

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 12:42:18 ; Search time 424 Seconds
(without alignments)
12591.144 Million cell updates/sec

Title: US-10-030-271-1
Perfect score: 909
Sequence: 1 atggcgcctaccgcggctgcac.....tcagtrgtgatgagcctgcac 909

Scoring table: OLGCO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : N_Geneseq_16Dec04:*

1: geneeqn1980s:*\n2: geneeqn1990s:*\n3: geneeqn2000s:*\n4: geneeqn2001s:*\n5: geneeqn2001bs:*\n6: geneeqn2002as:*\n7: geneeqn2002bs:*\n8: geneeqn2003as:*\n9: geneeqn2003bs:*\n10: geneeqn2003cs:*\n11: geneeqn2003ds:*\n12: geneeqn2004as:*\n13: geneeqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	909	100.0	909	5	AAE27407 Human apo
2	909	100.0	1883	5	AAE27408 Human apo
3	858	94.4	981	10	ADC79259 Human DED
4	858	94.4	1230	6	ABA94362 Human APR
5	858	94.4	1230	6	AAH40080 Human DED
6	858	94.4	1924	6	AAH59062 Human DED
7	858	94.4	1979	12	ADQ86891 Human tum
8	858	94.4	2045	3	AAA95790 Apoptosis
9	858	94.4	2045	3	AAH33283 Human col
10	768	84.5	2044	3	AAH18296 Lung canc
11	538	59.2	1966	6	AAH52603 CDNA sequ
12	531	58.4	1570	4	AAH99646 Human pro
13	334	36.7	626	4	AAH07925 Human CDN
14	281	30.9	1042	4	AAI60747 Human pol
15	281	30.9	1067	5	AAI58961 Human pol
16	281	30.9	1067	5	ADQ9183 DNA encod
17	281	30.9	1067	5	ADH48943 Novel hum
18	277	30.5	11084	12	ADQ18808 Human bof
19	252	27.7	303	6	AAH40075 Human DED
20	252	27.7	303	6	AAH59057 Human DED

21	187	20.6	1084	6	ABL39692 Human NS
22	187	19.5	1106	5	ABL39693 Human NS
23	177	19.5	603	6	AAE93937 Primer BP
24	151	16.6	451	9	ACH41209 Human foe
25	96	10.6	484	9	ACH25056 Human adu
26	25	2.8	25	10	ADC79263 Human DED
27	22	2.4	838	5	ADL44878 Human ova
28	21	2.3	323	5	ADL39650 Human ova
29	20	2.2	21	5	AAE27413 Human apo
30	20	2.2	23	5	AAE27416 Human apo
31	20	2.2	2610	9	ACC59397 Microbial
32	20	2.2	2673	11	ABD04389 Pseudomon
33	20	2.2	2715	11	ABD04082 Pseudomon
34	20	2.2	2814	11	ABD04271 Pseudomon
35	19	2.1	360	10	ADH78561 35 amino
36	19	2.1	579	13	ADH55265 Novel can
37	19	2.1	606	5	AAH52281 Human ARP
38	19	2.1	943	6	ABH70016 CDNA enco
39	19	2.1	943	9	ADA01379 Human PRO
40	19	2.1	943	9	ADA43808 Human CDN
41	19	2.1	943	9	ADA43576 Human CDN
42	19	2.1	943	9	ADA01251 Human PRO
43	19	2.1	943	9	ADA01135 Human CDN
44	19	2.1	943	9	ADA43632 Human CDN
45	19	2.1	943	9	ADA06954 Human PRO
46	19	2.1	943	9	ADA08442 Novel hum
47	19	2.1	943	9	ADH99735 Human PRO
48	19	2.1	943	9	ADH87018 Human PRO
49	19	2.1	943	9	ADH66173 Human CDN
50	19	2.1	943	10	ADH99851 Human PRO
51	19	2.1	943	10	ADH99506 Novel hum
52	19	2.1	943	10	ADH66057 Human CDN
53	19	2.1	943	10	ADH66057 Human CDN
54	19	2.1	943	10	ADH66057 Human CDN
55	19	2.1	943	10	ADH66057 Human CDN
56	19	2.1	943	10	ADH66057 Human CDN
57	19	2.1	943	10	ADH66057 Human CDN
58	19	2.1	943	10	ADH66057 Human CDN
59	19	2.1	943	10	ADH66057 Human CDN
60	19	2.1	943	10	ADH66057 Human CDN
61	19	2.1	943	10	ADH66057 Human CDN
62	19	2.1	943	10	ADH66057 Human CDN
63	19	2.1	943	10	ADH66057 Human CDN
64	19	2.1	943	10	ADH66057 Human CDN
65	19	2.1	943	10	ADH66057 Human CDN
66	19	2.1	943	10	ADH66057 Human CDN
67	19	2.1	943	10	ADH66057 Human CDN
68	19	2.1	943	10	ADH66057 Human CDN
69	19	2.1	943	10	ADH66057 Human CDN
70	19	2.1	943	10	ADH66057 Human CDN
71	19	2.1	943	10	ADH66057 Human CDN
72	19	2.1	943	10	ADH66057 Human CDN
73	19	2.1	943	10	ADH66057 Human CDN
74	19	2.1	943	10	ADH66057 Human CDN
75	19	2.1	943	10	ADH66057 Human CDN
76	19	2.1	943	10	ADH66057 Human CDN
77	19	2.1	943	10	ADH66057 Human CDN
78	19	2.1	943	10	ADH66057 Human CDN
79	19	2.1	943	10	ADH66057 Human CDN
80	19	2.1	943	10	ADH66057 Human CDN
81	19	2.1	943	10	ADH66057 Human CDN
82	19	2.1	943	10	ADH66057 Human CDN
83	19	2.1	943	10	ADH66057 Human CDN
84	19	2.1	943	10	ADH66057 Human CDN
85	19	2.1	943	10	ADH66057 Human CDN
86	19	2.1	943	10	ADH66057 Human CDN
87	19	2.1	943	10	ADH66057 Human CDN
88	19	2.1	943	10	ADH66057 Human CDN
89	19	2.1	943	10	ADH66057 Human CDN
90	19	2.1	943	10	ADH66057 Human CDN
91	19	2.1	943	10	ADH66057 Human CDN
92	19	2.1	943	10	ADH66057 Human CDN
93	19	2.1	943	10	ADH66057 Human CDN

94	19	2.1	943	12	AD619885	Human	PRO	C 167	18	2.0	527	9	AC116894	AC116894 DNA clone
95	19	2.1	943	12	AD677463	Human	CDN	C 168	18	2.0	558	9	AC116892	AC116892 DNA clone
96	19	2.1	943	12	AD656339	Human	PRO	C 169	18	2.0	598	9	AC116893	AC116893 DNA clone
97	19	2.1	943	12	AD639387	Human	PRO	C 170	18	2.0	618	6	ABK73212	ABK73212 Bacillus
98	19	2.1	943	12	AD638572	Human	CDN	C 171	18	2.0	628	9	AC116900	AC116900 DNA clone
99	19	2.1	943	12	ADG11125	Human	CDN	C 172	18	2.0	629	9	AC116902	AC116902 DNA clone
100	19	2.1	943	12	ADG11009	Human	CDN	C 173	18	2.0	632	9	AC116901	AC116901 DNA clone
101	19	2.1	943	12	ADH31537	Human	PRO	C 174	18	2.0	697	13	ADQ54233	ADQ54233 Novel can
102	19	2.1	943	12	ADH38785	Human	CDN	C 175	18	2.0	767	6	AB576791	AB576791 Frog embry
103	19	2.1	943	12	ADH29420	Human	CDN	C 176	18	2.0	809	6	ABQ33820	ABQ33820 Oligonuclei
104	19	2.1	943	12	ADH23723	Human	CDN	C 177	18	2.0	809	6	ABQ33821	ABQ33821 Oligonuclei
105	19	2.1	943	12	ADH27053	Human	CDN	C 178	18	2.0	918	4	AA554068	AA554068 Pseudomon
106	19	2.1	943	12	ADH38921	Novel	hum	C 179	18	2.0	918	8	ACA42159	ACA42159 Pseudomon
107	19	2.1	943	12	ADH26937	Human	CDN	C 180	18	2.0	918	12	ADQ25331	ADQ25331 P. aerugin
108	19	2.1	943	12	ADH38205	Novel	hum	C 181	18	2.0	918	12	ADQ25329	ADQ25329 P. aerugin
109	19	2.1	943	12	ADH38901	Human	CDN	C 182	18	2.0	927	8	ACA45425	ACA45425 Pseudomon
110	19	2.1	943	12	ADH23839	Human	CDN	C 183	18	2.0	1011	11	ABD14470	ABD14470 Pseudomon
111	19	2.1	943	12	ADH40214	Human	PRO	C 184	18	2.0	1056	3	AAZ49478	AAZ49478 Xylitol d
112	19	2.1	943	12	ADH40099	Human	PRO	C 185	18	2.0	1163	5	AA545101	AA545101 CDNA enco
113	19	2.1	943	12	ADH31421	Human	PRO	C 186	18	2.0	1179	12	ADM80103	ADM80103 SpiRamyci
114	19	2.1	943	12	ADH29299	Human	CDN	C 187	18	2.0	1179	12	ADN97619	ADN97619 S. ambofac
115	19	2.1	943	12	ADH49514	Novel	hum	C 188	18	2.0	1258	5	AA545289	AA545289 CDNA enco
116	19	2.1	943	12	ADH51978	Novel	hum	C 189	18	2.0	1266	8	ACA42690	ACA42690 Pseudomon
117	19	2.1	943	12	ADH49833	Novel	hum	C 190	18	2.0	1273	2	AAZ20428	AAZ20428 Human sec
118	19	2.1	943	12	ADH52434	Novel	hum	C 191	18	2.0	1273	10	ADD90212	ADD90212 Novel hum
119	19	2.1	943	12	ADH52550	Novel	hum	C 192	18	2.0	1273	10	ADG90031	ADG90031 Human CDN
120	19	2.1	943	12	ADH58547	Novel	hum	C 193	18	2.0	1311	8	ACA26866	ACA26866 Pseudomon
121	19	2.1	943	12	ADH51862	Novel	hum	C 194	18	2.0	1314	5	AA64885	AA64885 Bordetella
122	19	2.1	943	12	ADH58423	Novel	hum	C 195	18	2.0	1355	5	AA665574	AA665574 Human pro
123	19	2.1	943	12	AD113620	Novel	hum	C 196	18	2.0	1388	12	ADQ68764	ADQ68764 Human tum
124	19	2.1	943	12	ADK00876	Human	PRO	C 197	18	2.0	1388	13	ADQ85685	ADQ85685 Human tum
125	19	2.1	943	12	ADL008617	Human	PRO	C 198	18	2.0	1409	5	AA688080	AA688080 Human FLE
126	19	2.1	1285	6	AB190412	Human	CDN	C 199	18	2.0	1412	11	ABD11817	ABD11817 Pseudomon
127	19	2.1	1742	6	AB211501	Human	pol	C 200	18	2.0	1432	13	ACN40506	ACN40506 Tumour-as
128	19	2.1	1742	12	ADMA4019	Novel	hum	C 201	18	2.0	1447	5	ABX71274	ABX71274 Human bra
129	19	2.1	1852	13	ADQ85413	Human	tum	C 202	18	2.0	1448	6	ABQ54670	ABQ54670 Human ova
130	19	2.1	1870	13	ADN95938	Human	BEC	C 203	18	2.0	1646	3	AA676512	AA676512 Human ORF
131	19	2.1	1870	13	ADP55303	Human	PRO	C 204	18	2.0	1695	11	ABD11715	ABD11715 Pseudomon
132	19	2.1	1871	12	ADMG6334	Human	FLJ	C 205	18	2.0	1809	11	ABD14263	ABD14263 Pseudomon
133	19	2.1	2019	11	ABD07232	Pseudomon		C 206	18	2.0	1890	13	ABD33429	ABD33429 Human can
134	19	2.1	2247	4	AB129951	Drosophila		C 207	18	2.0	1899	6	AB211986	AB211986 Human pol
135	19	2.1	2417	5	ADM19574	Novel	hum	C 208	18	2.0	1899	12	ADMA4504	ADMA4504 Novel hum
136	19	2.1	2527	3	ADQ25121	Human	sof	C 209	18	2.0	1922	6	AB168889	AB168889 Kidney ca
137	19	2.1	2528	3	AA251797	Full leng		C 210	18	2.0	1922	6	AB168628	AB168628 Kidney ca
138	19	2.1	2528	10	AD619854	Human	Bcl	C 211	18	2.0	1922	6	AB170020	AB170020 Pancreas
139	19	2.1	2533	10	AD678552	575 amino		C 212	18	2.0	1922	6	AB162350	AB162350 Colon ade
140	19	2.1	2534	3	AA251804	Full leng		C 213	18	2.0	1922	6	AB168275	AB168275 Kidney ca
141	19	2.1	2534	10	AD61991	Human	Bcl	C 214	18	2.0	1922	6	ABK64494	ABK64494 Human den
142	19	2.1	2605	10	ADP68191	Human	MP5	C 215	18	2.0	1922	6	ABN95603	ABN95603 Gene #210
143	19	2.1	2605	10	ADG32699	Human	DNA	C 216	18	2.0	1922	8	ACA64898	ACA64898 Human MT1
144	19	2.1	2605	13	ADP24151	Breast ca		C 217	18	2.0	1922	9	AA157584	AA157584 Human met
145	19	2.1	2605	13	ADP24151	Breast ca		C 218	18	2.0	1944	6	ABA93761	ABA93761 Human tes
146	19	2.1	2611	5	ADM19321	Novel hum		C 219	18	2.0	1953	12	ADP71877	ADP71877 Renal tox
147	19	2.1	2739	8	ADA70899	Rice gene		C 220	18	2.0	1970	10	ADP31957	ADP31957 Human nov
148	19	2.1	2748	11	ABD07169	Pseudomon		C 221	18	2.0	2005	10	AB142238	AB142238 Toxigenicly
149	19	2.1	4756	4	AB103648	Drosophila		C 222	18	2.0	2283	12	ADQ64827	ADQ64827 Novel hum
150	19	2.1	5268	4	AB129950	Drosophila		C 223	18	2.0	2332	10	ADP63500	ADP63500 Human gen
151	19	2.1	5760	6	AB578661	M. echino		C 224	18	2.0	2332	10	ADP63500	ADP63500 Human gen
152	19	2.1	15462	4	AAK74459	Human	imm	C 225	18	2.0	2376	11	ABD12137	ABD12137 Pseudomon
153	19	2.1	15462	5	ABA21217	Human	ner	C 226	18	2.0	2412	11	ADM03644	ADM03644 Human CDN
154	19	2.0	142	10	ADP38268	Synchrotron		C 227	18	2.0	2569	12	ADQ17411	ADQ17411 Human sof
155	19	2.0	385	8	ABK35833	Bovine ES		C 228	18	2.0	2676	12	ADJ39546	ADJ39546 Plant CDN
156	19	2.0	393	8	ABX39164	Bovine ES		C 229	18	2.0	2745	8	ABZ20402	ABZ20402 Oncofoeta
157	19	2.0	426	8	ABX42473	Bovine ES		C 230	18	2.0	2745	12	ADQ22503	ADQ22503 Human sof
158	19	2.0	435	9	AAK78270	Human	imm	C 231	18	2.0	2753	6	ABT03399	ABT03399 Ovary cel
159	19	2.0	442	9	AC116898	DNA clone		C 232	18	2.0	2997	12	ADP45491	ADP45491 Human KIA
160	19	2.0	442	9	AC116896	DNA clone		C 233	18	2.0	3016	6	ABZ11184	ABZ11184 Human pol
161	19	2.0	460	9	AC116904	Human	foe	C 234	18	2.0	3120	12	ADK43144	ADK43144 Human N-a
162	19	2.0	482	9	AC116897	DNA clone		C 235	18	2.0	3156	2	AAV18471	AAV18471 T-cell su
163	19	2.0	508	9	AC116899	DNA clone		C 236	18	2.0	3399	10	ADCS9315	ADCS9315 DNA enco
164	19	2.0	510	9	AC116897	DNA clone		C 237	18	2.0	3403	3	AB1265975	AB1265975 Drosophila
165	19	2.0	513	6	ABK78152	Bacillus		C 238	18	2.0	3414	6	ABT07557	ABT07557 Human bre
166	19	2.0	513	6	ABK78152	Bacillus		C 239	18	2.0	3414	6	ABT07557	ABT07557 Human bre

240	18	2.0	4989	8	AAD54622	Aad54622 Human Mas	C 313	17	1.9	358	2	AAV86648	AAV86648 EST clone
241	18	2.0	5341	10	ADD29667	Add29667 Human tum	C 314	17	1.9	382	6	ABL82930	Ab182930 Human ova
C 242	18	2.0	5735	6	ABK94936	Abk94936 Human nov	C 315	17	1.9	386	6	ABL82848	Ab182848 Human ova
C 243	18	2.0	5735	6	ABK94980	Abk94980 Human nov	C 316	17	1.9	389	12	ADK13892	Adk13892 Murine PS
C 244	18	2.0	5768	6	ABL61797	Ab161797 COLon ade	C 317	17	1.9	394	6	ABV94314	Abv94314 Human pan
C 245	18	2.0	6032	10	ADG71667	Adg71667 Chlamydom	C 318	17	1.9	396	6	ADA60082	Ada60082 Soybean v
C 246	18	2.0	6222	4	ABL26974	Ab126974 Drosophill	C 319	17	1.9	405	12	ADP64240	Adp64240 Soybean c
C 247	18	2.0	7512	13	ADRA84505	Adr84505 Aspergill	C 320	17	1.9	396	11	ABD09167	Abd09167 Pseudomon
C 248	18	2.0	7826	12	AD022140	Ad022140 Human sof	C 321	17	1.9	410	12	ADP64035	Adp64035 Maize car
C 249	18	2.0	9873	4	AAK89905	Aak89905 Human dig	C 322	17	1.9	419	3	AAK52656	Aak52656 Arabidops
C 250	18	2.0	9873	4	AAK35986	Aa135986 Human mus	C 323	17	1.9	422	8	AB218661	Ab218661 Group IIT
C 251	18	2.0	9973	8	ABX58974	Abx58974 CDNA enco	C 324	17	1.9	425	12	ADP64026	Adp64026 Maize car
C 252	18	2.0	9973	12	ADJ29724	Adj29724 Human mus	C 325	17	1.9	430	12	ADP64026	Adp64026 Maize car
C 253	18	2.0	12851	10	ADMG7168	Adg71688 Chlamydom	C 326	17	1.9	432	2	AAV69391	Aav69391 H. contor
C 254	18	2.0	30943	12	ADN97550	Adn97550 S ambotac	C 327	17	1.9	432	11	ABV14652	Abv14652 Pseudomon
C 255	18	2.0	30943	12	ADN97550	Adn97550 S ambotac	C 328	17	1.9	437	8	ABX37295	Abx37295 Bovine RS
C 256	18	2.0	32229	13	ADR67012	Adr67012 Human can	C 329	17	1.9	444	8	ABX91608	Abx91608 Murine ge
C 257	18	2.0	35026	3	AAA64890	Aaa64890 Bordetell	C 330	17	1.9	449	8	ACH40180	Ach40180 Human foe
C 258	18	2.0	52211	11	ACN44892	Acn44892 Mouse gen	C 331	17	1.9	450	6	ABL87323	Ab187323 Human ova
C 259	18	2.0	68732	13	ABD33428	Abd33428 Human can	C 332	17	1.9	458	4	AA185286	Aa185286 Human pol
C 260	18	2.0	89873	13	ABD32846	Abd32846 Mouse can	C 333	17	1.9	458	4	AA186353	Aa186353 Human pol
C 261	18	2.0	105219	11	ACN44286	Acn44286 Human gen	C 334	17	1.9	459	8	ACA54500	Acc54500 Prokaryot
C 262	18	2.0	128600	6	ABK83461	Abk83461 Human CDN	C 335	17	1.9	465	4	AA116090	Aa116090 Probe #60
C 263	18	2.0	176594	6	ABD33387	Abd33387 Murine ca	C 336	17	1.9	465	4	ABA58643	Abas58643 Human foe
C 264	18	2.0	326014	6	ABK89296	Abk89296 Human gen	C 337	17	1.9	465	4	AA138318	Aa138318 Probe #70
C 265	18	2.0	340449	8	AA152198	Aa152198 Human kin	C 338	17	1.9	465	4	ABA27635	Abat7635 Probe #61
C 266	18	2.0	340449	8	AA152198	Aa152198 Human kin	C 339	17	1.9	465	4	AAK32491	Aak32491 Human bon
C 267	17	1.9	60	6	ABN59247	Abn59247 Human spl	C 340	17	1.9	465	4	AAK06775	Aak06775 Human bra
C 268	17	1.9	141	6	AB212551	Ab212551 Arabidops	C 341	17	1.9	465	4	ABK32199	Abk32199 Human liv
C 269	17	1.9	141	6	ACH83922	Ach83922 Human gen	C 342	17	1.9	465	6	ABK07276	Abk07276 Human gen
C 270	17	1.9	158	3	ACB30409	Ac30409 Human sec	C 343	17	1.9	473	4	AA190094	Aa190094 Human pol
C 271	17	1.9	164	12	ACH91070	ACH91070 Human gen	C 344	17	1.9	477	3	ACA55129	Aac55129 Arabidops
C 272	17	1.9	164	6	ADP64007	Adp64007 Maize car	C 345	17	1.9	477	4	ABL25519	Ab125519 Drosophill
C 273	17	1.9	166	6	ABN79237	Abn79237 Human gly	C 346	17	1.9	479	9	ACH27184	ACH27184 Human adu
C 274	17	1.9	202	12	ADP64037	Adp64037 Maize car	C 347	17	1.9	483	9	ACH27861	ACH27861 Human adu
C 275	17	1.9	222	12	ADK43201	Adk43201 Human pro	C 348	17	1.9	495	9	ACH34100	ACH34100 Human end
C 276	17	1.9	232	7	ADSG7042	Adsg7042 Corn seed	C 349	17	1.9	497	13	ACH05313	ACH05313 Novel can
C 277	17	1.9	241	6	ABN18672	Abn18672 Human ORF	C 350	17	1.9	515	5	AA521950	Aa521950 Human col
C 278	17	1.9	246	9	ADA60064	Ada60064 Soybean v	C 351	17	1.9	523	4	AAH06261	Aah06261 Human CDN
C 279	17	1.9	246	12	ADP64144	Adp64144 Soybean c	C 352	17	1.9	528	11	ABD08387	ABD08387 Pseudomon
C 280	17	1.9	255	9	ADA60058	Ada60058 Soybean v	C 353	17	1.9	531	12	ACH70593	ACH70593 Human gen
C 281	17	1.9	255	12	ADP64138	Adp64138 Soybean c	C 354	17	1.9	533	9	ACH23692	ACH23692 Human adu
C 282	17	1.9	257	6	ABL79682	Ab179682 Human ova	C 355	17	1.9	572	9	ACH40027	ACH40027 Human foe
C 283	17	1.9	259	9	ADA60054	Ada60054 Soybean v	C 356	17	1.9	572	9	ACH40027	ACH40027 Human foe
C 284	17	1.9	259	12	ADP64134	Adp64134 Soybean c	C 357	17	1.9	582	12	ACH70221	ACH70221 Human gen
C 285	17	1.9	266	9	ADA60051	Ada60051 Soybean v	C 358	17	1.9	586	12	ACH77370	ACH77370 Human gen
C 286	17	1.9	266	12	ADP64131	Adp64131 Soybean c	C 359	17	1.9	588	12	ACH77377	ACH77377 Human gen
C 287	17	1.9	278	11	ADT94498	Adt94498 Colon can	C 360	17	1.9	591	12	ADO00355	Ado00355 Novel hum
C 288	17	1.9	280	10	ABX83021	Abx83021 Corn ear-	C 361	17	1.9	591	12	ADN98786	Adn98786 Novel hum
C 289	17	1.9	283	12	ADP64032	Adp64032 Maize car	C 362	17	1.9	606	5	ABV57788	Abv57788 Human pro
C 290	17	1.9	287	9	ADA60055	Ada60055 Soybean v	C 363	17	1.9	651	13	ADO56232	ADO56232 Novel can
C 291	17	1.9	287	12	ADP64135	Adp64135 Soybean c	C 364	17	1.9	652	6	ABQ43193	Abq43193 Oligonuci
C 292	17	1.9	290	9	ADA60052	Ada60052 Soybean v	C 365	17	1.9	652	6	ABQ43192	Abq43192 Oligonuci
C 293	17	1.9	290	12	ADP64132	Adp64132 Soybean c	C 366	17	1.9	669	4	AAH05181	Aah05181 Human CDN
C 294	17	1.9	296	12	ADP64133	Adp64133 Soybean c	C 367	17	1.9	696	12	ADL81748	Adl81748 P. aerugi
C 295	17	1.9	299	12	ADP63896	Adp63896 Maize car	C 368	17	1.9	713	6	ABK76957	Abk76957 Frog emb
C 296	17	1.9	329	12	ADP63896	Adp63896 Maize car	C 369	17	1.9	716	13	ADP26096	Adp26096 Breast ca
C 297	17	1.9	332	12	ADP63895	Adp63895 Maize car	C 370	17	1.9	727	4	AA197835	Aa197835 Human neu
C 298	17	1.9	332	12	ADP63895	Adp63895 Maize car	C 371	17	1.9	735	10	ADK55838	Adk55838 Plant DNA
C 299	17	1.9	347	4	ABA71220	Abat71220 Human foe	C 372	17	1.9	758	6	ABK77298	Abk77298 Frog emb
C 300	17	1.9	347	4	AA151454	Aa151454 Probe #15	C 373	17	1.9	769	10	ADD34431	Add34431 Mouse mlt
C 301	17	1.9	347	4	ABA37529	Abat71220 Human foe	C 374	17	1.9	780	4	AB111313	Ab111313 Drosophill
C 302	17	1.9	347	4	ABA37529	Abat71220 Human foe	C 375	17	1.9	822	10	ADDI6673	Add16673 DNA (Segi
C 303	17	1.9	347	4	AAK45513	Aak45513 Human bon	C 376	17	1.9	858	8	ADA70840	Ada70840 Rice gene
C 304	17	1.9	347	4	AAK19519	Aak19519 Human bta	C 377	17	1.9	872	6	ABK34512	Abk34512 Human CDN
C 305	17	1.9	347	4	ABK45199	Abk45199 Human liv	C 378	17	1.9	875	3	AAFI5034	Aafi5034 TyriChoder
C 306	17	1.9	347	6	ABK19781	Abk19781 Human gen	C 379	17	1.9	912	10	ADH48573	Adh48573 O-acetylS
C 307	17	1.9	348	10	ADBS5845	Adbs5845 Human gen	C 380	17	1.9	912	10	ADH48573	Adh48573 Experimen
C 308	17	1.9	351	6	ABO55849	Abos55849 Human gen	C 381	17	1.9	933	13	ADSI4773	Adsi4773 Pseudomon
C 309	17	1.9	351	6	ABO55849	Abos55849 Human gen	C 382	17	1.9	962	4	AAH32213	Aah32213 Human olf
C 310	17	1.9	352	3	AAK44118	Aak44118 Arabidops	C 383	17	1.9	962	4	ADD17518	Add17518 DNA (Segi
C 311	17	1.9	354	11	ABD13946	Abd13946 Pseudomon	C 384	17	1.9	962	10	ADK58212	Adk58212 Plant DNA
C 312	17	1.9	354	12	ACH84293	ACH84293 Human gen	C 385	17	1.9	962	10	ADK57482	Adk57482 Plant DNA

386	17	1.9	962	11	ADM45007	Adm45007 Insect re	C 455	17	1.9	1686	8	ABX56030	Abx56030 M. echino
387	17	1.9	969	11	ABD10237	Abd10237 Pseudomon	C 460	17	1.9	1711	10	ADD13642	Add13642 C. glutam
388	17	1.9	983	12	ACH87261	ACH87261 Human gen	C 461	17	1.9	1717	3	AACT8069	Aac78069 Human can
389	17	1.9	1008	11	ABD10349	Abd10349 Pseudomon	C 462	17	1.9	1730	3	AAA26383	Aaa26383 Human sec
390	17	1.9	1011	2	AAx86962	Aax86962 Human tum	C 463	17	1.9	1730	12	ADL17444	Adl17444 Novel hum
391	17	1.9	1012	4	AA559715	AA559715 Propionib	C 464	17	1.9	1742	6	AA562540	Aaa62540 CDNA sequ
392	17	1.9	1012	8	ACR64644	ACr64644 Propionib	C 465	17	1.9	1752	6	AB154635	Ab154635 Levam lru
393	17	1.9	1020	12	ADJ43382	Adj43382 Plant cDN	C 466	17	1.9	1766	5	AAAD04277	Aad04277 Short for
394	17	1.9	1045	2	AAV74137	Aav74137 Human FLA	C 467	17	1.9	1766	5	AAAD04276	Aad04276 Short for
395	17	1.9	1045	6	AAAD43203	AAa43203 Human FLA	C 468	17	1.9	1830	4	AAH15765	Aah15765 Human cDN
C 396	17	1.9	1050	6	AAAS3949	AAa33949 ORF8 sequ	C 469	17	1.9	1840	5	AA585767	Aaa85767 DNA encod
C 397	17	1.9	1050	6	AAAL43629	AAa43629 Rhodococc	C 470	17	1.9	1876	10	ADAS53225	Ada53225 Human cod
C 398	17	1.9	1050	6	ABKS1847	ABs1847 R. erythri	C 471	17	1.9	1879	5	AAAD04274	Aad04274 Long form
C 400	17	1.9	1056	6	AAAD27248	AAa27248 Rhodococc	C 472	17	1.9	1879	5	AAAD04275	Aad04275 Long form
C 401	17	1.9	1056	6	AAAD31760	AAa31760 Corn lbcv	C 473	17	1.9	1888	13	ACN43748	Acn43748 Human dia
C 402	17	1.9	1107	11	ABD00807	ABd00807 Klebsiell	C 474	17	1.9	1894	13	ACN43747	Acn43747 Human dia
C 403	17	1.9	1116	9	AAEF71205	AAef1205 Corynebac	C 475	17	1.9	1908	8	ACN53411	Acn53411 Prokaryot
C 404	17	1.9	1137	5	ADB83240	ADb83240 Human cDN	C 476	17	1.9	1927	2	AAAD047841	Aad047841
C 405	17	1.9	1137	5	AA587537	AAe87537 DNA encod	C 477	17	1.9	1935	12	ADL70564	Adl70564
C 406	17	1.9	1137	5	AA587536	AAe87536 DNA encod	C 478	17	1.9	1951	6	AA562304	Aaa62304 CDNA sequ
C 407	17	1.9	1139	3	AAZ43923	AAz43923 Human DEB	C 479	17	1.9	1973	1	AAAN91045	Aan91045 Gene encd
C 408	17	1.9	1142	3	AAZ43924	AAz43924 Murine DE	C 480	17	1.9	1974	8	ACCA24277	Acca24277 Murine Cl
C 409	17	1.9	1174	5	AA585037	AA585037 DNA encod	C 481	17	1.9	1978	13	ACN43745	Acn43745 Human dia
C 410	17	1.9	1200	6	AAV74138	Aav74138 Mouse FLA	C 482	17	1.9	2000	6	AB199444	Ab199444 Mouse lbc
C 411	17	1.9	1236	10	ADP94930	ADp94930 Mouse FLA	C 483	17	1.9	2005	2	AAQ71303	Aaq71303 Mouse cbc
C 412	17	1.9	1253	3	AAAC51678	AAc51678 Zea maye	C 484	17	1.9	2010	8	ABX17536	Abx17536 Human cbc
C 413	17	1.9	1253	3	AAQ70661	AAq70661 SCFV pRAS	C 485	17	1.9	2014	13	ADQ38799	Adq38799 Human SNP
C 414	17	1.9	1273	2	AAQ74636	AAq74636 Aspergill	C 486	17	1.9	2044	13	AD548703	Ad548703 Bacterial
C 415	17	1.9	1279	8	ACC50966	ACC50966 Human bla	C 487	17	1.9	2067	8	ACAA27186	ACAa27186 Prokaryot
C 416	17	1.9	1279	8	ACC50999	ACC50999 Human bla	C 488	17	1.9	2079	5	ABV24761	Abv24761 Human pro
C 417	17	1.9	1279	11	ADN38839	ADn38839 Cancer/an	C 489	17	1.9	2085	8	ACA40672	ACA40672 Prokaryot
C 418	17	1.9	1279	12	ADM87422	ADM87422 Human EST	C 490	17	1.9	2100	5	AA987825	Aa987825 Human lat
C 419	17	1.9	1296	2	AAQ70660	AAq70660 SCFV pRAS	C 491	17	1.9	2100	12	ADL70562	Adl70562 Cervical
C 420	17	1.9	1307	6	AB199926	ABi99926 Rat mucoc	C 492	17	1.9	2127	4	AB111312	Ab111312 Drosophi
C 421	17	1.9	1312	6	AB199926	ABi99926 Rat mucoc	C 493	17	1.9	2130	11	ABD14485	ABd14485 Pseudomon
C 422	17	1.9	1316	8	AB876373	ABt76373 CDNA encd	C 494	17	1.9	2186	12	ADL70566	Adl70566
C 423	17	1.9	1316	8	ACR12835	ACr12835 Human cer	C 495	17	1.9	2187	11	ABD08438	ABD08438
C 424	17	1.9	1316	12	ADU75173	ADj75173 Marker ge	C 496	17	1.9	2212	13	ACN38839	Acn38839 Tumour-as
C 425	17	1.9	1316	12	ADJ75293	ADj75293 Marker ge	C 497	17	1.9	2220	10	ADB63585	Adb63585 Human cDN
C 426	17	1.9	1332	8	ADA70436	Ada70436 Rice gene	C 498	17	1.9	2232	12	AD020098	Ado20098 Human PRO
C 427	17	1.9	1340	4	AB109137	ABi09137 Drosophi	C 499	17	1.9	2239	13	AD087327	Ad087327 Human tum
C 428	17	1.9	1344	3	AAAC98034	AAc98034 Human col	C 500	17	1.9	2261	6	AAH14367	Aah14367 Human cDN
C 429	17	1.9	1352	11	ABD09111	ABd09111 Pseudomon	C 501	17	1.9	2261	4	ABK46133	ABk46133 CDNA encd
C 430	17	1.9	1356	2	AAQ70659	AAq70659 SCFV pRAS	C 502	17	1.9	2308	11	ADM03580	Adm03580 Human cDN
C 431	17	1.9	1359	12	AD042037	ADa042037 Human cel	C 503	17	1.9	2347	5	AA588827	Aaa88827 DNA encod
C 432	17	1.9	1361	3	AA888832	AAa88832 Maize ste	C 504	17	1.9	2367	2	AAV44448	Aav44448 Mycobacte
C 433	17	1.9	1379	2	AAQ08978	AAq08978 Mouse ade	C 505	17	1.9	2367	2	AAV64557	Aav64557 M. tuberc
C 434	17	1.9	1385	3	AAAC48022	AAc48022 Zea maye	C 506	17	1.9	2367	2	AAZ19146	Aaz19146 M. tuberc
C 435	17	1.9	1397	12	ADM80821	ADM80821 Human CAD	C 507	17	1.9	2367	2	AAZ19358	Aaz19358 M. tuberc
C 436	17	1.9	1398	13	ADT66719	ADt66719 Rat 26S p	C 508	17	1.9	2371	12	ADM66938	Adm66938 Human pro
C 437	17	1.9	1417	12	ADJ62811	ADj62811 Human cDN	C 509	17	1.9	2381	8	ABX55998	Abx55998 Gene encd
C 438	17	1.9	1417	12	ADJ62812	ADj62812 Human cDN	C 510	17	1.9	2406	11	ABD14099	ABd14099 Pseudomon
C 439	17	1.9	1432	8	AAAC48011	AAc48011 Zea maye	C 511	17	1.9	2413	4	AA160272	AAi60272 Human pol
C 440	17	1.9	1458	8	ACAC32203	ACa32203 Prokaryot	C 512	17	1.9	2419	4	ABL25542	ABl25542 Drosophi
C 441	17	1.9	1471	4	AA159312	AAi59312 Human pool	C 513	17	1.9	2460	2	AAV44303	Aav44303 Human sec
C 442	17	1.9	1488	8	ACA27255	ACa27255 Prokaryot	C 514	17	1.9	2460	5	AA968477	AAf968477 Human cDN
C 443	17	1.9	1518	4	AA501474	AAa01474 Human sec	C 515	17	1.9	2496	2	AAQ80750	Aaq80750 T. flavus
C 444	17	1.9	1518	10	ADP94924	ADf94924 Human gen	C 516	17	1.9	2496	2	AAV65780	Aav65780 Thermus f
C 445	17	1.9	1523	10	ADAS2444	Ada52444 Human cod	C 517	17	1.9	2496	6	ADE53382	Ad53382 T. flavus
C 446	17	1.9	1536	4	AAAF61016	AAf61016 P. putida	C 518	17	1.9	2496	7	AD192601	Ad192601 T. flavus
C 447	17	1.9	1550	2	AAAT09256	AAa09256 Human ara	C 519	17	1.9	2496	9	ADB16311	Adb16311 DNA encod
C 448	17	1.9	1551	2	AAAX19627	AAx19627 Arthrobac	C 520	17	1.9	2496	9	ACF05365	Acf05365 Thermus i
C 449	17	1.9	1581	6	AAH66268	AAh66268 C. glutami	C 521	17	1.9	2496	9	ACF05366	Acf05366 Thermus i
C 450	17	1.9	1628	5	AAH59913	AAh59913 Novel hum	C 522	17	1.9	2496	9	ACF05364	Acf05364 Thermus i
C 451	17	1.9	1629	8	AAAF71204	AAf71204 Corynebac	C 523	17	1.9	2496	9	ACF05363	Acf05363 Thermus i
C 452	17	1.9	1656	8	ACAA43651	ACa43651 Prokaryot	C 524	17	1.9	2511	11	ABD10528	ABd10528 Pseudomon
C 453	17	1.9	1662	6	AAK63616	AAk63616 Rat sequ	C 525	17	1.9	2511	5	AAAD07667	Aad07667 Human sec
C 454	17	1.9	1662	10	ADBS5257	ADb5257 Toxicity-	C 526	17	1.9	2525	2	AAV02016	Aav02016 DNA encod
C 455	17	1.9	1662	10	ADBS5937	ADb55937 Primary r	C 527	17	1.9	2527	2	AAZ00313	Aaz00313 Human tum
C 456	17	1.9	1662	12	ABT42496	ABt42496 Toxicity	C 528	17	1.9	2536	10	ADP94952	Adp94952 Human gen
C 457	17	1.9	1662	12	ADP73011	ADp73011 Renal tox	C 529	17	1.9	2537	4	AAK52190	Aak52190 Human pol
C 458	17	1.9	1680	10	ACF68722	ACf68722 Phototrab	C 531	17	1.9	2538	2	AAK21398	Aak21398 Central f

C 532	17	1.9	2542	6	ABL63691	Abi63691 Breast ca	605	17	1.9	3930	3	AAZ44744	Aaz44744 Human KLI
C 533	17	1.9	2542	6	ABL67221	Abi67221 Thyroid c	606	17	1.9	3930	5	AAD08139	Aad08139 Human kin
C 534	17	1.9	2550	4	AA59640	AA59640 Human cel	607	17	1.9	3930	8	AB557217	Ab557217 Human kin
C 535	17	1.9	2575	2	AA185781	AA185781 Human Muc	608	17	1.9	3930	10	ADG63389	Adg63389 Human CDN
C 536	17	1.9	2575	5	AA158486	AA158486 Human pol	609	17	1.9	3954	3	AACT5733	Aac75733 Human ORF
C 537	17	1.9	2575	5	ADQ98701	Adq98701 DNA encod	610	17	1.9	4638	10	AD102662	Adi102662 Human CDN
C 538	17	1.9	2575	9	ADB48461	Adb48461 Novel hum	611	17	1.9	4722	12	ADQ85612	Adq85612 Human tum
C 539	17	1.9	2587	12	ADQ63163	Adq63163 Novel hum	612	17	1.9	4722	12	ADQ84694	Adq84694 Human tum
C 540	17	1.9	2592	2	AAZ41355	Aaz41355 Human nor	613	17	1.9	4722	13	ADQ83469	Adq83469 Human tum
C 541	17	1.9	2602	11	ACN43022	Acn43022 Human dia	614	17	1.9	4722	13	ADQ84235	Adq84235 Human tum
C 542	17	1.9	2616	11	ABD14247	Abd14247 Pseudomon	615	17	1.9	4722	13	ADQ86713	Adq86713 Human tum
C 543	17	1.9	2629	13	ACN43021	Acn43021 Human dia	616	17	1.9	4744	6	ABN96962	Abn96962 Gene #346
C 544	17	1.9	2649	10	ADL13617	Adl13617 Osteoartrh	617	17	1.9	4950	6	ABK83470	Abk83470 Human CDN
C 545	17	1.9	2692	10	ADL13618	Adl13618 Osteoartrh	618	17	1.9	4950	6	ABK13302	Abk13302 DNA encod
C 546	17	1.9	2736	4	ABL25518	Abi25518 Drosophill	619	17	1.9	4950	13	ACN40396	Acn40396 Tumour-as
C 547	17	1.9	2756	4	ABL12176	Abi12176 Drosophill	620	17	1.9	4950	13	ADR52806	Adr52806 Drug ther
C 548	17	1.9	2793	13	ADS64243	Ads64243 Bacterial	621	17	1.9	4993	10	ADP74197	Adp74197 Human nov
C 549	17	1.9	2793	13	ADS63868	Ads63868 Bacterial	622	17	1.9	5075	12	ADP04059	Adp04059 Human col
C 550	17	1.9	2803	12	ADQ22316	Adq22316 Human sof	623	17	1.9	5372	8	ABX10239	Abx10239 Human CDN
C 551	17	1.9	2804	3	AAFP21915	Aaf21915 Human bre	624	17	1.9	5385	6	ABL99888	Abi99888 Human sec
C 552	17	1.9	2825	4	ABL16532	Abi16532 Drosophill	625	17	1.9	5408	13	ADS09831	Ads09831 Human the
C 553	17	1.9	2836	8	ADA53209	Ada53209 Human cod	626	17	1.9	5429	4	ABL12170	Abi12170 Drosophill
C 554	17	1.9	2850	8	ACA44145	Ac444145 Prokaryot	627	17	1.9	5434	4	AB567750	Ab567750 Human int
C 555	17	1.9	2859	13	ADS63497	Ads63497 Bacterial	628	17	1.9	5569	5	ABV24840	Abv24840 Human ova
C 556	17	1.9	2875	8	ABX70971	Abx70971 Novel hum	629	17	1.9	5570	5	ADP16917	Adp16917 Human pro
C 557	17	1.9	2886	10	ACD19394	Acdi19394 CDNA enco	630	17	1.9	5682	10	ADP81684	Adp81684 Leukemia
C 558	17	1.9	2897	12	ADQ85666	Adq85666 Human tum	631	17	1.9	5733	13	ACN39104	Acn39104 Tumour-as
C 559	17	1.9	2897	13	ADQ83578	Adq83578 Human tum	632	17	1.9	6040	4	AA106077	AA106077 Human rep
C 560	17	1.9	2909	10	ADG93394	Adg93394 Maize lrp	633	17	1.9	6040	4	ABL98642	Abi98642 Human tes
C 561	17	1.9	2970	6	AB567320	Ab567320 Breast gp	634	17	1.9	6044	4	AA106074	AA106074 Human rep
C 562	17	1.9	2973	8	ACFP34508	Acfp34508 Gene enco	635	17	1.9	6044	4	AA106076	AA106076 Human rep
C 563	17	1.9	2973	10	ACD19393	Acdi19393 CDNA enco	636	17	1.9	6044	4	ABL98639	Abi98639 Human tes
C 564	17	1.9	2984	12	ADQ96263	Adq96263 T cell ac	637	17	1.9	6044	4	ABL98631	Abi98631 Human tes
C 565	17	1.9	2984	6	ABH01095	Abh01095 Brevibact	638	17	1.9	6044	4	ABL98641	Abi98641 Human tes
C 566	17	1.9	3001	4	AAH88439	Aah88439 CNS disor	639	17	1.9	6083	4	AA546715	AA546715 Tumour su
C 567	17	1.9	3001	4	AAH15723	Aah15723 Human CDN	640	17	1.9	6621	4	ACC46588	Acc46588 Human dlt
C 568	17	1.9	3048	4	AB118019	Abi118019 Drosophill	641	17	1.9	6621	4	ABL26680	Abi26680 Drosophill
C 569	17	1.9	3129	13	ADT43898	Adt43898 Bacterial	642	17	1.9	6765	6	ABK83783	Abk83783 Human CDN
C 570	17	1.9	3148	12	ADK43180	Adk43180 Human PTP	643	17	1.9	6765	6	ADS99929	Ads99929 Human ape
C 571	17	1.9	3167	6	ABK34683	Abk34683 Human CDN	644	17	1.9	6765	12	ADP13354	Adp13354 Renal cel
C 572	17	1.9	3171	4	ABL26681	Abi26681 Drosophill	645	17	1.9	6797	4	ABL18018	Abi18018 Drosophill
C 573	17	1.9	3187	8	AB235872	Ab235872 Human sec	646	17	1.9	7186	8	ACC46573	Acc46573 Human dlt
C 574	17	1.9	3203	10	ADB62175	Adb62175 Human CDN	647	17	1.9	7373	4	AA541749	AA541749 Genomic s
C 575	17	1.9	3211	4	AAH34203	Aah34203 Human col	648	17	1.9	7373	4	ABA06610	Ab406610 Human gen
C 576	17	1.9	3244	10	AAD49459	Aad49459 Human yes	649	17	1.9	7373	6	ABV84147	Abv84147 Human pol
C 577	17	1.9	3279	13	ADK43402	Adk43402 Human PTP	650	17	1.9	7655	10	ADC27426	Adc27426 CDNA enco
C 578	17	1.9	3345	13	ACN43026	Acn43026 Human dia	651	17	1.9	8443	10	ADC27428	Adc27428 CDNA enco
C 579	17	1.9	3420	10	ADC73044	Adc73044 Triametes	652	17	1.9	8880	4	AAK83253	Aak83253 Human imm
C 580	17	1.9	3431	8	AB234816	Ab234816 Coding se	653	17	1.9	10835	4	AA559527	Aa559527 Propionib
C 581	17	1.9	3431	13	ACN37667	Acn37667 Tumour-as	654	17	1.9	10835	8	ACF64456	Acf64456 Propionib
C 582	17	1.9	3448	4	ABL09136	Abi09136 Drosophill	655	17	1.9	10976	13	ABD32650	Abd32650 Human can
C 583	17	1.9	3480	10	ADC73046	Adc73046 Triametes	656	17	1.9	11796	8	ABX10231	Abx10231 Human CDN
C 584	17	1.9	3483	13	ACN43025	Acn43025 Human dia	657	17	1.9	11796	10	ADG39785	Adg39785 Human CDN
C 585	17	1.9	3517	12	ADJ67698	Adj67698 KiF1C DNA	658	17	1.9	12508	3	AA553941	AA553941 12.5 kb p
C 586	17	1.9	3517	12	ADJ67696	Adj67696 KiF1C DNA	659	17	1.9	12508	6	AAAD27240	AAad27240 Rhodococc
C 587	17	1.9	3517	12	ADJ67695	Adj67695 KiF1C DNA	660	17	1.9	12523	6	AA143619	AA143619 Rhodococc
C 588	17	1.9	3518	12	ADJ67697	Adj67697 KiF1C DNA	661	17	1.9	12523	6	ABK51837	Abk51837 Rhodococc
C 589	17	1.9	3518	12	ADJ67699	Adj67699 KiF1C DNA	662	17	1.9	14044	4	AAFP54793	Aafp54793 Nucleotid
C 590	17	1.9	3540	13	ADS45801	Ads45801 Bacteri	663	17	1.9	17606	5	AAFP83655	Aafp83655 Human COL
C 591	17	1.9	3546	13	ACN43024	Acn43024 Human dia	664	17	1.9	17606	5	AA521772	AA521772 Human gen
C 592	17	1.9	3573	13	ACN43023	Acn43023 Human dia	665	17	1.9	20158	10	ADL13614	Adl13614 Osteoartrh
C 593	17	1.9	3615	12	ACA56656	Ac456656 Human big	666	17	1.9	20158	4	AAK82721	Aak82721 Human imm
C 594	17	1.9	3615	12	AD156452	Ad156452 Human pol	667	17	1.9	21635	11	ACN44628	Acn44628 Mouse gen
C 595	17	1.9	3615	12	ADK43194	Adk43194 Human pro	668	17	1.9	23024	4	AAFP25499	Aafp25499 Nucleotid
C 596	17	1.9	3630	13	ADQ85894	Adq85894 Human tum	669	17	1.9	32351	12	ADQ59404	Adq59404 Human can
C 597	17	1.9	3630	13	ADQ84819	Adq84819 Human tum	670	17	1.9	33023	6	ABN96853	Abn96853 Gene #335
C 598	17	1.9	3634	5	ABD33170	Abd33170 Murine ca	671	17	1.9	33023	13	ADP13378	Adp13378 Renal cel
C 599	17	1.9	3642	5	AA585083	AA585083 DNA encod	672	17	1.9	33023	12	ADT93877	Adt93877 Non-smell
C 600	17	1.9	3643	12	ADK43401	Adk43401 Human PTP	673	17	1.9	35183	13	ABD33355	Abd33355 Murine ca
C 601	17	1.9	3779	13	ADQ6756	Adq6756 Full leng	674	17	1.9	42000	3	AA463349	Aa463349 Streptom
C 602	17	1.9	3781	12	ADQ87056	Adq87056 Human tum	675	17	1.9	43712	12	ADQ18757	Adq18757 Human sof
C 603	17	1.9	3781	12	ADQ85867	Adq85867 Human tum	676	17	1.9	45993	6	AA036070	Aa036070 Human liv
C 604	17	1.9	3781	13	ACN40680	Acn40680 Tumour-as	677	17	1.9	48037	4	AAK84729	Aak84729 Human imm

678	17	1.9	48037	4	AAK85983	AAK85983 Human imm	751	16	1.8	150	6	ABL01772	ABL01772 Human MSH
679	17	1.9	48045	4	AAK84730	AAK84730 Human imm	752	16	1.8	150	12	ADP43117	ADP43117 MSH2 exon
680	17	1.9	48045	4	AAK85984	AAK85984 Human imm	753	16	1.8	173	8	ABX52457	ABX52457 Bovine
681	17	1.9	55998	9	ADA02975	ADA02975 Mouse Anp	754	16	1.8	183	12	ACH85312	ACH85312 Human gen
682	17	1.9	55998	10	ADB72713	ADB72713 Mouse Anp	755	16	1.8	186	9	ACH03443	ACH03443 Human lat
683	17	1.9	55998	10	ADC85455	ADC85455 Mouse Anp	756	16	1.8	192	5	AAS65862	AAS65862 DNA encod
684	17	1.9	55998	12	ADM74570	ADM74570 Murine ca	757	16	1.8	201	13	ADS41306	ADS41306 Human aut
685	17	1.9	58857	3	AAH58471	AAH58471 Nucleotid	758	16	1.8	201	13	ADS41305	ADS41305 Human aut
686	17	1.9	63164	3	AAH63348	AAH63348 Streptomy	759	16	1.8	201	13	ADS40308	ADS40308 Human aut
687	17	1.9	67212	13	ABD33426	ABD33426 Murine ca	760	16	1.8	216	4	ABA72518	ABA72518 Human foe
688	17	1.9	69770	10	ADC86870	ADC86870 WFS1 vari	761	16	1.8	216	4	AAI52931	AAI52931 Probe #21
689	17	1.9	70782	12	ADO58147	ADO58147 Angiococc	762	16	1.8	216	4	AAK47095	AAK47095 Human bon
690	17	1.9	70782	12	ADO58147	ADO58147 Angiococc	763	16	1.8	216	4	AAK20942	AAK20942 Human bra
691	17	1.9	70782	12	ADO58147	ADO58147 Angiococc	764	16	1.8	216	4	ABSA4685	ABSA4685 Human gen
692	17	1.9	75252	11	ACN44450	ACN44450 Human gen	765	16	1.8	216	6	ABSA21325	ABSA21325 Human liv
693	17	1.9	80959	8	AAI51405	AAI51405 Human sec	766	16	1.8	220	2	AAO20723	AAO20723 B. hermsli
694	17	1.9	84830	12	ADL81732	ADL81732 P. aerugi	767	16	1.8	227	2	AAH85309	AAH85309 Human sin
695	17	1.9	87464	11	ACN44788	ACN44788 Mouse gen	768	16	1.8	227	4	AAI27044	AAI27044 Probe #16
696	17	1.9	94001	13	ADJ33491	ADJ33491 Human LAR	769	16	1.8	227	4	ABA75314	ABA75314 Human foe
697	17	1.9	102790	13	ABD32649	ABD32649 Human can	770	16	1.8	227	4	ABSA5878	ABSA5878 Probe #24
698	17	1.9	103464	13	ABD33278	ABD33278 Murine ca	771	16	1.8	227	4	ABSA3964	ABSA3964 Probe #18
699	17	1.9	107280	13	ABD33169	ABD33169 Murine ca	772	16	1.8	227	4	AAK49947	AAK49947 Human bon
700	17	1.9	110000	2	AAV30458_3	Continuation (4 of	773	16	1.8	227	4	AAK23869	AAK23869 Human bra
701	17	1.9	110000	2	AAV30458_3	Continuation (4 of	774	16	1.8	227	4	ABSA49593	ABSA49593 Human liv
702	17	1.9	110000	4	AAI99682_27	Continuation (28 o	775	16	1.8	228	8	ABX47690	ABX47690 Bovine ES
703	17	1.9	110000	4	AAI99682_27	Continuation (28 o	776	16	1.8	232	9	ADA60050	ADA60050 Soybean v
704	17	1.9	110000	4	AAI99683_27	Continuation (28 o	777	16	1.8	232	12	ADPE4130	ADPE4130 Soybean v
705	17	1.9	110000	4	AAI99683_27	Continuation (28 o	778	16	1.8	241	10	ACAS5485	ACAS5485 Human sig
706	17	1.9	110000	10	ACF67367_15	Continuation (16 o	779	16	1.8	241	12	ADIS5281	ADIS5281 Human pol
707	17	1.9	110000	11	ADM27081_00	AAH88703 Hyperther	780	16	1.8	242	9	ADA60057	ADA60057 Soybean v
708	17	1.9	123219	4	AAH88703	AAH88703 Human DNA	781	16	1.8	242	9	ADA60063	ADA60063 Soybean v
709	17	1.9	138627	12	ADQ97183	ADQ97183 Human can	782	16	1.8	242	12	ADPE4143	ADPE4143 Soybean c
710	17	1.9	176001	12	ADK43203	ADK43203 Human pro	783	16	1.8	242	12	ADPE4137	ADPE4137 Soybean c
711	17	1.9	186739	12	ADK43195	ADK43195 Human pro	784	16	1.8	246	4	AAK57464	AAK57464 Human imm
712	17	1.9	200000	9	ADAO47190	ADAO47190 DNA seque	785	16	1.8	246	9	ADA60060	ADA60060 Soybean v
713	17	1.9	226475	9	AAH58279	AAH58279 Human tum	786	16	1.8	246	9	ADA60059	ADA60059 Soybean v
714	17	1.9	248878	10	ACPF65381	ACPF65381 Phototrab	787	16	1.8	246	12	ADPE4139	ADPE4139 Soybean c
715	17	1.9	272022	12	ADQ97126	ADQ97126 Human can	788	16	1.8	246	12	ADPE4140	ADPE4140 Soybean c
716	17	1.9	330973	11	ACN44846	ACN44846 Human gen	789	16	1.8	248	6	ABN76668	ABN76668 Human ORF
717	17	1.9	334462	10	ADC24763	ADC24763 Human w11	790	16	1.8	248	9	ADA60062	ADA60062 Soybean v
718	17	1.9	337022	12	ADQ59416	ADQ59416 Human can	791	16	1.8	248	12	ADPE4142	ADPE4142 Soybean c
719	17	1.9	349980	5	AAH68527	AAH68527 C. glutami	792	16	1.8	249	9	ADA60065	ADA60065 Soybean v
720	17	1.9	349980	5	AAH68528	AAH68528 C. glutami	793	16	1.8	249	12	ADPE4145	ADPE4145 Soybean c
721	16	1.8	16	6	AAH40092	AAH40092 Human DED	794	16	1.8	253	3	AAK32443	AAK32443 Human sec
722	16	1.8	16	6	AAH59074	AAH59074 Integrin #1	795	16	1.8	255	6	ABL37449	ABL37449 Human col
723	16	1.8	16	17	AAA22755	AAA22755 Integrin	796	16	1.8	255	6	ABL36911	ABL36911 Human col
724	16	1.8	16	20	ABZ98661	ABZ98661 Human try	797	16	1.8	258	12	ADQ21814	ADQ21814 Human sof
725	16	1.8	16	10	ABD31692	ABD31692 Human try	798	16	1.8	258	13	ADQ21814	ADQ21814 Human sof
726	16	1.8	16	12	ADJ60540	ADJ60540 Oligonuc	799	16	1.8	264	6	ABN15934	ABN15934 Human ORF
727	16	1.8	16	12	ADK43355	ADK43355 Human PTP	800	16	1.8	266	9	ADA60061	ADA60061 Soybean v
728	16	1.8	16	12	ADK43233	ADK43233 Antisense	801	16	1.8	266	12	ADPE4141	ADPE4141 Soybean c
729	16	1.8	16	12	ADQ46029	ADQ46029 Human o11	802	16	1.8	273	10	ACD97961	ACD97961 Human col
730	16	1.8	16	23	ABN83374	ABN83374 Mononucle	803	16	1.8	274	12	ADPE3916	ADPE3916 Maize car
731	16	1.8	16	25	ACC47832	ACC47832 Human Hlx	804	16	1.8	276	8	ACA26440	ACA26440 Prokaryot
732	16	1.8	16	29	ABK83200	ABK83200 Iron upta	805	16	1.8	276	11	ABD16447	ABD16447 Pseudom
733	16	1.8	16	41	ADG16991	ADG16991 Anti-salm	806	16	1.8	281	9	ADA60056	ADA60056 Soybean v
734	16	1.8	16	47	AAH86394	AAH86394 Sp6 anti-	807	16	1.8	281	12	ADPE4136	ADPE4136 Soybean c
735	16	1.8	16	60	ABN38637	ABN38637 Human sp1	808	16	1.8	291	6	ABO91162	ABO91162 M. capaul
736	16	1.8	16	65	ABN27987	ABN27987 Rat spliic	809	16	1.8	295	7	ADSB6892	ADSB6892 Corn seed
737	16	1.8	16	65	ABN58427	ABN58427 Mouse spl	810	16	1.8	297	11	ABD16005	ABD16005 Pseudom
738	16	1.8	16	66	ABO49187	ABO49187 ecPyr con	811	16	1.8	299	6	ABN22757	ABN22757 Human ORF
739	16	1.8	16	66	ABSA5985	ABSA5985 Chimeric	812	16	1.8	304	2	AAQ60270	AAQ60270 Human bra
740	16	1.8	16	66	ADG16986	ADG16986 Anti-salm	813	16	1.8	305	2	AAV52943	AAV52943 Human UNC
741	16	1.8	16	80	ADM95586	ADM95586 Rat antia	814	16	1.8	309	6	ABL74370	ABL74370 Corn tabs
742	16	1.8	16	90	ADH35231	ADH35231 Primer #5	815	16	1.8	314	3	AAA96834	AAA96834 Nucleotid
743	16	1.8	16	91	ACG91112	ACG91112 Human gen	816	16	1.8	314	5	AAH88903	AAH88903 Human BAT
744	16	1.8	16	92	AAH28566	AAH28566 Human sec	817	16	1.8	314	5	ABK89237	ABK89237 Human BAT
745	16	1.8	16	121	ABR80371	ABR80371 MSH2 muta	818	16	1.8	314	12	ADH35220	ADH35220 Human mut
746	16	1.8	16	121	ABR80370	ABR80370 MSH2 muta	819	16	1.8	315	3	AAA31619	AAA31619 Plant mic
747	16	1.8	16	121	ADQ71305	ADQ71305 Human mic	820	16	1.8	315	4	ABL23727	ABL23727 Drosophi1
748	16	1.8	16	144	ABL59553	ABL59553 Rat OSF1	821	16	1.8	317	2	AAO61187	AAO61187 Human bra
749	16	1.8	16	146	AAH36098	AAH36098 Human col	822	16	1.8	321	11	ABD16139	ABD16139 Pseudom
750	16	1.8	150	2	AAQ93939	AAQ93939 Human MSH	823	16	1.8	332	10	ADSB5087	ADSB5087 Farneey1

824	16	1.8	348	6	ABN23094	Abn23094 Human ORF	C 897	16	1.8	508	9	ACH18628	Ach18628 Human adu
825	16	1.8	360	3	AAC09023	Aac09023 Human sec	C 898	16	1.8	510	2	AAC47652	Aac47652 Arabidops
C 826	16	1.8	361	8	ABX37223	Abx37223 Bovine ES	C 899	16	1.8	513	3	AAx98247	Aax98247 Nucleotid
827	16	1.8	364	8	ABX11546	Abx11546 CDNA encd	C 900	16	1.8	514	11	ACN80427	Acn80427 Breast ca
828	16	1.8	374	4	AA125184	AA125184 Probe #15	C 901	16	1.8	515	12	ACH69777	Ach69777 Human gen
829	16	1.8	374	4	ABx70956	Abx70956 Human foe	C 902	16	1.8	525	9	ACH18501	Ach18501 Human adu
830	16	1.8	374	4	AA151147	AA151147 Probe #19	C 903	16	1.8	525	10	ADBS5684	Adbs5684 Toxicity-
831	16	1.8	374	4	ABx37382	Abx37382 Probe #15	C 904	16	1.8	529	10	AAD05542	Aad05542 Human sec
832	16	1.8	374	4	AAK45194	AAK45194 Human bon	C 905	16	1.8	530	12	ACH71556	Ach71556 Human gen
833	16	1.8	374	4	AAK19226	AAK19226 Human bra	C 906	16	1.8	533	10	ABX57454	Abx57454 Arabidops
834	16	1.8	374	4	ABx44866	Abx44866 Human liv	C 907	16	1.8	535	6	ABx69544	Abx69544 Novel mur
835	16	1.8	374	4	ABx19444	Abx19444 Human gen	C 908	16	1.8	535	12	ACH68059	Ach68059 Human gen
C 836	16	1.8	375	13	ADT44415	Adt44415 Bacterial	C 909	16	1.8	537	11	ABD17566	Abd17566 Pseudomon
C 837	16	1.8	383	6	ABX88199	Abx88199 Human col	C 910	16	1.8	538	5	AD169273	Ad169273 Human ova
C 838	16	1.8	391	8	ABX35794	Abx35794 Bovine ES	C 911	16	1.8	538	5	AD175619	Ad175619 Human ova
C 839	16	1.8	393	4	AA110228	AA110228 Human bre	C 912	16	1.8	538	12	ACH70226	Ach70226 Human ful
C 840	16	1.8	399	12	ADP93186	Adp93186 Cotton ex	C 913	16	1.8	540	12	ADM80058	Adm80058 Spirampci
C 841	16	1.8	400	5	ABV33317	Abv33317 Human pro	C 914	16	1.8	540	12	ADN97574	Adn97574 S ambotac
C 842	16	1.8	400	5	ABV42240	Abv42240 Human pro	C 915	16	1.8	544	13	ACHS18530	Achs18530 Human MRP
C 843	16	1.8	410	8	ABX40316	Abx40316 Bovine ES	C 916	16	1.8	545	12	ACH78377	Ach78377 Human gen
C 844	16	1.8	410	5	AAx67584	AAx67584 Novel hum	C 917	16	1.8	546	11	ABD12467	Abd12467 Pseudomon
C 845	16	1.8	412	4	AAx57086	AAx57086 CDNA encd	C 918	16	1.8	552	12	ACH89579	Ach89579 Human gen
C 846	16	1.8	412	4	AAK58371	AAK58371 Human lmm	C 919	16	1.8	553	4	AAx44710	Aax44710 Human ful
C 847	16	1.8	412	4	ABK43490	Abk43490 DNA encd	C 920	16	1.8	555	12	ACH67155	Ach67155 Human gen
C 848	16	1.8	412	10	ADB93264	Adb93264 Human CDN	C 921	16	1.8	556	4	AA117849	AA117849 Probe #77
C 849	16	1.8	412	12	AD153877	Ad153877 CDNA encd	C 922	16	1.8	556	4	ABx62804	Abx62804 Human foe
C 850	16	1.8	417	10	ADH28961	Adh28961 Human chr	C 923	16	1.8	556	4	AA142820	AA142820 Probe #11
C 851	16	1.8	423	4	AAK57725	AAK57725 Human lmm	C 924	16	1.8	556	4	ABx30094	Abx30094 Probe #85
C 852	16	1.8	423	9	ACH14533	Ach14533 Human adu	C 925	16	1.8	556	4	AAK17007	AAK17007 Human bon
C 853	16	1.8	424	3	AAc02693	Aac02693 Human sec	C 926	16	1.8	556	4	AAK11204	AAK11204 Human bra
C 854	16	1.8	424	3	AAx89681	AAx89681 Mouse Exo	C 927	16	1.8	556	4	ABx36689	Abx36689 Human liv
C 855	16	1.8	426	3	AAx89682	AAx89682 Mouse Exo	C 928	16	1.8	559	13	ADS62161	Ads62161 Bacterial
C 856	16	1.8	429	6	ABL89486	ABL89486 Human pol	C 929	16	1.8	560	10	ADT72426	Adt72426 DNA Seq I
C 857	16	1.8	429	6	ABX48348	Abx48348 Bovine ES	C 930	16	1.8	561	10	ADJ92290	Adj92290 Mouse hai
C 858	16	1.8	442	5	ABV12172	Abv12172 Human pro	C 931	16	1.8	562	6	ABO56554	ABO56554 Human col
C 859	16	1.8	444	8	ABX41536	Abx41536 Bovine ES	C 932	16	1.8	563	10	ACD94817	ACD94817 Human col
C 860	16	1.8	444	11	ABD00840	ABD00840 K1ebsle11	C 933	16	1.8	564	5	ADL40855	ADL40855 Human ova
C 861	16	1.8	447	5	ADL38910	Adl38910 Human ova	C 934	16	1.8	566	4	AAx27472	AAx27472 CDNA encd
C 862	16	1.8	450	3	AAc02173	Aac02173 Human sec	C 935	16	1.8	566	10	ADB93650	Adb93650 Human CDN
C 863	16	1.8	454	3	AAc41478	Aac41478 Zee maye	C 936	16	1.8	566	10	ABT40376	ABT40376 Toxicity
C 864	16	1.8	455	5	ABV46106	Abv46106 Human pro	C 937	16	1.8	566	12	ACH70093	Ach70093 Human gen
C 865	16	1.8	456	6	ABK45904	ABK45904 CDNA encd	C 938	16	1.8	566	12	ACH69990	Ach69990 Human gen
C 866	16	1.8	459	9	ACH27308	Ach27308 Human adu	C 939	16	1.8	567	3	AAx08041	Aax08041 Fusarilm
C 867	16	1.8	462	5	AAx87821	AAx87821 DNA encd	C 940	16	1.8	569	4	AA118832	AA118832 Probe #87
C 868	16	1.8	462	5	ABY03003	ABY03003 Human pro	C 941	16	1.8	569	4	ABx63830	ABx63830 Human foe
C 869	16	1.8	465	5	AAx74705	AAx74705 DNA encd	C 942	16	1.8	569	4	ABx43955	ABx43955 Probe #12
C 870	16	1.8	465	8	ABx00879	ABx00879 Somatocra	C 943	16	1.8	569	4	ABx31011	ABx31011 Probe #94
C 871	16	1.8	465	10	ABx258928	ABx258928 Human som	C 944	16	1.8	569	4	AAK38060	AAK38060 Human bon
C 872	16	1.8	468	6	ABK45064	ABK45064 CDNA encd	C 945	16	1.8	569	4	AAK12341	AAK12341 Human bra
C 873	16	1.8	468	6	ABN73893	Abn73893 Bovine em	C 946	16	1.8	571	10	ABx56935	ABx56935 Arabidops
C 874	16	1.8	468	9	ACH12973	Ach12973 Human adu	C 947	16	1.8	573	11	ACH9587	Ach9587 Pseudomon
C 875	16	1.8	469	9	ACH16876	Ach16876 Human adu	C 948	16	1.8	573	11	ACH9587	Ach9587 Pseudomon
C 876	16	1.8	471	6	ABU93396	ABU93396 Arabidops	C 949	16	1.8	573	12	ACH91587	Ach91587 Human gen
C 877	16	1.8	471	6	ACH35175	Ach35175 Human end	C 950	16	1.8	578	12	ACH77412	ACH77412 Human gen
C 878	16	1.8	471	9	ACH36314	Ach36314 Human end	C 951	16	1.8	579	11	ABD02989	ABD02989 Pseudomon
C 879	16	1.8	471	11	ABD17275	ABD17275 Pseudomon	C 952	16	1.8	579	11	ABD07528	ABD07528 Pseudomon
C 880	16	1.8	473	4	AAx26332	AAx26332 Human cdn	C 953	16	1.8	580	5	ABV58878	ABV58878 Human pro
C 881	16	1.8	473	8	ABX73673	ABX73673 Human nov	C 954	16	1.8	580	5	ABx59877	ABx59877 Human foe
C 882	16	1.8	474	9	ACH32532	Ach32532 Human end	C 955	16	1.8	583	4	ABx59877	ABx59877 Human foe
C 883	16	1.8	474	12	ACH83927	Ach83927 Human gen	C 956	16	1.8	583	4	AA139650	AA139650 Probe #85
C 884	16	1.8	475	9	ACH43718	Ach43718 Human foe	C 957	16	1.8	583	4	AAK34127	AAK34127 Human bon
C 885	16	1.8	477	12	ADJ44735	ADJ44735 Plant CDN	C 958	16	1.8	583	4	ABx33925	ABx33925 Human bra
C 886	16	1.8	478	4	AAH98628	AAH98628 Human EST	C 959	16	1.8	583	6	ABx08891	ABx08891 Human liv
C 887	16	1.8	484	9	ACH39852	Ach39852 Human foe	C 960	16	1.8	584	3	AAx09173	AAx09173 Human pen
C 888	16	1.8	486	9	AAc05720	AAc05720 Human sec	C 961	16	1.8	585	11	ABD06024	ABD06024 Pseudomon
C 889	16	1.8	486	11	ACH99971	ACH99971 K1ebsle11	C 962	16	1.8	587	6	ABx62827	ABx62827 Rat seque
C 890	16	1.8	490	9	ACH44274	ACH44274 Human foe	C 963	16	1.8	587	10	ADBS5789	ADBS5789 Toxicity-
C 891	16	1.8	492	11	ABD16297	ABD16297 Pseudomon	C 964	16	1.8	587	12	ACH69640	ACH69640 Human gen
C 892	16	1.8	500	6	ABN62652	ABN62652 Human can	C 965	16	1.8	587	12	ADP72121	ADP72121 Renal tox
C 893	16	1.8	505	10	ADBS1554	ADBS1554 Arabidops	C 966	16	1.8	588	4	AAx31178	AAx31178 Human dia
C 894	16	1.8	506	2	AAV02884	AAV02884 Human HMG	C 967	16	1.8	588	6	ABK71795	ABK71795 Human dit
C 895	16	1.8	507	6	ABT07257	ABT07257 Human CPG	C 968	16	1.8	591	11	ABD08032	ABD08032 Pseudomon
C 896	16	1.8	507	11	ABD05999	ABD05999 Pseudomon	C 969	16	1.8	591	13	ADQ51836	ADQ51836 Novel can

c	970	16	1.8	592	3	AAFI1381	AAFI1381	Aspergill
c	971	16	1.8	593	5	AA505448	AA505448	Mammalian
c	972	16	1.8	597	4	AAH78212	AAH78212	Nucleotid
c	973	16	1.8	597	5	AA505467	AA505467	Mammalian
c	974	16	1.8	597	10	ABT23375	ABT23375	Breast ca
c	975	16	1.8	598	13	ACN53714	ACN53714	Cotton an
c	976	16	1.8	601	10	ADK58253	ADK58253	Plant DNA
c	977	16	1.8	603	6	ABO57337	ABO57337	Human col
c	978	16	1.8	603	13	ADQ56284	ADQ56284	Novel can
c	979	16	1.8	606	2	AAV71928	AAV71928	MORT1 iso
c	980	16	1.8	606	2	AAV71929	AAV71929	MORT1 iso
c	981	16	1.8	606	6	ABO54671	ABO54671	Human ova
c	982	16	1.8	606	10	ADK55837	ADK55837	Plant DNA
c	983	16	1.8	607	10	ADBA4764	ADBA4764	Primary r
c	984	16	1.8	608	10	ADQ57026	ADQ57026	Novel can
c	985	16	1.8	608	13	ADK55977	ADK55977	Plant DNA
c	986	16	1.8	608	13	ADQ53001	ADQ53001	Novel can
c	987	16	1.8	609	13	ADT44525	ADT44525	Bacterial
c	988	16	1.8	611	10	ADDI4687	ADDI4687	DNA (Segi
c	989	16	1.8	615	2	AAO91084	AAO91084	Human her
c	990	16	1.8	615	4	AAH22905	AAH22905	Codon opt
c	991	16	1.8	615	10	ADK41226	ADK41226	CHO expre
c	992	16	1.8	621	11	ABDI1930	ABDI1930	Pseudomon
c	993	16	1.8	621	4	AAH06272	AAH06272	Human CDN
c	994	16	1.8	622	10	ADCT2543	ADCT2543	DNA Seg I
c	995	16	1.8	624	11	ABD05800	ABD05800	Pseudomon
c	996	16	1.8	626	10	ADDI4690	ADDI4690	DNA (Segi
c	997	16	1.8	627	2	AAV71930	AAV71930	MORT1 iso
c	998	16	1.8	635	13	ADQ79142	ADQ79142	Novel can
c	999	16	1.8	636	11	ABDI06775	ABDI06775	Pseudomon
c	1000	16	1.8	639	11	ABDI4656	ABDI4656	Pseudomon

ALIGNMENTS

RESULT	1
AAAF27407	
ID	AAF27407 standard; cDNA; 909 BP.
XX	
AC	AAF27407;
XX	
DT	24-APR-2001 (first entry)
DE	Human apoptosis-associated factor NT2RM1000558 partial cDNA, SEQ ID NO:1.
XX	
KW	Human; apoptosis-associated factor; NT2RM1000558; death effector domain;
KW	DEB; caspase family cleavage domain; pro-apoptotic; drug screening;
KW	cell proliferation; ischemic disease; chronic viral disease; ss.
XX	
OS	Homo sapiens.
PN	WO200104300-A1.
XX	
PD	18-JAN-2001.
XX	
PF	06-JUL-2000; 2000MO-JP004516.
XX	
PR	08-JUL-1999; 99JP-00194179.
PR	18-OCT-1999; 99US-0159586P.
XX	
PA	(HELI-) HELIX RES INST.
XX	
I	Oca T, Isogai T, Nishikawa T, Kawai Y, Miyoshi S, Satoh S;
XX	
DR	WPI; 2001-138348/14.
DR	P-PDB; AAB60386.
PT	Polynucleotide encoding an apoptosis-associated factor protein with death
PT	effector domain and caspase family-cleavage domain, useful in regulating
XX	diseases with cell proliferation.
XX	
S	Claim 1; Page 41-43; 53pp; Japanese.

	Query Match	100.0%	Score 909;	DB 5;	Length 909;	
	Best Local Similarity	100.0%	Pred. No. 0;			
	Matches 909;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0	
XX	The invention relates to a novel human apoptosis-associated factor					
CC	(AAB60386, AAB60387), designated NT2RM1000558, which contains a death					
CC	effector domain (DED) and a caspase family cleavage domain and is capable					
CC	of inducing apoptosis in cells. The invention also relates to nucleic					
CC	acids encoding the protein (AA27407, AA27408); variants of the protein					
CC	(particularly dominant negative variants); vectors and host cells					
CC	comprising a nucleic acid which encodes an apoptosis-associated factor					
CC	of the invention; the recombinant production of the protein; an antibody					
CC	against the protein; and methods of screening for compounds which can					
CC	regulate apoptosis. The apoptosis-related factor is useful in regulating					
CC	diseases associated with cell proliferation and in screening drug					
CC	candidates e.g., for regulating cell proliferation or cell death in					
CC	ischemic diseases and chronic viral diseases. The present sequence					
CC	represents cDNA encoding a substantial proportion of the human apoptosis-					
CC	associated factor NT2RM1000558					
XX						
SQ	Sequence 909 BP; 139 A; 284 C; 332 G; 154 T; 0 U; 0 Other;					
QY	1	ATGGCGCTATCCGGGTGACCCCGGCCCGCTCTGGAGAGAGATGATGCTTGAAC	60			
DB	1	ATGGCGCTATCCGGGTGACCCCGGCCCGCTCTGGAGAGAGATGATGCTTGAAC	60			
QY	61	TACGGGATGCTGTGCTTCAACCGTATGTTCCAGATGATGGGGCACTGAACGATGC	120			
DB	61	TACGGGATGCTGTGCTTCAACCGTATGTTCCAGATGATGGGGCACTGAACGATGC	120			
QY	121	GAGCTGAGACTCTTGCCCTTTCTGTGATGATGAGCTCTTGCGCGCCGCGAGACTTATGCC	180			
DB	121	GAGCTGAGACTCTTGCCCTTTCTGTGATGATGAGCTCTTGCGCGCCGCGAGACTTATGCC	180			
QY	181	CGGCGCCCGCAAGCGCTTGAAGTCTCTGCTGAGACTGAGCGCCGCGGAGATGGCGGAG	240			
DB	181	CGGCGCCCGCAAGCGCTTGAAGTCTCTGCTGAGACTGAGCGCCGCGGAGATGGCGGAG	240			
QY	241	AGCAACTGCGGAGCTGAGGCAATCTCTGCGCGCTGAGCGCCGCGCAAGACTTGTCGACG	300			
DB	241	AGCAACTGCGGAGCTGAGGCAATCTCTGCGCGCTGAGCGCCGCGCAAGACTTGTCGACG	300			
QY	301	CACCTGGCGGCAGCGGCGCGCACTGTCTCCGAACGCTATAGCTATGCGACCTTC	360			
DB	301	CACCTGGCGGCAGCGGCGCGCACTGTCTCCGAACGCTATAGCTATGCGACCTTC	360			
QY	361	AGCTCTTCAAGAAGAGAGAGAGATGATGCTGCGCGCTGCGGCAATCAAGATGTTTGA	420			
DB	361	AGCTCTTCAAGAAGAGAGAGATGATGCTGCGCGCTGCGGCAATCAAGATGTTTGA	420			
QY	421	AATTCTCAGCAGGCTCAGTGGAGAGACAGGCTCCGCCCAACAGCGGAGCGGCGAGT	480			
DB	421	AATTCTCAGCAGGCTCAGTGGAGAGACAGGCTCCGCCCAACAGCGGAGCGGCGAGT	480			
QY	481	CGGGCGCGGCCCACTGTGTGTGCCAGACGCGCGGAGAGGGGCGCCAGCGGCAACCCAG	540			
DB	481	CGGGCGCGGCCCACTGTGTGTGCCAGACGCGCGGAGAGGGGCGCCAGCGGCAACCCAG	540			
QY	541	CAGCAGTCAAGACCCCGCCAGACTTCTCTTAAGGCAAAATGATCCTGTGACATCCGGCTC	600			
DB	541	CAGCAGTCAAGACCCCGCCAGACTTCTCTTAAGGCAAAATGATCCTGTGACATCCGGCTC	600			
QY	601	CGGGTTGAGCAGATCTGCGAGCATGAGCGCAAGCTTGTGAGCAGAGGCGTGGCATCCCG	660			
DB	601	CGGGTTGAGCAGATCTGCGAGCATGAGCGCAAGCTTGTGAGCAGAGGCGTGGCATCCCG	660			
QY	661	CGGCGCCAGCGCTGGCGCGGCACTGACGCTGTTTGGGAGGCGCACCGCAGTGTGGCG	720			
DB	661	CGGCGCCAGCGCTGGCGCGGCACTGACGCTGTTTGGGAGGCGCACCGCAGTGTGGCG	720			
QY	721	TCAAGGAGCCTGGGCTGTGTGTTGTGACATCAAGTTCTAGAGCTTCTTATGTGAC	780			

Db 721 TCAGAGGACCTGGGCTGTGGTTGTGACATCAAGTTCTCAGAGCTCTCTATCTGAC 780
Qy 781 GCGTTCTGGGGGAGATTAAGTGGTGGGCGCCCTGCTGAGAGCCCTGCGGGCGGTGTTCCG 840
Db 781 GCGTTCTGGGGGAGATTAAGTGGTGGGCGCCCTGCTGAGAGCCCTGCGGGCGGTGTTCCG 840
Qy 841 ACTGAGGCGCTGCGAGAGGCTGTGGGCGGAGGCTGTTGCGCTGCTGATGATGAT 900
Db 841 ACTGAGGCGCTGCGAGAGGCTGTGGGCGGAGGCTGTTGCGCTGCTGATGATGAT 900
Qy 901 GAGGCTGAC 909
Db 901 GAGGCTGAC 909
RESULT 2
AAFP27408
ID AAFP27408 standard; cDNA; 1883 BP.
AC AAFP27408;
XX 24-APR-2001 (first entry)
DT Human apoptosis-associated factor NT2RML000558 cDNA, SEQ ID NO:3.
DE Human apoptosis-associated factor; NT2RML000558; death effector domain;
KW DEB; caspase family cleavage domain; pro-apoptotic; drug screening;
KM cell proliferation; ischemic disease; chronic viral disease; ss.
XX Homo sapiens.
OS
XX MO200104300-A1.
PN 18-JAN-2001.
PD 06-JUL-2000; 2000MO-JP004516.
PF 08-JUL-1999; 99JUL-00194179.
PR 18-OCT-1999; 99JUL-0159586P.
XX (HELI-) HELIX RES INST.
PA Ota T, Isegai T, Nishikawa T, Kawai Y, Miyoshi S, Satoh S;
PI MPI. 2001-138348/14.
DR P-ESDB; AAB60387.
XX Polynucleotide encoding an apoptosis-associated factor protein with death
PT effector domain and caspase family-cleavage domain, useful in regulating
PT diseases with cell proliferation.
PS Claim 3; Page 44-47; 53pp; Japanese.
XX
XX The invention relates to a novel human apoptosis-associated factor
CC (AAB60386, AAB60387), designated NT2RML000558, which contains a death
CC effector domain (DED), and a caspase family cleavage domain and is capable
CC of inducing apoptosis in cells. The invention also relates to nucleic
CC acids encoding the protein (AAFP27407, AAFP27408); variants of the protein
CC (particularly dominant negative variants); vectors and host cells
CC comprising a nucleic acid which encodes an apoptosis-associated factor
CC of the invention; the recombinant production of the protein; an antibody
CC against the protein; and methods of screening for compounds which can
CC regulate apoptosis. The apoptosis-related factor is useful in regulating
CC diseases associated with cell proliferation and in screening drug
CC candidates e.g., for regulating cell proliferation or cell death in
CC ischemic diseases and chronic viral diseases. The present sequence
CC represents a full-length cDNA encoding the human apoptosis-associated
CC factor NT2RML000558
XX
SQ Sequence 1883 BP; 343 A; 595 C; 588 G; 357 T; 0 U; 0 Other;
Query Match 100.0%; Score 909; DB 5; Length 1883;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGGCGATACCGGGGTGACCCCGGCGCGGCTGGGAGAGATGAGTGCCTGACATAC 60
Db 124 ATGGGCGATACCGGGGTGACCCCGGCGCGGCTGGGAGAGATGAGTGCCTGACATAC 183
Qy 61 TACGGGATGCTGCGCTTCAACGATATGTTGAGGTGTGGGCGGCAACGACAGTGC 120
Db 184 TACGGGATGCTGCGCTTCAACGATATGTTGAGGTGTGGGCGGCAACGACAGTGC 243
Qy 121 GAGCTGAGCTCTGCTGCTTCTGCTGATGAGGCTCTCGGCGCGCGGAGGCTTACCC 180
Db 244 GAGCTGAGCTCTGCTGCTTCTGCTGATGAGGCTCTCGGCGCGGAGGCTTACCC 303
Qy 181 CGGGCCCGGAGGCGCTGAGAGCTCTGCTGAGAGCTGAGGCGCGGAGGAGTGGCGGAG 240
Db 304 CGGGCCCGGAGGCGCTGAGAGCTCTGCTGAGAGCTGAGGCGCGGAGGAGTGGCGGAG 363
Qy 241 AGCAACCTGCGGCTGCTGCTGCGGCAACTCTGCGCGGCTGAGCGCGGCAACCTGCTGCG 300
Db 364 AGCAACCTGCGGCTGCTGCTGCGGCAACTCTGCGCGGCTGAGCGCGGCAACCTGCTGCG 423
Qy 301 CACTGGGCGCGAGCGCGCGCGGCAAGTGTCTTCCAGAACGCTATAGCTATAGGACCTTC 360
Db 424 CACTGGGCGCGAGCGCGCGCGGCAAGTGTCTTCCAGAACGCTATAGCTATAGGACCTTC 483
Qy 361 AGCTTTTAAAGAGAGACAGAGGTAGTGCCTGCGCGGCTGCGGCAAGTGTGCA 420
Db 484 AGCTTTTAAAGAGAGACAGAGGTAGTGCCTGCGCGGCTGCGGCAAGTGTGCA 543
Qy 421 AATTCTCAGACAGGCTCACTGGGAGACAGAGCTTCCCGCAACCAACGCGGAGCGGAGT 480
Db 544 AATTCTCAGACAGGCTCACTGGGAGACAGAGCTTCCCGCAACCAACGCGGAGCGGAGT 603
Qy 481 CGGGCCCGGCGGAGTGTGTGTCCAGACGCGCGGCGGAGAGGCGCGGCGGAGCGGAGT 540
Db 604 CGGGCCCGGCGGAGTGTGTGTCCAGACGCGCGGCGGAGAGGCGCGGCGGAGCGGAGT 663
Qy 541 CAGCAGTACAGAGCGCGGCGGAGGCTTCTCTGAGGCGAAGTACCTGTGACATCCGGCTC 600
Db 664 CAGCAGTACAGAGCGCGGCGGAGGCTTCTCTGAGGCGAAGTACCTGTGACATCCGGCTC 723
Qy 601 CGGGTTCCAGACAGATTAAGTGCAGAGCATGCGGCGGCGGCTTGGAGCAGGCGGCGGATCCCG 660
Db 724 CGGGTTCCAGACAGATTAAGTGCAGAGCATGCGGCGGCGGCTTGGAGCAGGCGGCGGATCCCG 783
Qy 661 CGGGCCCGGCGGAGTGTGTGTCCAGACGCGCGGCGGAGAGGCGGCGGAGGCGGAGT 720
Db 784 CGGGCCCGGCGGAGTGTGTGTCCAGACGCGCGGCGGAGAGGCGGCGGAGGCGGAGT 843
Qy 721 TCAGAGGACCTGGGCTGTGGTTGTGACATCAAGTTCTCAGAGCTCTCTATCTGAC 780
Db 844 TCAGAGGACCTGGGCTGTGGTTGTGACATCAAGTTCTCAGAGCTCTCTATCTGAC 903
Qy 781 GCGTTCTGGGGGAGATTAAGTGGTGGGCGCCCTGCTGAGAGCCCTGCGGGCGGTGTTCCG 840
Db 904 GCGTTCTGGGGGAGATTAAGTGGTGGGCGCCCTGCTGAGAGCCCTGCGGGCGGTGTTCCG 963
Qy 841 ACTGAGGCGCTGCGAGAGGCTGTGGGCGGAGGCTGTTGCGCTGCTGATGATGAT 900
Db 964 ACTGAGGCGCTGCGAGAGGCTGTGGGCGGAGGCTGTTGCGCTGCTGATGATGAT 1023
Qy 901 GAGGCTGAC 909
Db 1024 GAGGCTGAC 1032
RESULT 3
ADC79259
ID ADC79259 standard; cDNA; 981 BP.
AC ADC79259;
XX
XX

DT 01-JAN-2004 (first entry)
 XX Human DEDD2 encoding cDNA SEQ ID NO:1.
 DE human; death effector domains containing DNA-binding protein;
 XX DED-containing DNA-binding protein; DEDD2; cell death; gene therapy;
 KW cytosolic; cancer; chronic myeloid leukaemia; gene; ss.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 1..981
 FT CDS /tag= a
 FT /product= "DEDD2"
 FI
 XX MO2003054195-A1.
 XX
 XX 03-JUL-2003.
 XX
 XX 20-DEC-2002; 2002MO-JP013371.
 XX
 XX 20-DEC-2001; 2001JP-00387854.
 XX 18-JUL-2002; 2002JP-00209458.
 XX
 XX (MORG) MORINAGA MILK IND CO LTD.
 XX
 XX Suzu S, Hageshita H, Nomaguchi K, Yamada M, Hayasawa H;
 XX WPI; 2003-569246/53.
 XX
 XX P-PSDB; ADC79260.
 XX
 XX DNA encoding cell death proteins for treatment of kidney, large intestine
 PT and prostate cancers and leukemia.
 PT
 XX Claim 2; Page 18-20; 26pp; Japanese.
 XX
 XX The present sequence encodes a human death effector domains (DED)
 CC containing DNA-binding protein (DEDD) protein, designated DEDD2, that
 CC causes cell death. Also described: (1) primer and probe for investigation
 CC of the DEDD2 gene; and (2) reagents for gene therapy. DEDD2 has
 CC cytosolic activity. DEDD2 can be used in the diagnosis and treatment of
 CC cancers of the kidney, large intestine and prostate, and acute and
 CC chronic myeloid leukaemia.
 CC
 XX Sequence 981 BP; 151 A; 303 C; 363 G; 164 T; 0 U; 0 Other;
 SQ
 Query Match 94.4%; Score 858; DB 10; Length 981;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 361 AGCTCTCAAGAGAGACAGAGGTAAGTCCGTCGCGCAGTCAAGCAGTTCTGCA 420
 DB 361 AGCTCTCAAGAGAGACAGAGGTAAGTCCGTCGCGCAGTCAAGCAGTTCTGCA 420
 QY 421 AATTTCACGACGAGTCAAGTGGAGACAGGCTCCCCCAACCAAGCGGACGGGAGT 480
 DB 421 AATTTCACGACGAGTCAAGTGGAGACAGGCTCCCCCAACCAAGCGGACGGGAGT 480
 QY 481 CGGGGCGGGCCAGTGTGTGTCAGACGAGGCGGAGAGGGGCGCCAGCCGACCCAG 540
 DB 481 CGGGGCGGGCCAGTGTGTGTCAGACGAGGCGGAGAGGGGCGCCAGCCGACCCAG 540
 QY 541 CAGCAGTCAAGACCCCGCAGACCTTCTCTGTAAGGCAAGTGAACCTGTGACATCCGGCTC 600
 DB 541 CAGCAGTCAAGACCCCGCAGACCTTCTCTGTAAGGCAAGTGAACCTGTGACATCCGGCTC 600
 QY 601 CGGGTTGAGACGACGATCTGAGAGCATGGGCGAGCTTTGAGACGAGGCGTGGCATCCGG 660
 DB 601 CGGGTTGAGACGACGATCTGAGAGCATGGGCGAGCTTTGAGACGAGGCGTGGCATCCGG 660
 QY 661 CGGGCCCGAGGCGTGGGCGGCGAGCTGAGCGTGTGAGGCGAGGCGCAGGCGAGTGGCGC 720
 DB 661 CGGGCCCGAGGCGTGGGCGGCGAGCTGAGCGTGTGAGGCGAGGCGCAGGCGAGTGGCGC 720
 QY 721 TCAAGGACCTGGGCTGTGTGTGTGACATCAAGTTCTGACAGCTCTCTATCTGGAC 780
 DB 721 TCAAGGACCTGGGCTGTGTGTGTGACATCAAGTTCTGACAGCTCTCTATCTGGAC 780
 QY 781 GCCTTTGGGGGCACTACTAGTGGCGCCCTGCTGACAGGCGCTCGGGGGGCTGTCTTG 840
 DB 781 GCCTTTGGGGGCACTACTAGTGGCGCCCTGCTGACAGGCGCTCGGGGGGCTGTCTTG 840
 QY 841 ACTGAGGCGCTGCGAGAGGCTGTGGGCGGAGGCGTGTGCGCTGCTGAGTGGAT 900
 DB 841 ACTGAGGCGCTGCGAGAGGCTGTGGGCGGAGGCGTGTGCGCTGCTGAGTGGAT 900
 QY 901 GAGGCTGAC 909
 DB 901 GAGGCTGAC 909

RESULT 4
 ABA94362
 ID ABA94362 standard; DNA; 1230 BP.
 XX
 XX ABA94362;
 AC
 XX 26-MAR-2002 (first entry)
 DT
 XX Human APRG polypeptide (Incyte ID. 3102521CD1) encoding cDNA.
 XX
 KW APRG; apoptosis regulator; cytosolic; antiatherosclerotic; osteopathic;
 KW antiarteriosclerotic; hepatotropic; antipapillary; antihelminthic; human;
 KW antiallergic; antianemic; antiaschematic; antithyroid; anti-HIV; cancer;
 KW antiinflammatory; antidiabetic; antipain; antipapillary; antipapillary;
 KW immunosuppressive; dermatological; antitumor; antineoplastic; fungicide;
 KW antiarthritic; antibacterial; virucide; antiparasitic; protozoicide;
 KW tranquilizer; vulnerary; gynecological; vasotropic; gene therapy; ss.
 KW
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 127..1107
 FT CDS /tag= a
 FT /product= "APRG polypeptide"
 FI
 XX MO200192527-A2.
 XX
 XX 06-DEC-2001.
 XX
 XX 30-MAY-2001; 2001MO-US017581.
 XX

PD 23-MAY-2002.
 XX 15-NOV-2001; 2001WO-US044844.
 PF 17-NOV-2000; 2000US-00715893.
 PR 29-JUN-2001; 2001US-0301889P.
 XX (BURN-) BURNHAM INST.
 XX
 XX Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
 PI Stenner-Liemwen F;
 PI MPI: 2002-500222/53.
 DR P-PSDB: AAE24860.
 XX
 XX New polypeptide comprising a death domain or death effector domain,
 PT useful for discovery of drugs that suppress infection, inflammation,
 PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.
 XX
 PS Claim 19; Page 184-186; 209pp; English.

CC The invention relates to an isolated polypeptide comprising a death
 CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention
 CC is useful for identifying a binding agent, preferably a protein or a drug
 CC that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC
 CC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or
 CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent and
 CC detecting the association of the domain and the candidate binding agent,
 CC by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or
 CC chemical crosslinking, nuclear magnetic resonance (NMR), mass
 CC spectroscopy (MS) and FPA. The invention is useful for modulating the
 CC level of a cell process such as cell proliferation, cell adhesion, cell
 CC stress responses, responses to microbial infection and B cell
 CC immunoglobulin class switching, in particular apoptosis within a cell.
 CC Antibody specifically reactive with CTDD DD of C. trachomatis, C.
 CC muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the
 CC CTDD DD protein is useful for detecting a Chlamydia infection. The
 CC invention is useful for modulating the activity of oncogenic proteins,
 CC for treating a pathology caused by the oncogenic proteins and for
 CC treating bacterial infections by modulating the activity of bacterial
 CC proteins. The protein and antibody specific for it are useful for
 CC discovery of drugs that suppress infection, inflammation, allergy,
 CC sepsis, autoimmunity, allograft rejection and other diseases. The protein
 CC is useful for treating immune-based pathologies, pathologies associated
 CC with cell division, inflammatory diseases such as sepsis, fibrosis,
 CC arthritis, graft versus host disease. The invention is used in antisense
 CC therapy and gene therapy. The present sequence is human DED4 gene
 CC
 SQ Sequence 1924 BP; 360 A; 599 C; 594 G; 368 T; 0 U; 3 Other;

Query Match 94.4%; Score 858; DB 6; Length 1924;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGGCTATCGGGTCCAGCCCGGCTGGGAGGAGAGTGGCTGACAC 60
 DB 91 ATGGGCTATCGGGTCCAGCCCGGCTGGGAGGAGAGTGGCTGACAC 150
 QY 61 TACGGGATGCTGCTCCCTTCCAGCTATGTTCCAGGTGTGGGCGGCACTGACGAGTGC 120
 DB 151 TACGGGATGCTGCTCCCTTCCAGCTATGTTCCAGGTGTGGGCGGCACTGACGAGTGC 210
 QY 121 GAGCTGAGAGCTCTGGGCTTTTCTGCTGATGAGGCTCTGGGCGGCGGAGGCTTACCC 180
 DB 211 GAGCTGAGAGCTCTGGGCTTTTCTGCTGATGAGGCTCTGGGCGGCGGAGGCTTACCC 270
 QY 181 CGGGCCCGCAGGCGCTAGAGCTCTGCTGAGAGCTGAGAGCGCGGGGCGAGTGGCGAG 240
 DB 271 CGGGCCCGCAGGCGCTAGAGCTCTGCTGAGAGCTGAGAGCGCGGGGCGAGTGGCGAG 330
 QY 241 AGCAACTGTGGGCTGCTGGGCGCACTCTGCGCGGTGTGGCCGCGCACGACTGTGGCG 300
 DB 331 AGCAACTGTGGGCTGCTGGGCGCACTCTGCGCGGTGTGGCCGCGCACGACTGTGGCG 390

QY 301 CACCTGAGCGCGCAAGCGGCGCGGCACTGTCTCCAGAACGCTATAGTATGCACTCC 360
 DB 391 CACCTGAGCGCGCAAGCGGCGCGGCACTGTCTCCAGAACGCTATAGTATGCACTCC 450
 QY 361 AGCTTTTAAAGAGACAGAGGTATGCTGCGGCTCGGCACTCAAGAGTTCTGCA 420
 DB 451 AGCTTTTAAAGAGACAGAGGTATGCTGCGGCTCGGCACTCAAGAGTTCTGCA 510
 QY 421 AATTCTGACAGAGGTCACTGGGAGACAGAGCTCCCCCAACCAAGCGGCGAGT 480
 DB 511 AATTCTGACAGAGGTCACTGGGAGACAGAGCTCCCCCAACCAAGCGGCGAGT 570
 QY 481 CGGGCCCGGCGGCTGCTGCTGCAAGACAGCGGCGGAGAGGGGCCCGGCACTCCAG 540
 DB 571 CGGGCCCGGCGGCTGCTGCTGCAAGACAGCGGCGGAGAGGGGCCCGGCACTCCAG 630
 QY 541 CAGAGTGAAGAGCGCGGCGGCACTCTTCTGAAAGCAAGTGAATCCGGCTC 600
 DB 631 CAGAGTGAAGAGCGCGGCGGCACTCTTCTGAAAGCAAGTGAATCCGGCTC 690
 QY 601 CGGCTTCAGAGAGTACTGAGACATGAGCGCACTTGGAGAGAGGCGTGGCATCCCGG 660
 DB 691 CGGCTTCAGAGAGTACTGAGACATGAGCGCACTTGGAGAGAGGCGTGGCATCCCGG 750
 QY 661 CGGCCCCAGGCGCTGCGCGGCGAGCTGAGCGTGTGGGCGAGCCGACAGTCTGCGC 720
 DB 751 CGGCCCCAGGCGCTGCGCGGCGAGCTGAGCGTGTGGGCGAGCCGACAGTCTGCGC 810
 QY 721 TCAAGGAGCGTGGGCTGTGTTTGGTTCATCAAGTTCAGAGCTCTCTATCTGGAC 780
 DB 811 TCAAGGAGCGTGGGCTGTGTTTGGTTCATCAAGTTCAGAGCTCTCTATCTGGAC 870
 QY 781 GCTTCTGGGCGGCACTAGTGGCGCCCTGCTGAGAGCGCTGCGGAGCGTGTCTCG 840
 DB 871 GCTTCTGGGCGGCACTAGTGGCGCCCTGCTGAGAGCGCTGCGGAGCGTGTCTCG 930
 QY 841 ACTGAGGCGCTTGGCGAGAGGCTGTGGGCGGAGGCTGTTCGCTGCTGAGTGTGAT 900
 DB 931 ACTGAGGCGCTTGGCGAGAGGCTGTGGGCGGAGGCTGTTCGCTGCTGAGTGTGAT 990
 QY 901 GAGGCTGAC 909
 DB 991 GAGGCTGAC 999

RESULT 6
 AAD59062
 ID AAD59062 standard; cDNA, 1924 BP.

XX AAD59062;
 AC 18-DEC-2003 (first entry)
 DT
 XX Human DED4 full length gene.

XX Human, death Domain; DD; death effector domain; DED; cell proliferation;
 KW Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;
 KW neural growth factor receptor-interacting domain; cell adhesion;
 KW vasotropic; microbial infection; inflammation; allograft rejection; CTDD;
 KW cell stress response; benign prostatic hypertrophy; antibacterial; NIDD;
 KW apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;
 KW neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;
 KW keloid; gene; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 91..1044

FT /tag= a

FT /product= "Human DED4 protein"

FT /note= "No stop codon"

FT /partial


```
FT misc_signal 157..222
FT /*tag= b
FT /note= "Nuclear localisation sequence"
XX
XX US2003049702-A1.
XX
XX 13-MAR-2003.
XX
XX 15-NOV-2001; 2001US-00001254.
XX
XX 17-NOV-2000; 2000US-00715893.
XX 17-NOV-2000; 2000US-0367360P.
XX 29-JUN-2001; 2001US-0301889P.
XX
XX (REED/) REED J C.
XX (GODZIK/) GODZIK A.
XX (PAWL/) PAWLOWSKI K.
XX (FIOR/) FIORENTINO L.
XX (LEES/) LEES S H.
XX (ROTH/) ROTH W.
XX (STEN/) STENNEN-LIEWEN F.
XX
XX Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
XX Stenner-Liewen F;
XX MPI; 2002-500222/53.
XX P-PSDB; AAE38903.
XX
XX New polypeptide comprising a death domain or death effector domain,
XX useful for discovery of drugs that suppress infection, inflammation,
XX allergy, sepsis, autoimmunity, allograft rejection and other diseases.
XX
XX Claim 19; Page 42-44; 99pp; English.
XX
XX The present invention provides novel death domain (DD) and death effector
XX domain (DED) proteins and nucleic acids encoding them. The invention also
XX provides death domain containing protein such as Chlamydia trachomatis
XX death domain containing protein (CTDP) DD and neural growth factor
XX receptor-interacting death domain (NIDD) DD. The invention is useful for
XX identifying a binding agent (e.g. protein or drug) that binds a DD, DED
XX or NB-ARC domain from DMP3, IRAK4, CTDD, DED4 or NIDD with a candidate
XX binding agent and identifying an effective agent (e.g. protein or drug)
XX that modulates the association of a DD, DED or NB-ARC domain with protein
XX that binds the DD, DED or NB-ARC domain. The invention is also useful for
XX modulating the level of cell process such as apoptosis, cell adhesion,
XX cell proliferation, cell stress responses, responses to microbial
XX infection and B cell immunoglobulin class switching. DDs, DEDs and NB-ARC
XX domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are
XX useful for discovery of drugs that suppress infection, autoimmunity,
XX inflammation, allergy, allograft rejection, sepsis and other diseases.
XX DD, DED or NB-ARC domain proteins are used to treat infection, allergy,
XX autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte
XX hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis,
XX inflammatory hyperplasia and smooth muscle cell proliferation in arteries
XX following balloon angioplasty (restenosis). The invention is also used in
XX antibody therapy and gene therapy. The present sequence is human DED4
XX full length gene. The DED4 gene is located on chromosome 19
XX
XX Sequence 1924 BP; 360 A; 599 C; 594 G; 368 T; 0 U; 3 Other;
SQ
Query Match 94.4%; Score 858; DB 6; Length 1924;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGGGCGTATCCGGGTCGACCCCGGCGCCGCTGCTGGAGAGAGATGCTCTGACTAC 60
DB 91 ATGGGCGCTATCCGGGTCGACCCCGGCGCCGCTGCTGGAGAGAGATGCTCTGACTAC 150
QY 61 TACGGGATGCTGCTGCTGACCGTATGATGAGGTGCTGGGGGGGCAATGACCGAGTGC 120
DB 151 TACGGGATGCTGCTGCTGACCGTATGATGAGGTGCTGGGGGGGCAATGACCGAGTGC 210
QY 121 GAGCTGAGACTCTGCTTCTGCTGATGAGGCTCTGCGCGCCGAGAGGCTTAGCC 180
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DB 211 GAGCTGAGACTCTGCTTCTGCTGATGAGGCTCTGCGCGCCGAGAGGCTTAGCC 270
QY 181 CGGGCCCCACACCGGCTGAGCTCTGCTGAGAGTGGAGCCCGCGGGCAGTGGCGGAG 240
DB 271 CGGGCCCCACACCGGCTGAGCTCTGCTGAGAGTGGAGCCCGCGGGCAGTGGCGGAG 330
QY 241 AGCAACTGCGGCTGCTGAGGCAACTCTGCGCGGCTGAGGCGCGGCAAGACTGATGCACTCC 300
DB 331 AGCAACTGCGGCTGCTGAGGCAACTCTGCGCGGCTGAGGCGCGGCAAGACTGATGCACTCC 390
QY 301 CACCTGCGCGGCAAGGCGCGCGCGGCAAGTGTCTCCAGAACGCTATAGTACCTCC 360
DB 391 CACCTGCGCGGCAAGGCGCGCGCGGCAAGTGTCTCCAGAACGCTATAGTACCTCC 450
QY 361 AGCTTTTAAAGAGAGAGAGTGTGCTGCGCGCTGCGCGCTGCGGCAAGTGTGCA 420
DB 451 AGCTTTTAAAGAGAGAGAGTGTGCTGCGCGCTGCGCGCTGCGGCAAGTGTGCA 510
QY 421 AATTCTGAGAGGCTGAGTGGAGAGACAGGCTTCCCGCAACCAAGCGGCGGAGT 480
DB 511 AATTCTGAGAGGCTGAGTGGAGAGACAGGCTTCCCGCAACCAAGCGGCGGAGT 570
QY 481 CGGGGCGCGCGCAGTGTGTGTCAGAGCGCGCGGAGAGGCGCGGCAAGCGGCGGAG 540
DB 571 CGGGGCGCGCGCAGTGTGTGTCAGAGCGCGCGGAGAGGCGCGGCAAGCGGCGGAG 630
QY 541 CAGCAGTCAAGAGCCCGCAGAGCTTCTCTGTAAGGCAAGTGAACCTGTGACATCCGGCTC 600
DB 631 CAGCAGTCAAGAGCCCGCAGAGCTTCTCTGTAAGGCAAGTGAACCTGTGACATCCGGCTC 690
QY 601 CGGGTTGAGAGAGAGTACTGAGAGAGTGGGCGAGCTTGGAGAGAGGCGGATCCGG 660
DB 691 CGGGTTGAGAGAGAGTACTGAGAGAGTGGGCGAGCTTGGAGAGAGGCGGATCCGG 750
QY 661 CGGGCCCAAGCGCTGCGCGCGCGGAGCTGAGAGCTGTTTGGGCAAGCGGAGTGTGCGC 720
DB 751 CGGGCCCAAGCGCTGCGCGCGCGGAGCTGAGAGCTGTTTGGGCAAGCGGAGTGTGCGC 810
QY 721 TCAAGGAGCTGGGCTGTGTTGTGATCAATCAAGTCTCAGAGCTCTCTATCTGAGC 780
DB 811 TCAAGGAGCTGGGCTGTGTTGTGATCAATCAAGTCTCAGAGCTCTCTATCTGAGC 870
QY 781 GCTTCTGAGGCGACTTACTGAGTGGCGCCCTGCTGAGAGCCCTCGGGGCGTGTCCG 840
DB 871 GCTTCTGAGGCGACTTACTGAGTGGCGCCCTGCTGAGAGCCCTCGGGGCGTGTCCG 930
QY 841 ACTGAGGCGCTTCCGAGAGGCTGTGGGCGCGGAGGCTGTTGCTGCTGCTGAGTGTGAT 900
DB 931 ACTGAGGCGCTTCCGAGAGGCTGTGGGCGCGGAGGCTGTTGCTGCTGCTGAGTGTGAT 990
QY 901 GAGGCTGAC 909
DB 991 GAGGCTGAC 999
RESULT 7
AD086891
ID AD086891 standard; cDNA; 1979 BP.
XX
XX AD086891;
XX
XX 07-OCT-2004 (first entry)
XX
XX Human tumour-associated antigenic target (TAT) cDNA sequence #3766.
XX human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
XX cancer; cell proliferative disorder; gene; ss.
XX Homo sapiens.
XX
XX WO2004060270-A2.
XX
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22-JUL-2004.
 15-OCT-2003; 2003WO-US029126.
 18-OCT-2002; 2002US-0418988P.
 (GENTH) GENENTECH INC.
 (WUTD/) WU T D.
 (ZHOU/) ZHOU Y.
 Wu TD, Zhou Y;
 WPI: 2004-53430/51.
 New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer.
 Claim 1; SEQ ID NO 3766; 5504bp; English.
 The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identical to (a) or (b); (5) a chimeric polypeptide comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a combination of the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT CDNA sequence from the present invention.

Sequence 1979 BP; 365 A; 617 C; 627 G; 370 T; 0 U; 0 Other;
 Query Match 94.4%; Score 858; DB 12; Length 1979;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGGGCTATCGGCTGACCCCGGCTGGTGGAGAGATGCTGAGTAC 60
 151 ATGGGCTATCGGCTGACCCCGGCTGGTGGAGAGATGCTGAGTAC 220
 61 TACGGGATGCTGCTGCTTACCGTATGTTGAGAGTGTGGGCGGCACTGACGAGTGC 120
 221 TACGGGATGCTGCTGCTTACCGTATGTTGAGAGTGTGGGCGGCACTGACGAGTGC 280
 121 GAGCTGAGGCTCTGCTTCTGCTGATGAGGCTCTGCGGCGCCGAGGCTTACGC 180

281 GAGCTGAGGCTCTGCTTCTGCTGATGAGGCTCTGCGCGCCGAGGCTTACCC 340
 181 CGGGCCGAGCGGCTGAGCTCTGCTGAGAGTGAAGCGCGCGGAGTGCAG 240
 341 CGGGCCGAGCGGCTGAGCTCTGCTGAGAGTGAAGCGCGCGGAGTGCAG 400
 241 AGCAACCTGCGGCTGCTGAGGCACTCTGCGCGTGTGAGCGCGCACTGCTGCG 300
 401 AGCAACCTGCGGCTGCTGAGGCACTCTGCGCGTGTGAGCGCGCACTGCTGCG 460
 301 CACCTGCGGCGGCACTGCTGAGGCACTCTGCGCGTGTGAGCGCGCACTGCTGCG 360
 461 CACCTGCGGCGGCACTGCTGAGGCACTCTGCGCGTGTGAGCGCGCACTGCTGCG 520
 361 AGCTTCAAG 420
 521 AGCTTCAAG 580
 421 AATTCAG 480
 581 AATTCAG 640
 481 CGGGCCGAGCGGCTGAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 641 CGGGCCGAGCGGCTGAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 700
 541 CAGGCTGAG 600
 701 CAGGCTGAG 760
 601 CGGGTTCAG 660
 761 CGGGTTCAG 820
 821 CGGGTTCAG 880
 721 TCAAGGAG 780
 881 TCAAGGAG 940
 841 ACTGAG 900
 1001 ACTGAG 1060
 901 GAGGCTGAC 909
 1061 GAGGCTGAC 1069

RESULT 8
 ID AAA95790 standard; cDNA; 2045 BP.
 AAA95790,
 28-FEB-2001 (first entry)
 Apoptosis related gene 1 clone H1DOK36.
 Cytostatic; antiinflammatory; immunosuppressive; antiisclerotic; cardiac;
 vitrucidal; anti-AIDS; vasodilatory; anti-ischaemic; antiparkinsonian; ss;
 anti-Alzheimer; gene therapy; human; apoptosis; fusion protein; cancer;
 colon; breast; prostate; melanoma; lymphoma; inflammation; herpes;
 autoimmune disorder; multiple sclerosis; viral infection.
 Homo sapiens.

XX WO20056752-A2.
 PN
 XX 28-SEP-2000.
 PD
 XX 15-MAR-2000; 2000WO-US006642.
 PF
 XX 24-MAR-1999; 99US-0126018P.
 PR 17-JUN-1999; 99US-0139638P.
 PR 18-AUG-1999; 99US-0149449P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Ruben SM, Ni J, Young PA;
 PI
 XX WPI, 2000-587660/55.
 DR P-PSDB; AAB15551.
 XX
 PT Nucleic acids encoding human apoptosis associated protein, useful for the
 PT prevention, treatment and diagnosis of e.g. Alzheimer's and Parkinson's
 PT disease, inflammation and ischemic injury.
 XX
 PS Claim 1; Page 244-245; 273pp; English.

CC The invention relates to the isolation of genes encoding 9 human
 CC apoptosis-related proteins. The nucleotide sequences AAB95790-A95798
 CC encode the human apoptosis related proteins AAB15551-B15559. The genes
 CC can be used to generate fusion proteins by linking to the gene for the
 CC human immunoglobulin G Fc (IgG Fc) portion (AAB95799) for increasing the
 CC stability of the fusion protein as compared to the human protein only.
 CC The gene and encoded protein may be used in the prevention, treatment and
 CC diagnosis of diseases associated with inappropriate apoptosis associated
 CC protein expression, e.g. cancer (e.g. colon, breast and prostate cancer,
 CC melanomas and lymphomas), inflammation, autoimmune disorders (e.g.
 CC multiple sclerosis) and viral infections (e.g. herpes)

CC Sequence 2045 BP; 457 A; 620 C; 604 G; 364 T; 0 U; 0 Other;

Query Match 94.4%; Score 858; DB 3; Length 2045;

Best Local Similarity 99.9%; Pred. No. 0;
 Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCGCTATCCGGGTCGACCCCGGCGCTGCTGGAGAGGATGATGCTCGACTAC 60
 DB 121 ATGGCGCTATCCGGGTCGACCCCGGCGCTGCTGGAGAGGATGATGCTCGACTAC 180
 QY 61 TACGGGATCTGTGCTTCAACCGTATGTTGAGCTGTGGCGGGCAACTGACCGATGC 120
 DB 181 TACGGGATCTGTGCTTCAACCGTATGTTGAGCTGTGGCGGGCAACTGACCGATGC 240
 QY 121 GAGCTGAGACTCCTGCGCTTTGCTGCTGATGAGGCTCTGGGCGCCCGGAGGCTTAC 180
 DB 241 GAGCTGAGACTCCTGCGCTTTGCTGCTGATGAGGCTCTGGGCGCCCGGAGGCTTAC 300
 QY 181 CGGGCCCGGAGCGGCTTAGAGCTCTGCTGAGAGCTGAGCGCGGCGAGTCCGGCGAG 240
 DB 301 CGGGCCCGGAGCGGCTTAGAGCTCTGCTGAGAGCTGAGCGCGGCGAGTCCGGCGAG 360
 QY 241 AGCAACTGCGGCTGCTGGGGCAACTCTGCGCTGCTGGCGCCGCAAGCTGTCGGC 300
 DB 361 AGCAACTGCGGCTGCTGGGGCAACTCTGCGCTGCTGGCGCCGCAAGCTGTCGGC 420
 QY 301 CACCTGGCGGCAAGGCGCGCGCGGCAAGTCTCCGAAGCGTATGCTATGGCACTCC 360
 DB 421 CACCTGGCGGCAAGGCGCGCGCGGCAAGTCTCCGAAGCGTATGCTATGGCACTCC 480
 QY 361 AGCTTTCAAGAGGAGCAGAGGTAAGTGCCTGCTGCGCTGCGAGTCAAGCACTTCTCA 420
 DB 481 AGCTTTCAAGAGGAGCAGAGGTAAGTGCCTGCTGCGCTGCGAGTCAAGCACTTCTCA 540
 QY 421 AATTCTCAGCAGGCTCAGTGGAGACAGGCTCCCGCCCAACCAAGGCGGCGAGGT 480
 DB 541 AATTCTCAGCAGGCTCAGTGGAGACAGGCTCCCGCCCAACCAAGGCGGCGAGGT 600

QY 481 CGGGCCCGGAGCGGCTAGTGTGTCAGACGAGCGGCGGAGAGGAGGCCCGCAGCGCACTCCAG 540
 DB 601 CGGGCCCGGAGCGGCTAGTGTGTCAGACGAGCGGCGGAGAGGAGGCCCGCAGCGCACTCCAG 660
 QY 541 CAGCAGTACAGAGCCCGCAGACCTTCTCTGAAAGCAAGTGAACCTGTGACATCCGGCTC 600
 DB 661 CAGCAGTACAGAGCCCGCAGACCTTCTCTGAAAGCAAGTGAACCTGTGACATCCGGCTC 720
 QY 601 CGGGTTCCAGCAGATACTGCGAGATAGGCGCCAGGCTTGGAGCAGAGGCGTGCATCCGG 660
 DB 721 CGGGTTCCAGCAGATACTGCGAGATAGGCGCCAGGCTTGGAGCAGAGGCGTGCATCCGG 780
 QY 661 CGGGCCCGGAGCGCTGGCGGCGGAGCTGACAGCTGATGTTGGGCAAGCCAGCGAGTGC 720
 DB 781 CGGGCCCGGAGCGCTGGCGGCGGAGCTGACAGCTGATGTTGGGCAAGCCAGCGAGTGC 840
 QY 721 TCAGAGGACCTGGGCTGTGTGTTTGTGACATCAAGTTCTCAGAGCTCTCTATCTGAC 780
 DB 841 TCAGAGGACCTGGGCTGTGTGTTTGTGACATCAAGTTCTCAGAGCTCTCTATCTGAC 900
 QY 781 GCTTCTGGGCGGACTTACCTGATGTCGCGCCCTGTCAGAGCCCTGCGGGCGGTTCCTG 840
 DB 901 GCTTCTGGGCGGACTTACCTGATGTCGCGCCCTGTCAGAGCCCTGCGGGCGGTTCCTG 960
 QY 841 ACTGAGGCGCTTCGAGAGGCTGTGGGCGGAGGCTGTTGCTGCTGCTGATGAT 900
 DB 961 ACTGAGGCGCTTCGAGAGGCTGTGGGCGGAGGCTGTGCTGCTGCTGATGAT 1020
 QY 901 GAGGCTGAC 909
 DB 1021 GAGGCTGAC 1029

RESULT 9

AAH33283
 ID AAH33283 standard; cDNA; 2045 BP.

XX AAH33283;

AC 03-SEP-2001 (first entry)

DE Human colon cancer antigen encoding cDNA SEQ ID NO:339.

KM Human: colon cancer; colon cancer antigen; diagnosis; detection;

KM colorectal carcinoma; 88.

OS Homo sapiens.

PN WO200122920-A2.

PD 05-APR-2001.

PF 28-SEP-2000; 2000WO-US026524.

PR 29-SEP-1999; 99US-0157137P.

PR 03-NOV-1999; 99US-0163280P.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Barash SC, Birse CE, Rosen CA;

DR WPI, 2001-235357/24.

DR P-PSDB; AAG73852.

PS Nucleic acids encoding 4277 human colon cancer-associated polypeptides,

PT useful for preventing, diagnosing and/or treating colorectal cancers.

CC Claim 1; Page 2451; 9803pp; English.

CC AAH33943 to AAH37195 and AAG7788 represent human colon

CC cancer-associated nucleic acid molecules (N) and proteins (P), where the

CC proteins are collectively known as colon cancer antigens. The colon

Query Match 84.5%; Score 768; DB 3; Length 2044;
 Best Local Similarity 99.8%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;
 Matches 818; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ATGGCGCTATCCGGGTGACACCCCGCCGCTGCTGGAGAGAGATGAGTGCCTGACATAC 60
DB 121 ATGGCGCTATCCGGGTGACACCCCGCCGCTGCTGGAGAGAGATGAGTGCCTGACATAC 180
QY 61 TACGGGATGCTGCTGCTTACCGTATGTTGAGAGTGTGGGGGGGCAATGACCGAGTGC 120
DB 181 TACGGGATGCTGCTGCTTACCGTATGTTGAGAGTGTGGGGGGGCAATGACCGAGTGC 240
QY 121 GAGCTGGAGCTCTGGCCTTTGCTGATGATGAGGCTCTGGGCGCGCGAGAGCTTAAGCC 180
DB 241 GAGCTGGAGCTCTGGCCTTTGCTGATGATGAGGCTCTGGGCGCGCGAGAGCTTAAGCC 300
QY 181 CGGGCCCGGAGCGGCTTAGAGCTCTGCTGAGCTGAGACCGCGCGCGGAGTGGCGAG 240
DB 301 CGGGCCCGGAGCGGCTTAGAGCTCTGCTGAGCTGAGACCGCGCGCGGAGTGGCGAG 360
QY 241 AGCAACTGCGGCTGTGGGGCACTCTGCGGCTGCTGGCCCGCAGACCTGCTGCCG 300
DB 361 AGCAACTGCGGCTGTGGGGCACTCTGCGGCTGCTGGCCCGCAGACCTGCTGCCG 420
QY 301 CACCTGGCGCGGAGCGGCGCGCGCGGCGGCTCCAGAACGCTATGATAGGCACTCC 360
DB 421 CACCTGGCGCGGAGCGGCGCGCGCGGCGGCTCCAGAACGCTATGATAGGCACTCC 480
QY 361 AGCTCTTCAAGAGAGACAGAGGGTATGCTGCTGCGGCTGCGGAGTCAAGAGCTTGTGA 420
DB 481 AGCTCTTCAAGAGAGACAGAGGGTATGCTGCTGCGGCTGCGGAGTCAAGAGCTTGTGA 540
QY 421 AATTCTCAGACAGGCTGATGTTGGAGAGACGCTCCCCCAACCAAGCGGCGCGGAGT 480
DB 541 AATTCTCAGACAGGCTGATGTTGGAGAGACGCTCCCCCAACCAAGCGGCGCGGAGT 600
QY 481 CGGGGCGCGGCGGAGTGTGGTGCAGACGCGCGCGGAGAGGGGCGCGACCGGACCCAG 540
DB 601 CGGGGCGCGGCGGAGTGTGGTGCAGACGCGCGCGGAGAGGGGCGCGACCGGACCCAG 660
QY 541 CAGCAGTCAAGAGCCCGCAGACCTTCTCTGAAGGCAAGTGAATTGTGACATCCGGCTC 600
DB 661 CAGCAGTCAAGAGCCCGCAGACCTTCTCTGAAGGCAAGTGAATTGTGACATCCGGCTC 720
QY 601 CGGGTTCAGACAGATGCTGCTGCAAGCATGAGGCCAGCTTGGAGCAGGGCGTGCATCCG 660
DB 721 CGGGTTCAGACAGATGCTGCTGCAAGCATGAGGCCAGCTTGGAGCAGGGCGTGCATCCG 780
QY 661 CGGGCCCGGAGCGCTGGCGGGGAGCTGAGCGTGTGGGAGGCGACCGAGTGCAGCC 720
DB 781 CGGGCCCGGAGCGCTGGCGGGGAGCTGAGCGTGTGGGAGGCGACCGAGTGCAGCC 840
QY 721 TCAAGGAGCTGAGGCTCTGTGTTGTGATCAATCAAGTCTCAGAGCTCTTATCTGAGC 780
DB 841 TCAAGGAGCTGAGGCTCTGTGTTGTGATCAATCAAGTCTCAGAGCTCTTATCTGAGC 900
QY 781 GCGTTCGAGGCGAGCTAAGTGAAGTGGCGCGCTGCTGAG 819
DB 901 GCGTTCGAGGCGAGCTAAGTGAAGTGGCGCGCTGCTGAG 939

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RESULT 11

AA62603 standard; cDNA; 1966 BP.

AA62603;

14-FEB-2002 (first entry)

CDNA sequence #390 encoding novel human secreted protein.

Human secreted protein; hyperproliferative disorder; autoimmune disorder;

KW immune deficiency disorder; blood disorder; inflammatory disorder;
 KW infectious disorder; gene therapy; antimicrobial; hepatotropic;
 KW immunosuppressive; antineumatic; ss.

OS Homo sapiens.

PN WO200177291-A2.

PD 18-OCT-2001.

PF 29-MAR-2001; 2001WO-US010485.

PR 06-APR-2000; 2000US-0195604P.

PA (GENY) GENETICS INST INC.

PI Wong GG, Clark HF, Fectel K, Agoelino MJ, Howes SH, Resnick RJ;
 PI Gulukota K, Graham JR;

DR MPI; 2002-010900/01.

XX New polynucleotides encoding secreted proteins useful for treating e.g.
 PT asthma, HIV and Crohn's disease.

XX Claim 1, Page 280; 391pp; English.

XX The present invention relates to the isolation of novel cDNA sequences
 CC which encode human secreted proteins. The cDNA sequences have been
 CC derived from a variety of human tissues. The invention also provides a
 CC method for producing proteins from these polynucleotide sequences. The
 CC proteins are useful for identifying compounds that modulate their
 CC activity and production, and the cell is also useful for identifying
 CC compounds that modulate expression of the polynucleotide sequences
 CC encoding the secreted proteins. The sequences of the invention are useful
 CC for treating diseases such as hyperproliferative disorders (e.g. cancer),
 CC immune deficiency disorders (e.g. severe combined immunodeficiency
 CC (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders
 CC (e.g. thrombocytopenia), inflammatory disorders (e.g. arthritis) and
 CC infectious disorders (e.g. hepatitis). The polynucleotide sequences of
 CC the invention are also useful in gene therapy. AA62214-AA62838
 CC represent the cDNA sequences of the invention that encode for novel human
 CC secreted proteins

XX Sequence 1966 BP; 356 A; 618 C; 614 G; 378 T; 0 U; 0 Other;

QY Query Match 59.2%; Score 538; DB 6; Length 1966;

Best Local Similarity 99.8%; Pred. No. 2.9e-236;

Matches 588; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 ATGGCGCTATCCGGGTGACACCCCGCCGCTGCTGGAGAGAGATGAGTGCCTGACATAC 60
DB 50 ATGGCGCTATCCGGGTGACACCCCGCCGCTGCTGGAGAGAGATGAGTGCCTGACATAC 109
QY 61 TACGGGATGCTGCTGCTTACCGTATGTTGAGAGTGTGGGGGGGCAATGACCGAGTGC 120
DB 110 TACGGGATGCTGCTGCTTACCGTATGTTGAGAGTGTGGGGGGGCAATGACCGAGTGC 169
QY 121 GAGCTGGAGCTCTGGCCTTTGCTGATGATGAGGCTCTGGGCGCGCGAGAGCTTAAGCC 180
DB 170 GAGCTGGAGCTCTGGCCTTTGCTGATGATGAGGCTCTGGGCGCGCGAGAGCTTAAGCC 229
QY 181 CGGGCCCGGAGCGGCTTAGAGCTCTGCTGAGCTGAGACCGCGCGGAGTGGCGAG 240
DB 230 CGGGCCCGGAGCGGCTTAGAGCTCTGCTGAGCTGAGACCGCGCGGAGTGGCGAG 289
QY 241 AGCAACTGCGGCTGTGGGGCACTCTGCGGCTGCTGGCCCGCAGACCTGCTGCCG 300
DB 290 AGCAACTGCGGCTGTGGGGCACTCTGCGGCTGCTGGCCCGCAGACCTGCTGCCG 349
QY 301 CACCTGGCGCGGAGCGGCGCGGCGGAGTGTCTCCAGAACGCTATGATAGGCACTTCC 360
DB 350 CACCTGGCGCGGAGCGGCGCGGCGGAGTGTCTCCAGAACGCTATGATAGGCACTTCC 409

```


QY 361 AGCTCTTCAAGAGACAGAGGTAAGTCTCCCTCCGCTGCGAGTCAAGCACTTCTGCA 420
DB 410 AACTCTTTCAAGAGACAGAGGTAAGTCTCCCTCCGCTGCGAGTCAAGCACTTCTGCA 469
QY 421 AATTCTCAGCAGAGGTCAGTGGAGACAGAGCTCCCTCCCAAGCGAGCGAGGAGT 480
DB 470 AATTCTCAGCAGAGGTCAGTGGAGACAGAGCTCCCTCCCAAGCGAGCGAGGAGT 529
QY 481 CGGGGCGGGCCGAGTGTGTGTCAGACCGGCGGAGAGGGGCGCCAGCCGACCCGAG 540
DB 530 CGGGGCGGGCCGAGTGTGTGTCAGACCGGCGGAGAGGGGCGCCAGCCGACCCGAG 589
QY 541 CAGCAGTCAGAGAGCCCGGACGACCTTCTCTGAAGGCAAGTACCTGTG 589
DB 590 CAGCAGTCAGAGAGCCCGGACGACCTTCTCTGAAGGCAAGTACCTGTG 638

RESULT 12
AAH99646
ID AAH99646 standard; cDNA; 1570 BP.
XX
AC AAH99646;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human protein encoding cDNA sequence SEQ ID NO:481.
XX
XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW antiinflammatory; antineumatic; antiallergic; immunosuppressive;
KW antibacterial; endocrine; cardiac; central nervous system; vincide;
KW anti-HIV; fungicide; antimutagen; cardiovascular; antianemic; anaemia;
KW antiagregant; haemostatic; vulnery; antidiabetic; osteopathic; eczema;
KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
KW immunomodulator; gene therapy; antisense therapy; vaccine; inflammation;
KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW genetic diseases; haematopoietic disorder; platelet disorder; asthma;
KW thrombocytopenia; osteoporosis; severe combined immunodeficiency;
KW allergic rhinitis; diabetes; multiple sclerosis; depression;
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW neurological disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200153455-A2.
XX
PD 26-JUL-2001.
XX
PF 22-DEC-2000; 2000WO-US035017.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Dirmannac RT;
XX
XX WPI; 2001-457603/49.
DR P-PSDB; AAM25705.
XX
PT Isolated human polynucleotides encoding polypeptides, useful for the
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
XX
XX Claim 1; Page 552; 1217bp; English.
XX
XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC AAM25963. The proteins can have activities based on the tissues and cells
CC they are expressed in, such as: antiinflammatory; antirheumatic;
CC antiallergic; immunosuppressive; antibacterial; endocrine; cardiac;
CC central nervous system; vincide; anti-HIV; fungicide; antimutagen;
CC cardiovascular; antianemic; antiagregant; haemostatic; vulnery;

CC antiulcer; osteopathic; dermatological; antiallergic; antiaesthetic;
CC antidiabetic; cyostatic; neuroprotective; antidepressant; nootropic;
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production. The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders
XX
SQ Sequence 1570 BP; 311 A; 488 C; 466 G; 305 T; 0 U; 0 Other;
Query Match 58.4%; Score 531; DB 4; Length 1570;
Best Local Similarity 99.8%; Pred. No. 4.7e-233;
Matches 581; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 328 GTGCTCCAGAACGCTATAGCTATAGGCACTCCAGCTCTTCAAGAGACAGAGGTAAGC 387
DB 76 GTGCTCCAGAACGCTATAGCTATAGGCACTCCAGCTCTTCAAGAGACAGAGGTAAGC 135
QY 388 TGCCGTCCGCTGCGAGTCAAGAGTTCGCAATTCTCAGCAGGTCAGTGGAGACA 447
DB 136 TGCCGTCCGCTGCGAGTCAAGAGTTCGCAATTCTCAGCAGGTCAGTGGAGACA 195
QY 448 GCTTCCCTCCCAACCAAGCGGAGCGGAGTGGGGCGGCCCAAGTGTGTGCCAGA 507
DB 196 GCTTCCCTCCCAACCAAGCGGAGCGGAGTGGGGCGGCCCAAGTGTGTGCCAGA 255
QY 508 CGGCGGCGAGAGGGGGCGCCGACCGGACCCAGAGAGAGTGAAGCCCGGACGCTTCC 567
DB 256 CGGCGGCGAGAGGGGGCGCCGACCGGACCCAGAGAGAGTGAAGCCCGGACGCTTCC 315
QY 568 TCTGAAGCAAAAGTGAAGCTGTGAATCCGAGTCCGGGTTTCAGAGAGTACTGAGAGCAT 627
DB 316 TCTGAAGCAAAAGTGAAGCTGTGAATCCGAGTCCGGGTTTCAGAGAGTACTGAGAGCAT 375
QY 628 GGGGCAAGCTTGGAGACAGAGGCGTGGCATCCGGGGGCGCCAGGCGCTGGCCGAGCTG 687
DB 376 GGGGCAAGCTTGGAGACAGAGGCGTGGCATCCGGGGGCGCCAGGCGCTGGCCGAGCTG 435
QY 688 GACGCTTTGGAGAGGCGGACCGAGTGTGGCTCAAGAGGACCTGGGCTGTGGTTTGT 747
DB 436 GACGCTTTGGAGAGGCGGACCGAGTGTGGCTCAAGAGGACCTGGGCTGTGGTTTGT 495
QY 748 GACATCAAGTTCGAGAGCTTCTCTATCTGAGACGCTTCTGGGGCGACTACTGAGTGGC 807
DB 496 GACATCAAGTTCGAGAGCTTCTCTATCTGAGACGCTTCTGGGGCGACTACTGAGTGGC 555
QY 808 GCCCTGTGCAAGGCGCTGCGGGGCGTGTCTCTGACTGAGGCGCTTCCAGAGGCTGTGGGC 867
DB 556 GCCCTGTGCAAGGCGCTGCGGGGCGTGTCTCTGACTGAGGCGCTTCCAGAGGCTGTGGGC 615
QY 868 CGGAGAGCTGTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 909
DB 616 CGGAGAGCTGTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 657

RESULT 13
AAH07925
ID AAH07925 standard; cDNA; 626 BP.
XX
AC AAH07925;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA clone (5'-primer) SEQ ID NO:4760.
XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX Homo sapiens.
XX EPI074617-A2.
XX 07-FEB-2001.
XX 28-JUL-2000; 2000BP-00116126.
XX 29-JUL-1999; 990P-00248036.
PR 27-AUG-1999; 990P-00300253.
PR 11-JAN-2000; 2000JP-0018776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX (HELI-) HELIX RES INST.
XX Ota T, Isegai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-length CDNA defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNA.
XX Claim 1; SEQ ID NO 4760; 2537pp + Sequence listing; English.
XX The present invention describes primer sets for synthesizing 5602 full-length CDNA defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length CDNA. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length CDNA. The primers allow obtaining of the full-length
CC CDNA easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human CDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
XX Sequence 626 BP; 102 A; 207 C; 216 G; 98 T; 0 U; 3 Other;
SQ
XX
XX Query Match 36.7%; Score 334; DB 4; Length 626;
XX Best Local Similarity 99.7%; Pred. No. 9.2e-143;
XX Matches 384; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGGGCGTATCCGGTGCAGCCCGGCGCCGCTGCTGGAGAGAGATGCTCTGACTAC 60
DB 88 ATGGGCGTATCCGGTGCAGCCCGGCGCCGCTGCTGGAGAGAGATGCTCTGACTAC 147
QY 61 TACGGGATCTCTGCTTACCGTATGTTGAGAGTGTGGGGGGAACATGACCGAGTCC 120
DB 148 TACGGGATCTCTGCTTACCGTATGTTGAGAGTGTGGGGGGAACATGACCGAGTCC 207
QY 121 GAGCTGAGACTCTGCTGCTTTCGCTGAGTAGAGGCTCTGAGCGCGCGAGAGGCTTAGCC 180
DB 208 GAGCTGAGACTCTGCTGCTTTCGCTGAGTAGAGGCTCTGAGCGCGCGAGAGGCTTAGCC 267
QY 181 CGGGCCCGGAGCGGCTTAGAGCTCTGCTGAGCTGAGAGCGCGCGGAGAGTGCAGCGAG 240

DB 268 CGGGCCCGAGCGGCTTAGAGCTCTGCTGAGAGTGCAGCGCGCGGAGTGCAGCAG 327
QY 241 AGCAACTGCGGCTGCTGCTGAGCAACTCTGCGCGTGTGCGCCGCGAGCACTGTGCGG 300
DB 328 AGCAACTGCGGCTGCTGCTGAGCAACTCTGCGCGTGTGCGCCGCGAGCACTGTGCGG 387
QY 301 CACCTGCGCGCGAGCGGCGCGGCGGCACTGTCTCCAGAACGCTATAGTATGACACTCC 360
DB 388 CACCTGCGCGCGAGCGGCGCGGCGGCACTGTCTCCAGAACGCTATAGTATGACACTCC 447
QY 361 AGCTTTCAAGAGAGAGAGAGGTA 385
DB 448 AGCTTTCAAGAGAGAGAGAGGTA 472
RESULT 14
AA160747/c
ID AA160747 standard; CDNA, 1042 BP.
XX AA160747;
AC
XX
XX 22-OCT-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 4736.
DE
XX Human; nootropic; immunosuppressant; cyostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200153312-A1.
PN
XX
XX 26-JUL-2001.
PD
XX
XX 26-DEC-2000; 2000MO-US034263.
PF
XX
XX 23-DEC-1999; 990US-00471275.
PR
XX 21-JAN-2000; 2000US-00488725.
PR
XX 25-APR-2000; 2000US-0052317.
PR
XX 20-JUN-2000; 2000US-00598042.
PR
XX 19-JUL-2000; 2000US-00620312.
PR
XX 03-AUG-2000; 2000US-00653450.
PR
XX 14-SEP-2000; 2000US-00662191.
PR
XX 19-OCT-2000; 2000US-00693036.
PR
XX 29-NOV-2000; 2000US-00727344.
XX
XX (HSE-) HSESEQ INC.
PA
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Dimaenac RT;
XX
XX WPI: 2001-442253/47.
DR P-PSDB; AAH41591.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
XX as central nervous system injuries.
XX
XX Claim 1; SEQ ID NO 4736; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and the
XX encoded polypeptides (AAM38642-AAH42213) with nootropic,
XX immunosuppressant and cyostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

CC Utilization of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

XX Sequence 1042 BP, 182 A; 318 C; 334 G; 208 T; 0 U; 0 Other;

Query Match 30.9%; Score 281; DB 4; Length 1042;

Best Local Similarity 99.3%; Pred. No. 1.7e-118;

Matches 431; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGGCTATCCGGGTCCACCCCGGCGCTGCTGGAGAGAGATGAGTCTGACTAC 60
DB 955 ATGGGCTATCCGGGTCCACCCCGGCGCTGCTGGAGAGAGATGAGTCTGACTAC 896
QY 61 TACGGGATGCTGTCTTCACCGTATGTTGAGTGTGGGGGCACTGACGAGTGC 120
DB 895 TACGGGATGCTGTCTTCACCGTATGTTGAGTGTGGGGGCACTGACGAGTGC 836
QY 121 GAGCTGAGCTCTGCTGCTTCTGCTGATGAGAGCTCTGCGCGCGAGGCTTACGC 180
DB 835 GAGCTGAGCTCTGCTGCTTCTGCTGATGAGAGCTCTGCGCGCGAGGCTTACGC 776
QY 181 CGGGCCCGCAGCGGCTTGAAGCTCTGCTGAGCTGAGCGCGCGGCACTGCGGCGAG 240
DB 775 CGGGCCCGCAGCGGCTTGAAGCTCTGCTGAGCTGAGCGCGCGGCACTGCGGCGAG 716
QY 241 AGCAACTGCGGCTCTGGGGGCACTCCGCGCGGCTGCGCGCGCACTGCTGCGCG 300
DB 715 AGCAACTGCGGCTCTGGGGGCACTCCGCGCGGCTGCGCGCGCACTGCTGCGCG 656
QY 301 CACCTGCGCGCAGCGGCGCGCGCAGTGTCTCCAGAACGCTATAGTATGCACTCC 360
DB 655 CACCTGCGCGCAGCGGCGCGCGCAGTGTCTCCAGAACGCTATAGTATGCACTCC 596
QY 361 AGCTTTTCAAGAGAGACAGAGGTAGCTGCGCTGCGCGCTGCAAGCACTTCTGCA 420
DB 595 AGCTTTTCAAGAGAGACAGAGGTAGCTGCGCTGCGCGCTGCAAGCACTTCTGCA 536
QY 421 AATTCTCAGCAGGG 434
DB 535 AATTCTCAGCAGGG 522

RESULT 15

AA158961 standard; cDNA; 1067 BP.

AC AA158961;

DT 22-OCT-2001 (first entry)

DE Human polynucleotide SEQ ID NO 1164.

XX Human; nocotropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia; ss.

OS Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

PR 21-JAN-2000; 2000US-00488725.

PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

XX Tang YF, Liu C, Aundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
XX Zhou P, Goodrich R, Dermanac RT;

XX WPI; 2001-442253/47.

XX P-PEDB; AAM39805.

PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.

PS Claim 1; SEQ ID NO 1164; 10078pp; English.

CC The invention relates to human nucleic acids (AA157928-AA161369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nocotropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localized neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC inhibition of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

XX Sequence 1067 BP, 191 A; 349 C; 328 G; 199 T; 0 U; 0 Other;

Query Match 30.9%; Score 281; DB 4; Length 1067;

Best Local Similarity 99.3%; Pred. No. 1.7e-118;

Matches 431; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGGCTATCCGGGTCCACCCCGGCGCTGCTGGAGAGAGATGAGTCTGACTAC 60
DB 151 ATGGGCTATCCGGGTCCACCCCGGCGCTGCTGGAGAGAGATGAGTCTGACTAC 210
QY 61 TACGGGATGCTGTCTTCACCGTATGTTGAGAGTGTGGGGGCACTGACGAGTGC 120
DB 211 TACGGGATGCTGTCTTCACCGTATGTTGAGAGTGTGGGGGCACTGACGAGTGC 270
QY 121 GAGCTGAGCTCTGCGCTTCTGCTGATGAGAGCTCTGCGCGCGCGAGGCTTACGC 180
DB 271 GAGCTGAGCTCTGCGCTTCTGCTGATGAGAGCTCTGCGCGCGCGAGGCTTACGC 330
QY 181 CGGGCCCGCAGCGGCTTGAAGCTCTGCTGAGCTGAGCGCGCGGCACTGCGGCGAG 240
DB 331 CGGGCCCGCAGCGGCTTGAAGCTCTGCTGAGCTGAGCGCGCGGCACTGCGGCGAG 390
QY 241 AGCAACTGCGGCTCTGCGGCAACTCTGCTGCGCTGCTGCGCGCGCACTGCTGCGG 300
DB 391 AGCAACTGCGGCTCTGCGGCAACTCTGCTGCGCTGCTGCGCGCGCACTGCTGCGG 450
QY 301 CACCTGCGCGCAGCGGCGCGCGCGCAGTGTCTCCAGAACGCTATAGTATGAGCACTCC 360
DB 451 CACCTGCGCGCAGCGGCGCGCGCGCAGTGTCTCCAGAACGCTATAGTATGAGCACTCC 510
QY 361 AGCTTTTCAAGAGAGACAGAGGTAGCTGCGCTGCGCGCGCAGTCAAGCACTTCTGCA 420
DB 511 AGCTTTTCAAGAGAGACAGAGGTAGCTGCGCTGCGCGCGCAGTCAAGCACTTCTGCA 570
QY 421 AATTCTCAGCAGGG 434

Db |||||||
571 AATCTCAGCAGG 584

Search completed: February 12, 2005, 13:53:46
Job time : 484 secs

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OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 13:34:28 ; Search time 2502 Seconds
(without alignments)
13829.105 Million cell updates/sec

Title: US-10-030-271-1

Perfect score: 909
Sequence: 1 atggcgatccgcgggtcgac.....tcagtgatgagcgac 909

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 1903134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	858	94.4	1053	3	CR604307 full-length
2	858	94.4	1860	3	CR593642 full-length
3	858	94.4	1866	3	CR619301 full-length
4	858	94.4	1894	3	CR625070 full-length
5	607	66.8	1090	3	BM920838
6	586	64.5	800	4	BG685173
7	582	64.0	634	4	B1907024 603064980
8	582	64.0	905	4	B1910528 603068215
9	582	64.0	927	4	BG251151 602364954
10	582	64.0	947	4	B1910416 603068087
11	582	64.0	1062	5	BM908148 AGENCOURT
12	582	64.0	1131	2	BE907425 601500161
13	582	64.0	1510	3	CR599685 full-length
14	582	64.0	1586	3	CR590827 full-length
15	558	61.4	1089	5	BM925969 AGENCOURT
16	532	58.5	655	7	CK429257 OJ34512.Y
17	531	58.4	644	7	CN373290 170004241
18	531	58.4	993	4	BM559141 AGENCOURT
19	531	58.4	1051	5	BO073197 AGENCOURT
20	531	58.4	1161	5	BU902131 AGENCOURT
21	521	57.3	569	5	BP306442
22	515	56.7	793	5	BE883568 601508040
23	508	55.9	654	2	BE391120 601286078
24	506	55.7	506	2	BF656546 602119860

25	502	55.2	678	7	CN373294	CN373294 170005999
26	500	55.0	731	5	BQ923358	BQ923358 AGENCOURT
27	480	52.8	783	5	BU602002	BU602002 AGENCOURT
28	476	52.4	718	4	B1117988	B1117988 602867244
29	471	51.8	671	7	CN373287	CN373287 170004251
30	458	50.4	577	7	CN373291	CN373291 170004250
31	454	49.9	991	5	BQ956773	BQ956773 AGENCOURT
32	453	49.8	832	4	B1827768	B1827768 603075430
33	450	49.5	1028	5	BM928759	BM928759 AGENCOURT
34	450	49.5	1033	5	BM922715	BM922715 AGENCOURT
35	446	49.1	586	5	BP343733	BP343733 BP343733
36	446	49.1	780	6	CB994488	CB994488 AGENCOURT
37	442	48.6	831	6	CB992627	CB992627 AGENCOURT
38	440	48.4	1042	5	BQ072022	BQ072022 AGENCOURT
39	435	47.9	931	5	BX381775	BX381775 BX381775
40	432	47.5	580	5	BP211545	BP211545 BP211545
41	429	47.2	583	5	BP305292	BP305292 BP305292
42	427	47.0	817	6	CB990003	CB990003 AGENCOURT
43	426	46.9	891	5	BK458265	BK458265 BX458265
44	417	45.9	938	5	BU507654	BU507654 AGENCOURT
45	415	45.7	1151	5	BO947706	BO947706 AGENCOURT
46	410	45.1	837	4	B1769587	B1769587 603054964
47	407	44.8	1233	4	BM547754	BM547754 AGENCOURT
48	403	44.3	582	5	BP253687	BP253687 BP253687
49	393	43.2	402	7	CN373296	CN373296 170005999
50	388	42.7	425	7	AN245758	AN245758 2822785..5
51	387	42.6	826	6	CB991766	CB991766 AGENCOURT
52	385	42.4	1428	5	BM960582	BM960582 BP360582
53	385	42.4	1428	5	BM960670	BM960670 AGENCOURT
54	384	42.2	680	4	BG340752	BG340752 602462347
55	383	42.1	586	4	BM126446	BM126446 1F06C09.Y
56	381	41.9	573	5	BP352691	BP352691 BP352691
57	380	41.8	495	7	CR746989	CR746989 CR746989
58	380	41.8	567	6	CB154807	CB154807 K-EST0212
59	378	41.6	527	4	BM837565	BM837565 K-EST0113
60	375	41.3	643	7	CN373297	CN373297 170006000
61	372	40.9	586	5	BP254070	BP254070 BP254070
62	372	40.9	1313	5	BQ709748	BQ709748 AGENCOURT
63	368	40.5	657	7	CN373295	CN373295 170006000
64	368	40.5	1043	5	BU180173	BU180173 AGENCOURT
65	367	40.4	824	6	CB989607	CB989607 AGENCOURT
66	362	39.8	583	5	BP304786	BP304786 BP304786
67	353	38.8	690	4	BG706385	BG706385 602669711
68	349	38.4	574	7	CK819032	CK819032 1F06C09.Y
69	349	38.4	842	4	B1752583	B1752583 603028419
70	344	37.8	581	5	BP333294	BP333294 BP333294
71	343	37.7	878	4	B1756130	B1756130 603030029
72	340	37.4	479	7	CN373293	CN373293 170006000
73	334	36.7	474	4	BM700298	BM700298 UI-E-DW1-
74	325	35.8	415	7	CN373288	CN373288 170005326
75	302	33.2	465	6	CB153442	CB153442 K-EST0210
76	300	33.0	799	4	BG681575	BG681575 602628062
77	299	32.9	684	7	CN373289	CN373289 170006000
78	297	32.7	926	4	BG757042	BG757042 602710464
79	286	31.5	561	7	CN373292	CN373292 170004705
80	285	31.4	546	4	BM849284	BM849284 K-EST0129
81	285	31.4	549	4	BM853352	BM853352 K-EST0134
82	285	31.4	623	4	BG819012	BG819012 602781053
83	275	30.3	496	4	BG180215	BG180215 602329820
84	268	29.5	522	4	BM147424	BM147424 TCAAP1011
85	266	29.3	1046	5	BK342837	BK342837 7F65604.X
86	262	28.8	583	2	BE856624	BE856624 7F65604.X
87	262	28.8	587	5	BP306585	BP306585 BP306585
88	262	28.8	1481	5	BO071492	BO071492 AGENCOURT
89	254	27.9	421	6	CB153158	CB153158 K-EST0210
90	235	25.9	872	4	CB107743	CB107743 K-EST0147
91	235	25.9	872	4	BI253561	BI253561 603175851
92	235	25.9	872	4	BI757389	BI757389 603029320
93	230	25.3	532	2	BM837877	BM837877 K-EST0114
94	219	24.1	823	2	BE785785	BE785785 601478567
95	216	23.8	855	2	BE797255	BE797255 601507614
96	210	23.1	1021	5	BK384448	BK384448 BX384448
97	209	23.0	951	5	BK375652	BK375652 BX375652

98	204	22.4	993	4	BC766140	BC766140	602738347	171	31	3.4	884	4	BT151137	BT151137	602917084
99	188	20.7	762	4	BT600659	BT600659	603247545	C 172	30	3.3	161	2	AW794030	AW794030	MR1-UM000
100	173	19.0	924	5	BX442929	BX442929	BX442929	173	30	3.3	496	2	BF041764	BF041764	BP2500050
101	172	18.9	756	1	AL562850	AL562850	AL562850	174	30	3.3	650	6	CB557769	CB557769	AMGNNUC:M
102	169	18.6	951	4	BG122215	BG122215	602349767	175	30	3.3	821	7	CK598082	CK598082	AGENCOURT
103	166	18.3	635	2	BP339818	BP339818	602038892	176	29	3.2	333	5	BY348107	BY348107	BY348107
104	165	18.2	570	5	BP370313	BP370313	BP370313	177	29	3.2	340	5	BY351863	BY351863	BY351863
105	163	17.9	340	4	BM149931	BM149931	TCAP3011	178	29	3.2	344	5	BY184868	BY184868	BY184868
106	154	16.9	358	4	BM706675	BM706675	UI-E-COO-	179	29	3.2	346	6	CB693072	CB693072	AGENCOURT
107	154	16.9	371	4	BM706666	BM706666	UI-E-COO-	180	29	3.2	346	6	BY348272	BY348272	BY348272
108	148	16.3	974	6	CB130725	CB130725	K-EST0180	181	29	3.2	351	5	BY353184	BY353184	BY353184
109	146	16.1	206	5	BX328374	BX328374	BX328374	182	29	3.2	373	2	BB844365	BB844365	BB844365
110	145	16.0	763	4	BT520263	BT520263	603071122	183	29	3.2	379	2	BY023438	BY023438	BY023438
111	144	15.8	702	4	BG393347	BG393347	602411571	184	29	3.2	463	5	AM229739	AM229739	AM229739
112	143	15.7	469	5	BQ361597	BQ361597	RC4-OT024	185	29	3.2	474	5	BY255034	BY255034	BY255034
113	142	15.6	1192	5	BU190812	BU190812	AGENCOURT	186	29	3.2	476	2	AM227145	AM227145	AM227145
114	143	14.6	1129	5	BX372293	BX372293	BX372293	187	29	3.2	543	2	BE628235	BE628235	BE628235
115	133	14.6	1267	5	BM925194	BM925194	AGENCOURT	188	29	3.2	645	5	BD109330	BD109330	BD109330
116	129	14.2	642	2	BE781207	BE781207	601469135	189	29	3.2	673	4	BG963519	BG963519	BG963519
117	127	14.0	981	4	BM008603	BM008603	603618247	190	29	3.2	779	7	CK464017	CK464017	CK464017
118	120	13.2	874	1	AL519410	AL519410	AL519410	191	29	3.2	792	7	CO393836	CO393836	CO393836
119	120	13.2	200	2	BE242821	BE242821	TCAP1E21	192	29	3.2	802	4	BI649594	BI649594	BI649594
120	111	12.2	244	4	BM695503	BM695503	UI-E-COI-	193	29	3.2	900	6	CB589155	CB589155	CB589155
121	111	12.2	1146	4	BE870610	BE870610	601447719	194	28	3.1	240	9	CR185950	CR185950	CR185950
122	104	11.4	304	1	AA090354	AA090354	Y0170-Seq	195	27	3.0	361	4	BR837318	BR837318	BR837318
123	90	9.9	1123	5	BQ330921	BQ330921	AGENCOURT	196	25	2.8	334	4	AM158134	AM158134	AM158134
124	89	9.8	217	1	AA218681	AA218681	ZQ9608.r	197	25	2.8	404	2	AM159003	AM159003	AM159003
125	88	9.7	306	4	BM149218	BM149218	TCAP2011	198	25	2.8	525	8	BR860059	BR860059	BR860059
126	88	9.7	554	5	BX374863	BX374863	BX374863	199	25	2.8	771	7	CK803280	CK803280	CK803280
127	88	9.7	1091	5	BM150154	BM150154	TCAP5011	200	25	2.8	775	7	CY117797	CY117797	CY117797
128	84	9.2	224	4	AO171450	AO171450	HS_3073_A	201	25	2.8	835	7	CN328654	CN328654	CN328654
129	79	8.7	553	8	BI771166	BI771166	603054864	202	25	2.8	948	6	CD254010	CD254010	CD254010
130	77	8.5	916	2	BF695740	BF695740	601852476	203	25	2.8	1051	5	BX354590	BX354590	BX354590
131	77	8.5	915	2	AA725300	AA725300	a112b07.s	204	25	2.8	1061	5	BX374728	BX374728	BX374728
132	65	7.2	466	1	BF174916	BF174916	MYEA045.M	205	23	2.5	386	6	CB806813	CB806813	CB806813
133	61	7.2	122	2	BP233168	BP233168	602023718	206	23	2.5	419	6	CB799420	CB799420	CB799420
134	56	6.2	622	2	BY47525	BY47525	BY47525	207	23	2.5	539	1	AL925092	AL925092	AL925092
135	56	6.2	670	6	BQ951680	BQ951680	AGENCOURT	208	23	2.5	632	4	BM534241	BM534241	BM534241
136	56	6.2	769	5	AK011713	AK011713	Mus muscu	209	23	2.5	638	6	CA334090	CA334090	CA334090
137	56	6.2	898	5	AK089096	AK089096	Mus muscu	210	23	2.5	650	6	CD596064	CD596064	CD596064
138	56	6.2	1017	3	AU296471	AU296471	AU296471	211	23	2.5	684	7	CN083958	CN083958	CN083958
139	55	6.1	1199	3	BP158001	BP158001	BP158001	212	23	2.5	811	7	CP661528	CP661528	CP661528
140	55	6.1	820	1	BG404101	BG404101	602420009	213	22	2.4	1079	9	CI021177	CI021177	CI021177
141	55	5.9	1166	5	BX342836	BX342836	602420009	214	22	2.4	331	5	BY347412	BY347412	BY347412
142	54	5.7	1618	5	AK010701	AK010701	Mus muscu	215	22	2.4	422	1	AA511237	AA511237	AA511237
143	51	5.6	1025	6	BY101117	BY101117	BY101117	216	22	2.4	982	4	BG419147	BG419147	BG419147
144	50	5.5	1641	3	CD471681	CD471681	LeukoSE_4	217	21	2.3	251	2	BB606071	BB606071	BB606071
145	50	5.5	555	6	CK837899	CK837899	4063095.B	218	21	2.3	334	7	CP649266	CP649266	CP649266
146	44	4.8	706	7	BY1010940	BY1010940	PM2-UM005	219	21	2.3	362	5	BP147125	BP147125	BP147125
147	41	4.5	1017	6	BI048697	BI048697	UI-H-BT3-	220	21	2.3	373	5	CG289307	CG289307	CG289307
148	41	4.5	187	4	AM449244	AM449244	UI-H-BT3-	221	21	2.3	459	9	CG289316	CG289316	CG289316
149	40	4.4	383	2	BT108561	BT108561	602895012	222	21	2.3	459	9	CG289307	CG289307	CG289307
150	40	4.4	384	2	BB641783	BB641783	AGENCOURT	223	21	2.3	527	9	CG092204	CG092204	CG092204
151	38	4.2	763	4	BQ894996	BQ894996	Mus muscu	224	21	2.3	622	5	BP150734	BP150734	BP150734
152	38	4.2	935	5	BI151149	BI151149	602916901	225	21	2.3	676	6	CB647590	CB647590	CB647590
153	38	4.2	936	5	BX458264	BX458264	BX458264	226	21	2.3	819	9	CG298032	CG298032	CG298032
154	38	4.2	935	5	BX381774	BX381774	BX381774	227	21	2.3	855	9	CG298032	CG298032	CG298032
155	38	4.2	1008	5	BX375651	BX375651	BX375651	228	21	2.3	945	9	AI576572	AI576572	AI576572
156	36	4.0	935	5	BE666884	BE666884	150948.MA	229	20	2.2	197	1	BE096391	BE096391	BE096391
157	35	3.9	462	2	BE809924	BE809924	217308.MA	230	20	2.2	231	2	BE096761	BE096761	BE096761
158	35	3.9	545	2	CN787982	CN787982	4122243.B	231	20	2.2	288	2	BE095960	BE095960	BE095960
159	35	3.9	593	7	CK832751	CK832751	4056539.B	232	20	2.2	295	1	AI576594	AI576594	AI576594
160	35	3.9	634	7	CK956745	CK956745	4096973.B	233	20	2.2	327	2	BB096550	BB096550	BB096550
161	35	3.9	859	2	BF241187	BF241187	601880059	234	20	2.2	338	1	AI577932	AI577932	AI577932
162	33	3.6	859	2	BY234818	BY234818	BY234818	235	20	2.2	345	2	AM533372	AM533372	AM533372
163	33	3.5	378	5	BQ828297	BQ828297	LI61n2304	236	20	2.2	355	4	EM286915	EM286915	EM286915
164	32	3.5	537	5	CV106762	CV106762	AGENCOURT	237	20	2.2	360	1	AI574869	AI574869	AI574869
165	32	3.5	650	7	CK031162	CK031162	AGENCOURT	238	20	2.2	361	1	AM528910	AM528910	AM528910
166	32	3.5	735	7	CK838175	CK838175	4063565.B	239	20	2.2	377	1	AI602034	AI602034	AI602034
167	31	3.4	657	7	CK838175	CK838175	4063565.B	240	20	2.2	432	1	AI574862	AI574862	AI574862
168	31	3.4	657	7	CK838175	CK838175	4063565.B	241	20	2.2	432	1	AI574862	AI574862	AI574862
169	31	3.4	657	7	CK838175	CK838175	4063565.B	242	20	2.2	432	1	AI574862	AI574862	AI574862
170	31	3.4	657	7	CK838175	CK838175	4063565.B	243	20	2.2	432	1	AI574862	AI574862	AI574862

390	19	2.1	752	7	CF948639	CF948639	UI-M-HU-	463	18	2.0	79	9	CG712928	CG712928	111902960
391	19	2.1	753	4	BG769028	BG769028	602742963	464	18	2.0	88	9	CG799660	CG799660	111800380
392	19	2.1	759	4	AG030724	AG030724	Pan tlog1	465	18	2.0	90	9	CG708258	CG708258	1119008C0
393	19	2.1	766	9	AG581668	AG581668	Mus muscu	466	18	2.0	92	9	CG800743	CG800743	111801480
394	19	2.1	768	5	BX355175	BX355175	BX355175	467	18	2.0	92	9	CG708062	CG708062	1119005E0
395	19	2.1	777	7	CK306757	CK306757	SB02035A1	468	18	2.0	96	1	MA398502	MA398502	1119005E0
396	19	2.1	794	7	CN157609	CN157609	946327 MA	469	18	2.0	106	9	GG4270141	GG4270141	1119005E0
397	19	2.1	797	7	CN328875	CN328875	AGENCOURT	470	18	2.0	109	9	CG799342	CG799342	111801G1
398	19	2.1	799	6	CB997025	CB997025	AGENCOURT	471	18	2.0	117	9	CG733263	CG733263	111915B1
399	19	2.1	813	9	AL548800	AL548800	AL548800	472	18	2.0	118	6	CD942346	CD942346	1118014E1
400	19	2.1	830	6	CF994215	CF994215	AGENCOURT	473	18	2.0	118	6	CD955092	CD955092	1118014E1
401	19	2.1	834	6	CA496393	CA496393	AGENCOURT	474	18	2.0	118	6	CG728764	CG728764	1118014E1
402	19	2.1	839	5	AG314176	AG314176	Mus muscu	475	18	2.0	121	9	CG800161	CG800161	1118008A0
403	19	2.1	839	5	BUS09596	BUS09596	AGENCOURT	476	18	2.0	123	8	CG023002	CG023002	3591_1_32
404	19	2.1	842	4	BG763628	BG763628	602735842	477	18	2.0	129	9	CG712317	CG712317	1119025B1
405	19	2.1	844	8	CF243159	CF243159	AGENCOURT	478	18	2.0	131	9	CG800665	CG800665	1118014E1
406	19	2.1	845	8	BZ148659	BZ148659	CH230-441	479	18	2.0	132	9	CG712922	CG712922	1119029G0
407	19	2.1	847	4	BG296749	BG296749	602394512	480	18	2.0	132	9	CG716809	CG716809	1119046E0
408	19	2.1	850	4	BG919487	BG919487	602817686	481	18	2.0	132	9	CG724950	CG724950	1119083C0
409	19	2.1	851	1	AL549056	AL549056	AL549056	482	18	2.0	132	9	CG728665	CG728665	1119102D0
410	19	2.1	852	6	CA787600	CA787600	AGENCOURT	483	18	2.0	132	9	CG799158	CG799158	1118001A0
411	19	2.1	861	9	CG432941	CG432941	ZMBBCC004	484	18	2.0	132	9	CG806025	CG806025	1118006A0
412	19	2.1	866	9	CG671800	CG671800	OGUY755TV	485	18	2.0	132	9	CG806335	CG806335	1118068D1
413	19	2.1	867	5	BQ427693	BQ427693	AGENCOURT	486	18	2.0	133	9	CG716660	CG716660	1119046A0
414	19	2.1	871	1	AL528945	AL528945	AL528945	487	18	2.0	134	8	AZ577389	AZ577389	09C08 Sho
415	19	2.1	872	4	BG539339	BG539339	602567951	488	18	2.0	139	8	CG022559	CG022559	3591_1_2
416	19	2.1	874	8	BZ530271	BZ530271	OGAL1931C	489	18	2.0	139	8	CG713343	CG713343	1119031E0
417	19	2.1	884	9	CG836312	CG836312	ZMBBCC021	490	18	2.0	146	1	AL047726	AL047726	DXEP5860
418	19	2.1	886	5	BUS29064	BUS29064	AGENCOURT	491	18	2.0	148	9	CG037808	CG037808	3591_1_90
419	19	2.1	886	6	CD557530	CD557530	AGENCOURT	492	18	2.0	148	9	CG733081	CG733081	1118154A0
420	19	2.1	886	6	BX833398	BX833398	BX833398	493	18	2.0	149	9	CG716436	CG716436	1119045E0
421	19	2.1	900	6	CB994477	CB994477	AGENCOURT	494	18	2.0	149	9	CG725404	CG725404	1119085C0
422	19	2.1	918	4	BG770258	BG770258	602744843	495	18	2.0	151	8	AZ577701	AZ577701	13e12 Sho
423	19	2.1	923	5	BU148611	BU148611	AGENCOURT	496	18	2.0	151	9	CG716897	CG716897	1119046E0
424	19	2.1	924	5	CG370721	CG370721	OG2BES2TH	497	18	2.0	152	9	CG725510	CG725510	1119085E1
425	19	2.1	933	5	BU145513	BU145513	AGENCOURT	498	18	2.0	153	1	AT154457	AT154457	u601h10.r
426	19	2.1	940	7	CF664996	CF664996	AGENCOURT	499	18	2.0	155	8	CC021678	CC021678	3591_1_25
427	19	2.1	943	9	CNS03H95	CNS03H95	Tetraodon	500	18	2.0	155	7	CG801858	CG801858	1118025C1
428	19	2.1	944	9	CNS03H95	CNS03H95	AGENCOURT	501	18	2.0	156	7	CV306343	CV306343	1119085C0
429	19	2.1	950	5	BE900888	BE900888	601674304	502	18	2.0	156	7	CV306344	CV306344	1119085C0
430	19	2.1	951	2	BE900888	BE900888	601674304	503	18	2.0	156	9	CG728541	CG728541	111901E0
431	19	2.1	953	2	BE900888	BE900888	601674304	504	18	2.0	157	7	CV306373	CV306373	111901E0
432	19	2.1	956	2	BE900888	BE900888	601674304	505	18	2.0	157	7	CV306374	CV306374	111901E0
433	19	2.1	965	2	BE900888	BE900888	601674304	506	18	2.0	159	9	CG728541	CG728541	111901E0
434	19	2.1	975	2	BE900888	BE900888	601674304	507	18	2.0	160	9	CG799329	CG799329	1118001F0
435	19	2.1	1023	5	BQ115147	BQ115147	AGENCOURT	508	18	2.0	164	9	CG799335	CG799335	1118001F0
436	19	2.1	1037	1	AL551217	AL551217	AGENCOURT	509	18	2.0	166	6	CD733673	CD733673	4046433_1
437	19	2.1	1037	1	AL551217	AL551217	AGENCOURT	510	18	2.0	167	8	CG712894	CG712894	1119029F0
438	19	2.1	1078	1	AL533735	AL533735	AGENCOURT	511	18	2.0	167	8	CG712894	CG712894	1119029F0
439	19	2.1	1087	5	BX386150	BX386150	BX386150	512	18	2.0	169	4	BG089501	BG089501	u68f06.y
440	19	2.1	1088	9	CNS02MGM	CNS02MGM	Tetraodon	513	18	2.0	169	9	CG729632	CG729632	1119113G0
441	19	2.1	1109	5	BQ421980	BQ421980	AGENCOURT	514	18	2.0	170	8	CC023063	CC023063	3591_1_32
442	19	2.1	1112	8	BZ563120	BZ563120	pac82-164	515	18	2.0	171	8	CC029228	CC029228	3591_1_10
443	19	2.1	1127	5	BQ278930	BQ278930	AGENCOURT	516	18	2.0	171	9	CG799273	CG799273	1118001F0
444	19	2.1	1136	7	CR027826	CR027826	AGENCOURT	517	18	2.0	172	9	CG713168	CG713168	1119030F1
445	19	2.1	1188	3	CR721391	CR721391	Tetraodon	518	18	2.0	173	9	CG731635	CG731635	1119142E0
446	19	2.1	1195	5	BUS39777	BUS39777	AGENCOURT	519	18	2.0	176	8	CC028999	CC028999	3591_1_10
447	19	2.1	1195	5	AG053290	AG053290	Pan tlog1	520	18	2.0	177	8	CC020557	CC020557	3591_1_1
448	19	2.1	1217	8	BZ569571	BZ569571	pac82-164	521	18	2.0	182	9	CG729296	CG729296	1118001F0
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452	19	2.1	1411	3	CR7065329	CR7065329	Tetraodon	525	18	2.0	190	8	CC029499	CC029499	3591_1_11
453	19	2.1	2733	3	AK028295	AK028295	Mus muscu	526	18	2.0	191	8	CC021688	CC021688	3591_1_25
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456	18	2.0	72	8	CG725013	CG725013	1119083E1	529	18	2.0	198	9	CG713142	CG713142	1119045A0
457	18	2.0	74	8	CC032222	CC032222	3591_1_49	530	18	2.0	198	9	CG716712	CG716712	1119046B0
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459	18	2.0	74	9	CG729637	CG729637	1119113G1	532	18	2.0	199	9	CG728421	CG728421	1119100E0
460	18	2.0	77	9	CG725038	CG725038	1119083F1	533	18	2.0	199	9	CG728710	CG728710	1119102F0
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541	18	2.0	210	9	CG728623	1119102B0	C 614	18	2.0	319	7	W87133
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543	18	2.0	216	9	CG799456	1118002F0	C 616	18	2.0	321	5	BY446220
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546	18	2.0	220	2	BE938756	RC3-TN009	C 619	18	2.0	326	5	BY305781
547	18	2.0	221	9	CG728701	1119102F0	C 620	18	2.0	327	5	BY305782
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C 702	18	2.0	425	8	AZ336226	C 775	18	2.0	501	1	AA764559
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C 749	18	2.0	471	2	BE692879	C 822	18	2.0	539	2	AM610923
C 750	18	2.0	473	6	BY589761	C 823	18	2.0	541	4	BM791927
C 751	18	2.0	475	4	BI346249	C 824	18	2.0	541	9	CG565430
C 752	18	2.0	475	7	W07718	C 825	18	2.0	542	6	CD727848
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C 836	18	2.0	555	4	BJ256742	BJ256742	C 909	18	2.0	607	2	BE964533	BE964533	601658645
C 837	18	2.0	556	4	BP767143	BP767143	C 910	18	2.0	608	7	CO172807	CO172807	DG14-196f
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C 869	18	2.0	581	8	BH219763	BH219763 1006090D0	C 942	18	2.0	637	4	BM660454	BM660454	952037G06
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C 878	18	2.0	587	2	AK413062	AK413062	C 951	18	2.0	646	6	CD226409	CD226409	CCCL.45.C
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ALIGNMENTS

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RESULT 1
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DEFINITION full-length cDNA clone CS0DL006YLO9 of B cells (Ramos cell line)
ACCESSION CR604307
VERSION CR604307.1 GI:50485114
KEYWORDS HTC; cNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Feng Liang Email: fliang@life.techn.com URL:
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1053)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail: seque@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
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121 GAGCTGAGCTCTGCTGCTTCTGCTGATGAGTCTCTGCGCCCGGAGGCTTACCC 180
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DEFINITION full-length cDNA clone CS0DK010YK16 of HeLa cells Cot 25-normalized
of Homo sapiens (human).
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ACCESSION CR593642
VERSION HTS93642.1 GI:50474449
KEYWORDS HTC; CNSLT_cDNA.
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@life.technet.com URL :
http://fulllength.invitrogen.com/InvitrogenCorporation1600
Faraday Avenue
2 (bases 1 to 1860)
Genoscope.
REFERENCE
AUTHORS Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
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Best Local Similarity 99.9%; Pred. No. 0;
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DB 191 GAGCTGAGAGCTCTGGGCTTTCTGCTGATGATGAGCTCTGGGCGCGCGGAGGCTTAAAGC 250
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DB 431 AGCTCTTCAAAAGAGACAGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 490
QY 421 AATTCTCAGCAGGATGATGAGGAGAGAGGCTCCCGCCCAACCAAGCGGAGCGGAGT 480
DB 491 AATTCTCAGCAGGATGATGAGGAGAGAGGCTCCCGCCCAACCAAGCGGAGCGGAGT 550
QY 481 CGGGGCGGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540

DB 551 CGGGGCGGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 610
QY 541 CAGCAGTACAGAGCCCGGAGACCTTCTCTGAGGCAAGTACCTGATCCTCGGCTC 600
DB 611 CAGCAGTACAGAGCCCGGAGACCTTCTCTGAGGCAAGTACCTGATCCTCGGCTC 670
QY 601 CGGGTTCAGAGAGTATGCTGAGAGTACGAGGCTGCTGAGCAGGAGGCTGAGTCCCGG 660
DB 671 CGGGTTCAGAGAGTATGCTGAGAGTACGAGGCTGCTGAGCAGGAGGCTGAGTCCCGG 730
QY 661 CGGGCCAGGCGGCTGCGCGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 731 CGGGCCAGGCGGCTGCGCGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 790
QY 721 TCAAGGAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 791 TCAAGGAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 850
QY 781 GCTTCTGCGGCGGAGTACCTGAGTGGCGGCTGCTGAGGCGGCTGCGGCGGCTGCTGCTG 840
DB 851 GCTTCTGCGGCGGAGTACCTGAGTGGCGGCTGCTGAGGCGGCTGCGGCGGCTGCTGCTG 910
QY 841 ACTGAGGCTCTGCGAGAGGCTGCTGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB 911 ACTGAGGCTCTGCGAGAGGCTGCTGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 970
QY 901 GAGGCTGAC 909
DB 971 GAGGCTGAC 979

RESULT 3
CR619301
LOCUS 1866 bp mRNA linear HTC 21-JUL-2004
DEFINITION Full-length cDNA clone CSODC015Y24 of Neuroblastoma Cot
25-normalized of Homo sapiens (human).
ACCESSION CR619301
VERSION CR619301.1 GI:50500108
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@life.technet.com URL :
http://fulllength.invitrogen.com/InvitrogenCorporation1600
Faraday Avenue
2 (bases 1 to 1860)
Genoscope.
REFERENCE
AUTHORS Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
SOURCE location/Qualifiers
1..1866
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODC015Y24"
/tissue_type="Neuroblastoma Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Query Match 94.4%; Score 858; DB 3; Length 1866;
Best Local Similarity 99.9%; Pred. No. 0;

Matches	908; Conservative	0; Mismatches	1; Indels	0; Gaps	0;
Qy	1	ATGGCGCTATCCGGGTGACATCCCGGCCCCGCTGCTGGAGAGATGATGCTGGACTAC	60		
Db	76	ATGGCGCTATCCGGGTGACATCCCGGCCCCGCTGCTGGAGAGATGATGCTGGACTAC	135		
Qy	61	TACGGGATGCTGCTGCTTCAACCGTATGTTTCAAGGTGCTGGCGGCACTGACCGAGTGC	120		
Db	136	TACGGGATGCTGCTGCTTCAACCGTATGTTTCAAGGTGCTGGCGGCACTGACCGAGTGC	195		
Qy	121	GAGCTGAGAGCTCTGGGCTTTCTGCTGATGAGGCTCCGCGGCGCGGAGGCTTACGC	180		
Db	136	GAGCTGAGAGCTCTGGGCTTTCTGCTGATGAGGCTCCGCGGCGCGGAGGCTTACGC	255		
Qy	181	CGGGCCCGCAGCGGCTAGAGCTCTGCTGAGCTGAGCGCGCGCGGCAAGTGGCCGAG	240		
Db	256	CGGGCCCGCAGCGGCTAGAGCTCTGCTGAGCTGAGCGCGCGCGGCAAGTGGCCGAG	315		
Qy	241	AGCAACTGCGGCTGCTGCGGCACTCTGCGCGCTGCTGGCCCGCAGACTGCTGCGG	300		
Db	316	AGCAACTGCGGCTGCTGCGGCACTCTGCGCGCTGCTGGCCCGCAGACTGCTGCGG	375		
Qy	301	CACCTGGCGCGCAAGCGGCGCGGCGCGGCTGCTGAGAAAGCTATAGCTATGCACTCC	360		
Db	376	CACCTGGCGCGCAAGCGGCGCGGCGCGGCTGCTGAGAAAGCTATAGCTATGCACTCC	435		
Qy	361	AGCTCTTCAAAAGAGACAGAGGTAGCTGCGCTGCGTCCGCTGAGCTCAAGACTTCTCA	420		
Db	436	AGCTCTTCAAAAGAGACAGAGGTAGCTGCGCTGCGTCCGCTGAGCTCAAGACTTCTCA	495		
Qy	421	AATTTTCAGCAGAGGTCACTGAGGAGACAGGCTTCCCCCAACCAAGCGGCAAGCGGAGT	480		
Db	496	AATTTTCAGCAGAGGTCACTGAGGAGACAGGCTTCCCCCAACCAAGCGGCAAGCGGAGT	555		
Qy	481	CGGGCCCGGCGCAAGGTGCTGCTGAGCGGCGGCGGAGAGGGGCGCGGCGGCAAGCGG	540		
Db	556	CGGGCCCGGCGCAAGGTGCTGCTGAGCGGCGGCGGAGAGGGGCGCGGCGGCAAGCGG	615		
Qy	541	CAGCAGTCAAGAGCCCGGCGAGACTTCTCTGAAAGCAAGTGAAGCTGTGACATCCGAGTC	600		
Db	616	CAGCAGTCAAGAGCCCGGCGAGACTTCTCTGAAAGCAAGTGAAGCTGTGACATCCGAGTC	675		
Qy	601	CGGGTTCAGCAGAGTACTGCGAGATGAGGCGGCGGCTTGGAGCAGGAGGCTGGCATCCCGG	660		
Db	676	CGGGTTCAGCAGAGTACTGCGAGATGAGGCGGCGGCTTGGAGCAGGAGGCTGGCATCCCGG	735		
Qy	661	CGGGCCCGGCGCTGCGGCGAGCTGAGAGTGTGTTGGGCGGCGGCGGCAAGCGGAGTGGCG	720		
Db	736	CGGGCCCGGCGCTGCGGCGAGCTGAGAGTGTGTTGGGCGGCGGCGGCAAGCGGAGTGGCG	795		
Qy	721	TCAAGGAGCTGGGCTGTGTGTTGTGATCAATCAAGTTCTGAGAGCTCTCTATCTGAGC	780		
Db	796	TCAAGGAGCTGGGCTGTGTGTTGTGATCAATCAAGTTCTGAGAGCTCTCTATCTGAGC	855		
Qy	781	GCTTCTGGGCGGCTTACTGATGAGGCGGCTCTGCTGAGGCGGCTGGGGGCTGTTCTCG	840		
Db	856	GCTTCTGGGCGGCTTACTGATGAGGCGGCTCTGCTGAGGCGGCTGGGGGCTGTTCTCG	915		
Qy	841	ACTGAGGCGCTGCGAGAGGCTGTGGGCGGAGAGGCTGTTGCTGCTGCTGCTGATGTGAT	900		
Db	916	ACTGAGGCGCTGCGAGAGGCTGTGGGCGGAGAGGCTGTTGCTGCTGCTGCTGATGTGAT	975		
Qy	901	GAGGCTGAGC 909			
Db	976	GAGGCTGAGC 984			

RESULT 4
CR625070
LOCUS
DEFINITION
ACCESSION

CR625070
full-length cDNA clone CS0DC001Y18 of Neuroblastoma Cot
25-normalized of Homo sapiens (human).

1894 bp mRNA linear HTC 21-JUL-2004

VERSION	CR625070.1	GI:50505877
KEYWORDS	HTC; cDNA	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleostomi; Primates; Catarrhini; Hominoidea; Homo.	
AUTHORS	Li, W.B., Gruber, C., Jessee, J., and Polayes, D.	
TITLE	Full-length cDNA libraries and normalization	
JOURNAL	Unpublished	
REMARK	Contact : Feng Liang Email : fliang@life.techn.com URL : http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 1894)	
REFERENCE	Genoscope.	
AUTHORS	Direct Submission	
TITLE	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage ;	
JOURNAL	BP 191 91006 EVRY cedex - FRANCE (E-mail : seq@genoscope.cns.fr)	
COMMENT	- Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(4T) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.	
FEATURES	Location/Qualifiers	
source	1..1894	
	/organism="Homo sapiens"	
	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
	/clone="CS0DC001Y18"	
	/tissue_type="Neuroblastoma Cot 25-normalized"	
	/plasmid="pCMVSPORT_6"	
ORIGIN		
Query Match	94.4%; Score 858; DB 3; Length 1894;	
Best Local Similarity	99.9%; Pred. No. 0;	
Matches	908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1	ATGGCGCTATCCGGGTGACATCCCGGCCCCGCTGCTGGAGAGATGATGCTGGACTAC 60
Db	89	ATGGCGCTATCCGGGTGACATCCCGGCCCCGCTGCTGGAGAGATGATGCTGGACTAC 148
Qy	61	TACGGGATGCTGCTGCTTCAACCGTATGTTTCAAGGTGCTGGCGGCACTGACCGAGTGC 120
Db	149	TACGGGATGCTGCTGCTTCAACCGTATGTTTCAAGGTGCTGGCGGCACTGACCGAGTGC 208
Qy	121	GAGCTGAGAGCTCTGGGCTTTCTGCTGATGAGGCTCTGCGGCGGCGGAGGCTTAGCC 180
Db	209	GAGCTGAGAGCTCTGGGCTTTCTGCTGATGAGGCTCTGCGGCGGCGGAGGCTTAGCC 268
Qy	181	CGGGCCCGCAGCGGCTTGAAGCTCTGCTGAGCTGAGCGGCGGCGGCAAGTGGCGGAG 240
Db	269	CGGGCCCGCAGCGGCTTGAAGCTCTGCTGAGCTGAGCGGCGGCGGCAAGTGGCGGAG 328
Qy	241	AGCAACTGCGGCTGCTGCGGCACTCTGCGGCTGCTGGCCCGCAGACTGCTGCGG 300
Db	329	AGCAACTGCGGCTGCTGCGGCACTCTGCGGCTGCTGGCCCGCAGACTGCTGCGG 388
Qy	301	CACCTGGCGCGCAAGCGGCGCGGCGGAGTGTCTGAGAGGCTTATAGCTATGAGCACTCC 360
Db	389	CACCTGGCGCGCAAGCGGCGCGGCGGAGTGTCTGAGAGGCTTATAGCTATGAGCACTCC 448
Qy	361	AGCTCTTCAAAAGAGACAGAGGTAGCTGCGGCTGCGGCTGGGCAAGTGTCTGCA 420
Db	449	AGCTCTTCAAAAGAGACAGAGGTAGCTGCGGCTGCGGCTGGGCAAGTGTCTGCA 508
Qy	421	AATTTTCAGCAGAGGTCACTGAGGAGACAGGCTTCCCCCAACCAAGCGGCAAGCGGAGT 480
Db	509	AATTTTCAGCAGAGGTCACTGAGGAGACAGGCTTCCCCCAACCAAGCGGCAAGCGGAGT 568
Qy	481	CGGGCCCGGCGCAAGTGTGTTGCGAGCGGCGGCGGAGAGGGGCGGCGGCAAGCGGAG 540
Db	569	CGGGCCCGGCGCAAGTGTGTTGCGAGCGGCGGCGGAGAGGGGCGGCGGCAAGCGGAG 628

QY 541 CAGCAGTCAGAGAGCCGCGAGACCTTCTCTGAAGCAAGTACCTGTGACATCCGGCTC 600
 DB 629 CAGCAGTCAGAGAGCCGCGAGACCTTCTCTGAAGCAAGTACCTGTGACATCCGGCTC 688
 QY 601 CGGGTTTCAGAGAGTACTGCGAGCATGCGCCAGCCTTGGAGCAGGCGCTGGCATCCCGG 660
 DB 669 CGGGTTTCAGAGAGTACTGCGAGCATGCGCCAGCCTTGGAGCAGGCGCTGGCATCCCGG 748
 QY 661 CGGGCCCGAGCGCTGCGCGAGCATGCTGTGTTGGCCAGGCCACCGCATGTGCTGGCC 720
 DB 749 CGGGCCCGAGCGCTGCGCGAGCATGCTGTGTTGGCCAGGCCACCGCATGTGCTGGCC 808
 QY 721 TCAAGGAGACCTGAGGCTGTGTTGTGATCATCAAGTTCTGAGAGCTCTATCTGAC 780
 DB 809 TCAAGGAGACCTGAGGCTGTGTTGTGATCATCAAGTTCTGAGAGCTCTATCTGAC 868
 QY 781 GCGTTCTGGGGGAGCTACTGAGTGGCGCCCTGCTGACAGGCCCTGGGGGGCGTGTCTG 840
 DB 869 GCGTTCTGGGGGAGCTACTGAGTGGCGCCCTGCTGACAGGCCCTGGGGGGCGTGTCTG 928
 QY 841 ACTGAGGCGCTTCCGAGAGGCTGTGGCCCGGAGGCTGTTCGCTGTGTCAGTGTGAT 900
 DB 929 ACTGAGGCGCTTCCGAGAGGCTGTGGCCCGGAGGCTGTTCGCTGTGTCAGTGTGAT 988
 QY 901 GAGGCTGAC 909
 DB 989 GAGGCTGAC 997

RESULT 5
 LOCUS BM920838 1090 bp mRNA linear EST 12-MAR-2002
 DEFINITION AGENCOURT_6706034 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5752092
 5', mRNA sequence.
 ACCESSION BM920838
 VERSION BM920838.1 GI:139171217
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing By: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLNI at:
 http://image.llnl.gov
 Plate: L14M12785 row: 1 column: 13
 High quality sequence stop: 625.
 Location/Qualifiers
 1..1090
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5752092"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_115"
 /note="Organ: Pooled brain, lung, testis; Vector:
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27, and 1 male testis, age 69. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.

FEATURES

source

ORIGIN
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH_MGC Library."

Query Match 66.8%; Score 607; DB 5; Length 1090;
 Best Local Similarity 99.8%; Pred. No. 2.2e-297;
 Matches 657; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCGATATCCGGGTCGACCCCGGCGCTGGTGGAGAGATGATGCTGGACTAC 60
 DB 102 ATGGCGATATCCGGGTCGACCCCGGCGCTGGTGGAGAGATGATGCTGGACTAC 161
 QY 61 TACGGATGCTGTCCTTCAACCGTATGTTGAGTGTGGCGGCAACTGACCGAGTGC 120
 DB 162 TACGGATGCTGTCCTTCAACCGTATGTTGAGTGTGGCGGCAACTGACCGAGTGC 221
 QY 121 GAGCTGAGAGCTCTGGCTTTTCTGCTGATGAGGCTCTGCGCGCGGAGGCTTTAGCC 180
 DB 222 GAGCTGAGAGCTCTGGCTTTTCTGCTGATGAGGCTCTGCGCGCGGAGGCTTTAGCC 281
 QY 181 CGGGCCCGAGCGGCTGAGAGCTCTGCTGAGAGCTGAGAGCGCGGCGAGTGGCGGAG 240
 DB 282 CGGGCCCGAGCGGCTGAGAGCTCTGCTGAGAGCTGAGAGCGCGGCGAGTGGCGGAG 341
 QY 241 AGCAACTGCGGCTGCTGCGGCACTCTGCGCTGCTGAGCGCCCGCACGACTGTGCGG 300
 DB 342 AGCAACTGCGGCTGCTGCGGCACTCTGCGCTGCTGAGCGCCCGCACGACTGTGCGG 401
 QY 301 CACTGGGCGCGAGCGGCGCGCGCGCACTGTGTCGAGAACTGATAGTATGACACTTCC 360
 DB 402 CACTGGGCGCGAGCGGCGCGCGCGCACTGTGTCGAGAACTGATAGTATGACACTTCC 461
 QY 361 AGCTTTTAAAGAGAGAGAGGCTGAGCGTGTGCGCGCGCGCACTGAGAGAGTCTGCA 420
 DB 462 AGCTTTTAAAGAGAGAGGCTGAGCGTGTGCGCGCGCGCACTGAGAGAGTCTGCA 521
 QY 421 AATTCTCAGCAGAGGCTCAGTGGAGAGCAGGCTTCCCGCCCAACCAAGCGGCGGAGT 480
 DB 522 AATTCTCAGCAGAGGCTCAGTGGAGAGCAGGCTTCCCGCCCAACCAAGCGGCGGAGT 581
 QY 481 CGGGCCCGCGCGAGTGTGTGTCAGAGCGGCGGAGAGGCGCGCGAGCGGCGAG 540
 DB 582 CGGGCCCGCGCGAGTGTGTGTCAGAGCGGCGGAGAGGCGCGCGAGCGGCGAG 641
 QY 541 CAGCAGTCAGAGAGCCGCGAGACCTTCTCTGAAGCAAGTACCTGTGACATCCGGCTC 600
 DB 642 CAGCAGTCAGAGAGCCGCGAGACCTTCTCTGAAGCAAGTACCTGTGACATCCGGCTC 701
 QY 601 CGGGTTTCAGAGAGTACTGCGAGCATGCGCCAGCCTTGGAGCAGGCGCTGGCATCC 658
 DB 702 CGGGTTTCAGAGAGTACTGCGAGCATGCGCCAGCCTTGGAGCAGGCGCTGGCATCC 759

RESULT 6
 LOCUS BG685173 800 bp mRNA linear EST 01-MAY-2001
 DEFINITION 602637058P1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4746439 5',
 mRNA sequence.
 ACCESSION BG685173
 VERSION BG685173.1 GI:13916570
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: Louis M. Staedt, M.D., Ph.D.
 CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L16CML622 row: d column: 16
High quality sequence stop: 794.
Location/Qualifiers

FEATURES
source

1..800
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4764639"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH MGC 48"
/note="Organ: B-cells; Vector: pORF7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming,
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 64.5%; Score 586; DB 4; Length 800;
Best Local Similarity 100.0%; Pred. No. 1.1e-286;
Matches 586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

227 CGAGAGCAACTGCGGCTGCTGGGCAACTCTCTGGCGTGTGCGCCGACGACTTCT 296
119 CGAGAGCAACTGCGGCTGCTGGGCAACTCTCTGGCGTGTGCGCCGACGACTTCT 178
297 GCCGCACTGGGCGCCAGAGCGCGCGCGAGTGTCTCCAGAACGCTATGAGTAC 356
179 GCCGCACTGGGCGCCAGAGCGCGCGCGAGTGTCTCCAGAACGCTATGAGTAC 238
357 CTCGAGCTCTTCAAGAGAGACAGAGGAGTACGCTCCGCTCGCGAGTCAAGAGTTTC 416
239 CTCGAGCTCTTCAAGAGAGACAGAGGAGTACGCTCCGCTCGCGAGTCAAGAGTTTC 298
417 TGCAGATTTCTCAGCAGGGGTCACTGGAGACAGGCTCCCCCAACCAAGCGGCGGCG 476
299 TGCAGATTTCTCAGCAGGGGTCACTGGAGACAGGCTCCCCCAACCAAGCGGCGGCG 358
477 GAGTCGGGCGCGCCAGTGGTGTGCGAGACGCGCGGAGAGAGGCGCCAGCGCGCAC 536
359 GAGTCGGGCGCGCCAGTGGTGTGCGAGACGCGCGGAGAGAGGCGCCAGCGCGCAC 418
537 CCAGCAGCAGTCAAGAGCGCGCCAGACTTCTCTGAAAGCAAGTCACTGTGACATCCG 596
419 CCAGCAGCAGTCAAGAGCGCGCCAGACTTCTCTGAAAGCAAGTCACTGTGACATCCG 478
597 GCTCCGGGTGTGAGCAGAGTACTGGAGACATGGGCGACGCTTGGAGCGGGCGTGGCATC 656
479 GCTCCGGGTGTGAGCAGAGTACTGGAGACATGGGCGACGCTTGGAGCGGGCGTGGCATC 538
657 CCGGCGGCGCCAGCGGCTGGCGCGCGCAGCTGATGTTTGGGCGAGGCGACCGAGTGTCT 716
539 CCGGCGGCGCCAGCGGCTGGCGCGCGCAGCTGATGTTTGGGCGAGGCGACCGAGTGTCT 598
717 GCGCTCAAGGAGACCTGGGCTGTGGTGTGATCAATCAAGTCTCAGAGCTCTCTAATCT 776
599 GCGCTCAAGGAGACCTGGGCTGTGGTGTGATCAATCAAGTCTCAGAGCTCTCTAATCT 658
777 GGAAGCCTTCTGGGCGCACTACCTGAGTGGCGGCTGTGTCAGGCG 822
659 GGAAGCCTTCTGGGCGCACTACCTGAGTGGCGGCTGTGTCAGGCG 704

RESULT 7

B1907024 634 bp mRNA linear EST 16-OCT-2001
LOCUS 603064980F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5214211 5',
DEFINITION mRNA sequence.
ACCESSION B1907024
VERSION B1907024.1 GI:16169804
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 634)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L16ML1537 row: p column: 20
High quality sequence stop: 632.
Location/Qualifiers

FEATURES
source

1..634
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5214211"
/tissue_type="Leukocyte"
/lab_host="DH10B"
/note="Vector: pCMV-Sport6; Site 1: NotI; Site 2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."

ORIGIN

Query Match 64.0%; Score 582; DB 4; Length 634;
Best Local Similarity 100.0%; Pred. No. 1.2e-284;
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

328 GTGTCTCCAGAACCTATAGCTATGACACCTCCAGCTCTTCAAGAGAGACAGAGGTAGC 387
Db 32 GTGTCTCCAGAACCTATAGCTATGACACCTCCAGCTCTTCAAGAGAGACAGAGGTAGC 91
388 TGCCTGTGCGCTGGGCGAGTCAAGCAATTCTGCAAAATTTCTACAGAGGGTCACTGGAGACA 447
Db 92 TGCCTGTGCGCTGGGCGAGTCAAGCAATTCTGCAAAATTTCTACAGAGGGTCACTGGAGACA 151
448 GGTCTCCCCCAACCAAGCGCGCAGCGGAGAGTGTGGGGCGCGCCAGTGGTGTGCGACA 507
Db 152 GGTCTCCCCCAACCAAGCGCGCAGCGGAGAGTGTGGGGCGCGCCAGTGGTGTGCGACA 211
508 CCGGCGGAGAGAGGGGCGCCAGCGCAGCCAGCAGAGACAGTCAAGAGCCGCGACACTTCC 567
Db 212 CCGGCGGAGAGAGGGGCGCCAGCGCAGCCAGCAGAGACAGTCAAGAGCCGCGACACTTCC 271
568 TCTGAAGCAAAAGTACCTGTGACATCCGGCTCCGGGTTGGAGCAGAGTACTGGAGCAT 627
Db 272 TCTGAAGCAAAAGTACCTGTGACATCCGGCTCCGGGTTGGAGCAGAGTACTGGAGCAT 331
628 GGGCAGCCTTTGAGAGAGGGGAGTGGCATCCCGGCGGCGCCAGAGGCTGGGCGGCGACCTG 687
Db 332 GGGCAGCCTTTGAGAGAGGGGAGTGGCATCCCGGCGGCGCCAGAGGCTGGGCGGCGACCTG 391

QY 688 GACGTGTTGGGACAGCCACCGAGTGTGCGCTCAAGGAGACCTGGGCTCTGTGGTTGT 747
DB 392 GACGTGTTGGGACAGCCACCGAGTGTGCGCTCAAGGAGACCTGGGCTCTGTGGTTGT 451
QY 748 GACATCAAGTTCTCAGAGCTCTCTATCTGAGACGCTTCTGGGGGACTACTGAGTGGC 807
DB 452 GACATCAAGTTCTCAGAGCTCTCTATCTGAGACGCTTCTGGGGGACTACTGAGTGGC 511
QY 808 GCGCGCTGACAGCCCTGCGGGGCGGTGTTCCAGTCAAGAGCCCTCGAGAGGCTGTGGGC 867
DB 512 GCGCGCTGACAGCCCTGCGGGGCGGTGTTCCAGTCAAGAGCCCTCGAGAGGCTGTGGGC 571
QY 868 CCGGAGGCTGTGCGCTGCTGCTGATGATGAGGCTGAC 909
DB 572 CCGGAGGCTGTGCGCTGCTGCTGATGATGAGGCTGAC 613

RESULT 8
BI910528 905 bp mRNA linear EST 16-OCT-2001
LOCUS 603068215P1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5217218 5',
DEFINITION mRNA sequence.

ACCESSION BI910528
VERSION BI910528.1 GI:16173927
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM11545 row: n column: 03
High quality sequence stop: 863.

FEATURES
source location/Qualifiers
1..905
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5217218"
/tissue_type="leukocyte"
/lab_host="DH10B"
/clone_1ib="NIH_MGC_118"
/note="Vector: PCWV-SF0R76; Site 1: NotI; Site 2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."

ORIGIN

Query Match 64.0%; Score 582; DB 4; Length 905;
Best Local Similarity 100.0%; Pred. No. 1.2e-284;
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 328 GGTGTCCGAGACGCATAGTATGGACCTCAGCTCTTCAAGAGACAGAGGGTACG 387
DB 38 GTGTCCGAGACGCATAGTATGGACCTCAGCTCTTCAAGAGAGACAGAGGGTACG 97

QY 388 TGCCGTGCGCCGTGCGAGTCAAGCATTTCTGAAATTTCTAGCAGAGGTCAGTGGAGACA 447
DB 98 TGCCGTGCGCCGTGCGAGTCAAGCATTTCTGAAATTTCTAGCAGAGGTCAGTGGAGACA 157
QY 448 GGCTCCCCCACCACAGGCGAGGAGGTGCGGGGCCGGCCACAGTGTGTCCAGA 507
DB 158 GGCTCCCCCACCACAGGCGAGGAGGTGCGGGGCCGGCCACAGTGTGTCCAGA 217
QY 508 CCGCGCGGAGAGGGGGCCCCAGCGCACCCGACAGAGTCAAGAGCCCGCAGACTTCC 567
DB 218 CCGCGCGGAGAGGGGGCCCCAGCGCACCCGACAGAGTCAAGAGCCCGCAGACTTCC 277
QY 568 TCTGAAGCAAAAGTACCTGTGACATCCGAGCTCGGGTTTCTGAGCAGAGTACTCCAGCAT 627
DB 278 TCTGAAGCAAAAGTACCTGTGACATCCGAGCTCGGGTTTCTGAGCAGAGTACTCCAGCAT 337
QY 628 GGGCCAGCTTTGAGACAGGCGGTGACATCCCGGCGGCCCCAGGCGCTGGCGGAGCTG 687
DB 338 GGGCCAGCTTTGAGACAGGCGGTGACATCCCGGCGGCCCCAGGCGCTGGCGGAGCTG 397
QY 688 GACGTGTTGGGACAGCCACCGCAGTGTGCGCTCAAGGAGACCTGGGCTCTGTGGTTGT 747
DB 398 GACGTGTTGGGACAGCCACCGAGTGTGCGCTCAAGGAGACCTGGGCTCTGTGGTTGT 457
QY 748 GACATCAAGTTCTCAGAGCTCTCTATCTGAGACGCTTCTGGGGGACTACTGAGTGGC 807
DB 458 GACATCAAGTTCTCAGAGCTCTCTATCTGAGACGCTTCTGGGGGACTACTGAGTGGC 517
QY 808 GCGCTGCTGACAGGCGCTTGGGGGCGTGTCTGATGAGGCGCTTGGAGAGGCTGTGGGC 867
DB 518 GCGCTGCTGACAGGCGCTTGGGGGCGTGTCTGATGAGGCGCTTGGAGAGGCTGTGGGC 577
QY 868 CCGGAGGCTGTGCGCTGCTGCTGATGATGAGGCTGAC 909
DB 578 CCGGAGGCTGTGCGCTGCTGCTGATGATGAGGCTGAC 619

RESULT 9
BG251151 927 bp mRNA linear EST 13-FEB-2001
LOCUS 602364954P1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4473349 5',
DEFINITION mRNA sequence.

ACCESSION BG251151
VERSION BG251151.1 GI:12760967
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10295 row: k column: 14
High quality sequence stop: 715.

FEATURES

source

1..927

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4473349"
/tissue_type="adeno-carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_90"

LOCUS BM908148 1062 bp mRNA linear EST 12-MAR-2002
 DEFINITION AGENCOURT 6707554 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5745179
 5', mRNA sequence.
 ACCESSION BM908148
 VERSION BM908148.1 GI:19358527
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 1062)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT Robert Strausberg, Ph.D.
 EMAIL: cgapbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM12767 row: 1 column: 12
 High quality sequence stop: 651.
 Location/Qualifiers
 1..1062

FEATURES

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5745179"
 /tissue_type="medulla"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_119"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC library."

ORIGIN

Query Match 64.0%; Score 582; DB 5; Length 1062;
 Best Local Similarity 100.0%; Pred. No. 1.2e-284;
 Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 328 GTGTCTCCGAGACGCTATAGTATGACACCTCCAGCTCTTCAAGAGACAGAGGGTAC 387
 73 GTGTCTCCGAGACGCTATAGTATGACACCTCCAGCTCTTCAAGAGACAGAGGGTAC 132
 388 TCCGCTCCGCTGCGGACGTCAAGCAAGTCTTCAATTTCTACAGAGGCTCAGTGGAGACA 447
 133 TCCGCTCCGCTGCGGACGTCAAGCAAGTCTTCAATTTCTACAGAGGCTCAGTGGAGACA 192
 448 GGCTCCCCCCCCCAACCAAGCGGAGCGGCGGAGTCCGCGGCCCAAGTGTGTGCACA 507
 193 GGCTCCCCCCCCCAACCAAGCGGAGCGGCGGAGTCCGCGGCCCAAGTGTGTGCACA 252
 508 CGGCGCGGAGAGGGGCCCCAGCCGACCCAGACAGCACTAGAGCCGCCAGACCTTCC 567
 253 CGGCGCGGAGAGGGGCCCCAGCCGACCCAGACAGCACTAGAGCCGCCAGACCTTCC 312
 568 TTTGAAGGCAAGTGAAGTGTGATCATCGGCTTCCGGGTTGAGCAGAGTACTGAGACAT 627
 313 TTTGAAGGCAAGTGAAGTGTGATCATCGGCTTCCGGGTTGAGCAGAGTACTGAGACAT 372
 628 GGGCAGAGCTTTGAGAGAGGCGTGGATCCCGCGGCGGCCAGCGCTGGCGGGAGAGCTG 687
 373 GGGCAGAGCTTTGAGAGAGGCGTGGATCCCGCGGCGGCCAGCGCTGGCGGGAGAGCTG 432

QY 688 GACGTGTTTGGGACAGCCACCGACAGTGTGCGCTCAAGGACCTGAGGCTGTGTGTGT 747
 DB 433 GACGTGTTTGGGACAGCCACCGACAGTGTGCGCTCAAGGACCTGAGGCTGTGTGTGT 492
 QY 748 GACATCAAGTTCTCAGAGCTCTCTATTTGAGACGCTTCTGGGCGACTTACTGAGTGC 807
 DB 493 GACATCAAGTTCTCAGAGCTCTCTATTTGAGACGCTTCTGGGCGACTTACTGAGTGC 552
 QY 808 GCCCTGTGACAGGCGCTGCGGGGCGTGTTCCTGACCTGAGGCGCTGCGAGGCTGTGGC 867
 DB 553 GCCCTGTGACAGGCGCTGCGGGGCGTGTTCCTGACCTGAGGCGCTGCGAGGCTGTGGC 612
 QY 868 CGGAGGCTGTGTGCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 909
 DB 613 CGGAGGCTGTGTGCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 654

RESULT 12

LOCUS BS907425 1131 bp mRNA linear EST 20-OCT-2000
 DEFINITION 601500161P1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901934 5',
 mRNA sequence.
 ACCESSION BS907425
 VERSION BS907425.1 GI:10400971
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 1131)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT Robert Strausberg, Ph.D.
 EMAIL: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM9703 row: j column: 15
 High quality sequence stop: 686.
 Location/Qualifiers
 1..1131

FEATURES

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3901934"
 /tissue_type="epithelioid carcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_70"
 /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.1 kb. Library constructed by Life
 Technologies."

ORIGIN

Query Match 64.0%; Score 582; DB 2; Length 1131;
 Best Local Similarity 100.0%; Pred. No. 1.2e-284;
 Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 328 GTGTCTCCGAGACGCTATAGTATGACACCTCCAGCTCTTCAAGAGACAGAGGGTAC 387
 DB 30 GTGTCTCCGAGACGCTATAGTATGACACCTCCAGCTCTTCAAGAGACAGAGGGTAC 89
 QY 388 TCCGCTCCGCTGCGGACGTCAAGCAAGTCTTCAATTTCTACAGAGGCTCAGTGGAGACA 447
 DB 90 TCCGCTCCGCTGCGGACGTCAAGCAAGTCTTCAATTTCTACAGAGGCTCAGTGGAGACA 149
 QY 448 GGCTCCCCCCCCCAACCAAGCGGAGCGGCGGAGTCCGCGGCCCAAGTGTGTGCACA 507

DB 150 GGCCTCCCCCAACCAAGGCGAGCGGAGTCCGGGCGCCGCCAAGTGTGTGTCACAGA 209
QY 508 CGGCGCGGAGAGGGGCCCCAGCCGACCCGACAGCAGTCAAGAGCCCGCCAGACCTTCC 567
DB 210 CGGCGCGGAGAGGGGCCCCAGCCGACCCGACAGCAGTCAAGAGCCCGCCAGACCTTCC 269
QY 568 TCTGAAGGCAAGTGAACCTGTGACATCCGGCTCCGGGTTCCAGCAGAGTACTGCGACAT 627
DB 270 TCTGAAGGCAAGTGAACCTGTGACATCCGGCTCCGGGTTCCAGCAGAGTACTGCGACAT 329
QY 628 GGGCCAGCCTTGAAGAGGAGCGTGGAGTCCCGCGGAGCCGACGCGCTGGCGGAGAGCTG 687
DB 330 GGGCCAGCCTTGAAGAGGAGCGTGGAGTCCCGCGGAGCCGACGCGCTGGCGGAGAGCTG 389
QY 688 GACGTGTTGGGAGAGGAGCGGAGTGTGCTGCTCAAGAGGAGCTTGTGTGTGTGTGT 747
DB 390 GACGTGTTGGGAGAGGAGCGGAGTGTGCTGCTCAAGAGGAGCTTGTGTGTGTGTGTGT 449
QY 748 GACATCAAGTCTCTAGAGCTCTCTATCTGAGAGCGCTTCTGGGGGAGTACTGAGTGGC 807
DB 450 GACATCAAGTCTCTAGAGCTCTCTATCTGAGAGCGCTTCTGGGGGAGTACTGAGTGGC 509
QY 808 GCCCTGCTGAGAGCGGCGGAGCGTGTCTGCTGAGAGGCGCTGCGAGAGGCTGTGGGC 867
DB 510 GCCCTGCTGAGAGCGGCGGAGCGTGTCTGCTGAGAGGCGCTGCGAGAGGCTGTGGGC 569
QY 868 CGGAGGCTGTTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 909
DB 570 CGGAGGCTGTTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 611

RESULT 13
LOCUS CR599685 1510 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0D1069YH17 of Placenta Cot 25-normalized
ACCESSION CR599685
VERSION CR599685.1 GI:50480492
KEYWORDS HTC; cDNA; cDNA
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1510)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Paradey Avenue
2 (bases 1 to 1510)
REFERENCE CR599685
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES

Location/Qualifiers
1..1510

ORIGIN

Query Match 64.0%; Score 582; DB 3; Length 1510;
Best Local Similarity 100.0%; Pred. No. 1.2e-284;
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1069YH17"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 328 GTGTCTCCAGAACGCTATAGTATAGACACTTCCAGCTTCTTAAAGAGACAGAGGATGC 387
DB 29 GTGTCTCCAGAACGCTATAGTATAGACACTTCCAGCTTCTTAAAGAGACAGAGGATGC 88
QY 388 TGCCGTGCGCGCTCGGACATCAAGCATTTCTGCAATTTCTCAGCAGGAGTCACTGGAGACA 447
DB 89 TGCCGTGCGCGCTCGGACATCAAGCATTTCTGCAATTTCTCAGCAGGAGTCACTGGAGACA 148
QY 448 GGCCTCCCCCAACCAAGGAGAGCGGAGTCCGGGAGCGGAGGAGTGTGTGTGTGTGTGT 507
DB 149 GGCCTCCCCCAACCAAGGAGAGCGGAGTCCGGGAGCGGAGGAGTGTGTGTGTGTGTGT 208
QY 508 CGGCGCGGAGAGGGGCCCCAGCCGACCCGACAGCAGTGAAGAGCCCGCCAGACCTTCC 567
DB 209 CGGCGCGGAGAGGGGCCCCAGCCGACCCGACAGCAGTGAAGAGCCCGCCAGACCTTCC 268
QY 568 TCTGAAGGCAAGTGAACCTGTGACATCCGGCTCCGGGTTCCAGCAGAGTACTGCGAGCAT 627
DB 269 TCTGAAGGCAAGTGAACCTGTGACATCCGGCTCCGGGTTCCAGCAGAGTACTGCGAGCAT 328
QY 628 GGGCCAGCCTTGAAGAGGAGCGTGGAGTCCCGCGGAGCCGACGCGCTGGCGGAGAGCTG 687
DB 329 GGGCCAGCCTTGAAGAGGAGCGTGGAGTCCCGCGGAGCCGACGCGCTGGCGGAGAGCTG 388
QY 688 GACGTGTTGGGAGAGGAGCGGAGTGTGCTGCTCAAGAGGAGCTTGTGTGTGTGTGTGT 747
DB 389 GACGTGTTGGGAGAGGAGCGGAGTGTGCTGCTCAAGAGGAGCTTGTGTGTGTGTGTGT 448
QY 748 GACATCAAGTCTCTAGAGCTCTCTATCTGAGAGCGCTTCTGGGGGAGTACTGAGTGGC 807
DB 449 GACATCAAGTCTCTAGAGCTCTCTATCTGAGAGCGCTTCTGGGGGAGTACTGAGTGGC 508
QY 808 GCCCTGCTGAGAGCGGCGGAGCGTGTCTGCTGAGAGGCGCTGCGAGAGGCTGTGGGC 867
DB 509 GCCCTGCTGAGAGCGGCGGAGCGTGTCTGCTGAGAGGCGCTGCGAGAGGCTGTGGGC 568
QY 868 CGGAGGCTGTTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 909
DB 569 CGGAGGCTGTTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 610

RESULT 14
LOCUS CR590827 1586 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DE001VM11 of Placenta of Homo sapiens
ACCESSION CR590827
VERSION CR590827.1 GI:50471634
KEYWORDS HTC; cDNA; cDNA
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1586)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Paradey Avenue
2 (bases 1 to 1586)
REFERENCE CR590827
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

COMMENT

FEATURES

Source

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Location/Qualifiers
1. .1586
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cclone="CS0DEC01YM11"
/tissue_type="Placenta"
/plasmid="pCNAVSORT_6"
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ORIGIN

Query Match 64.0%; Score 582; DB 3; Length 1586;

OY	328	GGTGTCCAGAAACGCTATATAGCAATGGCAACCTCAGCTCTTTCAAAGAGGACACAAAGGGTAC	387
Db	111	GTGTCTCCAGAAACGCTATATAGCTATAGTGGACCTTCACGCTCTTTCAAAGAGGACAAAGGGTAC	170
OY	388	TGCGCTCGCCGTCGCGAGTCAGACGAGTTCTGCAAAATTCACAGCAGGGTCAAGTGGAGACA	447
Db	171	TGCGGTGCGCCGTCGCGAGTCAGACGAGTTCTGCAAAATTCACAGCAGGGTCAAGTGGAGACA	230
OY	448	GGCTTCCCCCACAACCAAGCGGCGACGGCGGAAGTCGGGGCCGCGCCAGTGTGTGTGCAGA	507
Db	231	GGCTTCCCCCACAACCAAGCGGCGACGGCGGAAGTCGGGGCCGCGCCAGTGTGTGTGCAGA	290
OY	508	CGGGCGGGGAGAGGGGGGCCCGACGGCCACCCCAAGACAGAGTCAGAGGCGCGGACCACTTCC	567
Db	291	CGGGCGGGGAGAGGGGGGCCCGACGGCCACCCCAAGACAGAGTCAGAGGCGCGGACCACTTCC	350
OY	568	TCTGAAGGCAAAAGTAGACCTGTGACATCCGGGCTCCGGGGTTCGAGCAGAGTACTCGAGCAT	627
Db	351	TCTGAAGGCAAAAGTAGACCTGTGACATCCGGGCTCCGGGGTTCGAGCAGAGTACTCGAGCAT	410
OY	628	GGGCGACGCTTGGAGACAGGGGCGTGGCATTCGCGCGGGCCCAAGGCGCTGGCGCGGACGCTG	687
Db	411	GGGCGACGCTTGGAGACAGGGGCGTGGCATTCGCGCGGGCCCAAGGCGCTGGCGCGGACGCTG	470
OY	688	GACGNGTTTGGGCAAGGCCACCGGACGTCGGGCTCAAAAGGGAACCTGGGCTCTGNGTTTGT	747
Db	471	GACGNGTTTGGGCAAGGCCACCGGACGTCGGGCTCAAAAGGGAACCTGGGCTCTGNGTTTGT	530
OY	748	GACATCAAGTTCTCAGAGCTCTCCTATCTGAGACGCGCTTCTGGGGCGCATTAACCTGAGTGGC	807
Db	531	GACATCAAGTTCTCAGAGCTCTCCTATCTGAGACGCGCTTCTGGGGCGCATTAACCTGAGTGGC	590
OY	808	GGCTTCTGTGCAGGGCCCTGTGGGGGCGTGTCTTGACTGAGGCCCTTGCAGAGGCTGTGTGGC	867
Db	591	GGCTTCTGTGCAGGGCCCTGTGGGGGCGTGTCTTGACTGAGGCCCTTGCAGAGGCTGTGTGGC	650
OY	868	CGGGAGGCGTGTGCGCTGCTGGTCAAGTGGAGTGGAGTGGAGCTGAC	909
Db	651	CGGGAGGCGTGTGCGCTGCTGGTCAAGTGGAGTGGAGTGGAGCTGAC	692

RESULT 15					
LOCUS	BM925969				
DEFINITION	BM925969	1089 bp	mDNA	linear	EST 12-MAR-2007
	AGENCOURT_6649774 NIH_MGC_114 Homo sapiens			cDNA clone IMAGE:57642727	
	5' mRNA sequence.				

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (pages 1 to 1089)	NIH-MGC	http://mgc.nci.nih.gov/	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
	Contact: Robert Strusberg, Ph.D.			Email: cgapbs-remail.nih.gov

FEATURES

Source

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLNL2817 row: h column: 01
High quality sequence start: 14
High quality sequence stop: 586.

Location/Qualifiers

Query Match 61.4%; Score 558; DB 5; Length 1089;

QY	1	ATTGAGCGTATCCGGGTGACCCCGGCGCCCGGTGCTGGGAGGAGAGATGAGCGCTTGACATAC	60
Db	71	ATTGGGCTATCCGGGTGCACCCCGGCGCCCGGTGCTGGGAGGAGAGATGAGCGCTTGACATAC	130
QY	61	TACGGGATGCTGTGCGCTTCAACCTATGTTTCGAGGCTGTGGCGGAGCACTGACCGAGTGC	120
Db	131	TACGGGATGCTGTGCGCTTCAACCTATGTTTCGAGGCTGTGGCGGAGCACTGACCGAGTGC	190
QY	121	GAGCTGAGCTTCCTGGCCCTTTCTGTGTGATGAGCTCTTGGCGCGCCGCGAGGCTTTAGCC	180
Db	191	GAGCTGAGCTTCCTGGCCCTTTCTGTGTGATGAGCTCTTGGCGCGCCGCGAGGCTTTAGCC	250
QY	181	CGGGCGCGGCAACGGGCTTGAAGCTCCTGTGAGCTGTGAGAGCGCGGGGCGAGTGGCGGCGAG	240
Db	251	CGGGCGCGGCAACGGGCTTGAAGCTCCTGTGAGCTGTGAGAGCGCGGGGCGAGTGGCGGCGAG	310
QY	241	AGCAACCTGCGAGCTGTGGGGCAACTCTCTGCGCGTGTGAGCCCGCGCAAGACTGTGTCGCG	300
Db	311	AGCAACCTGCGAGCTGTGGGGCAACTCTCTGCGCGTGTGAGCCCGCGCAAGACTGTGTCGCG	370
QY	301	CACCTGGCGGCGCAAGCGGCGCGCGCAGTGTCTCCAGAACGCTATAGCTATGAGCAACTTCC	360
Db	371	CACCTGGCGGCGCAAGCGGCGCGCGCAGTGTCTCCAGAACGCTATAGCTATGAGCAACTTCC	430
QY	361	AGCTCTTCAAAAGAGAGACAGAGGATGACTGCCGTGCCCTCGGCACTCAAGACGTTTGTGA	420
Db	431	AGCTCTTCAAAAGAGAGACAGAGGATGACTGCCGTGCCCTCGGCACTCAAGACGTTTGTGA	490
QY	421	AATTCTCAGCAGGGTCACTGGGAGACAGAGCTCCCCGCCCAACCAACCGGACGGCGGAGT	480
Db	491	AATTCTCAGCAGGGTCACTGGGAGACAGAGCTCCCCGCCCAACCAACCGGACGGCGGAGT	550
QY	481	CGGGGCGGGCCAGTGTGTGTGCCGAGCGGGCGGAGAGAGGGGCCCAAGCCGACCCGAG	540
Db	551	CGGGGCGGGCCAGTGTGTGTGCCGAGCGGGCGGAGAGAGGGGCCCAAGCCGACCCGAG	610
QY	541	CAGCAGTCAAGGCCCGCGCAAGACTTCTCTGTAAGGCAAAATGTAACCTGTGACATCCGGCTC	600
Db	611	CAGCAGTCAAGGCCCGCGCAAGACTTCTCTGTAAGGCAAAATGTAACCTGTGACATCCGGCTC	670

Qy 601 CCGGTTCCAGCAGAGTACTGCGAGCATGGGCCAGCCCTTGAAGCAGGGCGTGCAATCCCGG 660
Db 671 CCGGTTCCAGCAGAGTACTGCGAGCATGGGCCAGCCCTTGAAGCAGGGCGTGCAATCCCGG 730

Search completed: February 12, 2005, 15:25:37
Job time : 2618 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 13:38:08 / Search time 148 Seconds
(without alignments)
10049.835 Million cell updates/sec

Title: US-10-030-271-1
Perfect score: 909
Sequence: 1 atggcgctatccgggtcgac.....tcagtgatgagctgac 909

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	281	30.9	1067	4 US-09-620-312D-853	Sequence 853, App
2	20	2.2	2673	4 US-09-252-991A-2993	Sequence 2993, Ap
3	20	2.2	2715	4 US-09-252-991A-2686	Sequence 2686, Ap
4	20	2.2	2814	4 US-09-252-991A-2875	Sequence 2875, Ap
5	19	2.1	601	4 US-09-949-016-21931	Sequence 21931, A
6	19	2.1	601	4 US-09-949-016-21932	Sequence 21932, A
7	19	2.1	601	4 US-09-949-016-21933	Sequence 21933, A
8	19	2.1	601	4 US-09-949-016-21934	Sequence 21934, A
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10	19	2.1	601	4 US-09-949-016-84252	Sequence 84252, A
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13	19	2.1	601	4 US-09-949-016-84255	Sequence 84255, A
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15	19	2.1	878	4 US-09-270-767-27566	Sequence 27566, A
16	19	2.1	988	4 US-09-270-767-11903	Sequence 11903, A
17	19	2.1	1742	4 US-09-799-451-383	Sequence 383, App
18	19	2.1	2019	4 US-09-252-991A-5836	Sequence 5836, App
19	19	2.1	2528	4 US-09-394-142B-15	Sequence 15, Appl
20	19	2.1	2534	4 US-09-394-142B-19	Sequence 19, Appl
21	19	2.1	2748	4 US-09-252-991A-5773	Sequence 5773, Ap
22	19	2.1	14555	4 US-09-902-540-1096	Sequence 1096, Ap
23	19	2.1	32584	4 US-09-949-016-16766	Sequence 16766, A
24	19	2.1	60095	4 US-09-949-016-12419	Sequence 12419, A
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28	18	2.0	397	4 US-09-513-999C-34541	Sequence 34541, A
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30	18	2.0	601	4 US-09-949-016-33681	Sequence 33681, A
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32	18	2.0	969	4 US-09-902-540-8543	Sequence 8543, Ap
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37	18	2.0	1294	4 US-09-902-540-5865	Sequence 5865, Ap
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87	17	1.9	1050	3 US-09-655-270A-16	Sequence 16, Appl
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C 107	17	1.9	1323	4	US-09-902-540-2671	Sequence 2671, Ap	180	17	1.9	18508	4	US-09-949-016-13843	Sequence 13843, A
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C 252	16	1.8	513	3	US-09-199-637A-155	Sequence 155, App	325	16	1.8	627	3	US-09-064-414-5	Sequence 5, Appl1
C 253	16	1.8	531	4	US-09-902-540-8969	Sequence 8969, Ap	326	16	1.8	636	4	US-09-252-991A-5379	Sequence 5379, Ap
C 254	16	1.8	537	4	US-09-252-991A-16170	Sequence 16170, A	C 327	16	1.8	639	4	US-09-252-991A-13260	Sequence 13260, A
C 255	16	1.8	546	4	US-09-252-991A-11071	Sequence 11071, A	C 328	16	1.8	639	4	US-09-902-540-9299	Sequence 9299, Ap
C 256	16	1.8	573	4	US-09-252-991A-5367	Sequence 5367, Ap	C 329	16	1.8	669	2	US-08-896-410-3	Sequence 3, Appl1
C 257	16	1.8	579	4	US-09-252-991A-1593	Sequence 1593, Ap	C 330	16	1.8	684	4	US-09-252-991A-13602	Sequence 13602, A
C 258	16	1.8	579	4	US-09-252-991A-6132	Sequence 6132, Ap	331	16	1.8	702	2	US-08-800-751-4	Sequence 4, Appl1
C 259	16	1.8	585	4	US-09-252-991A-4628	Sequence 4628, Ap	332	16	1.8	702	2	US-08-990-818-4	Sequence 4, Appl1
C 260	16	1.8	591	4	US-09-252-991A-6636	Sequence 6636, Ap	C 333	16	1.8	702	4	US-09-252-991A-6046	Sequence 6046, Ap
C 261	16	1.8	593	4	US-09-669-751-48	Sequence 48, Appl	C 334	16	1.8	712	4	US-09-270-767-13449	Sequence 13449, A
C 262	16	1.8	597	4	US-09-669-751-67	Sequence 67, Appl	335	16	1.8	720	4	US-09-489-039A-6326	Sequence 6326, Ap
C 263	16	1.8	601	4	US-09-949-016-19938	Sequence 19938, A	336	16	1.8	723	4	US-09-791-540-5	Sequence 5, Appl1
C 264	16	1.8	601	4	US-09-949-016-22806	Sequence 22806, A	337	16	1.8	731	2	US-08-392-338A-10	Sequence 10, Appl
C 265	16	1.8	601	4	US-09-949-016-26995	Sequence 26995, A	338	16	1.8	731	3	US-09-166-750-10	Sequence 10, Appl
C 266	16	1.8	601	4	US-09-949-016-28199	Sequence 28199, A	339	16	1.8	731	3	US-09-166-093-10	Sequence 10, Appl
C 267	16	1.8	601	4	US-09-949-016-28433	Sequence 28433, A	340	16	1.8	731	3	US-09-172-019-10	Sequence 10, Appl
C 268	16	1.8	601	4	US-09-949-016-30077	Sequence 30077, A	341	16	1.8	731	3	US-09-166-094-10	Sequence 10, Appl
C 269	16	1.8	601	4	US-09-949-016-33283	Sequence 33283, A	342	16	1.8	731	4	US-09-443-213-10	Sequence 10, Appl
C 270	16	1.8	601	4	US-09-949-016-33284	Sequence 33284, A	343	16	1.8	735	3	US-09-079-970A-1	Sequence 1, Appl1
C 271	16	1.8	601	4	US-09-949-016-42975	Sequence 42975, A	C 344	16	1.8	762	3	US-09-199-637A-153	Sequence 153, App
C 272	16	1.8	601	4	US-09-949-016-46200	Sequence 46200, A	C 345	16	1.8	771	3	US-08-253-155A-17	Sequence 17, Appl
C 273	16	1.8	601	4	US-09-949-016-57560	Sequence 57560, A	346	16	1.8	771	3	US-09-079-970A-4	Sequence 4, Appl1
C 274	16	1.8	601	4	US-09-949-016-57561	Sequence 57561, A	347	16	1.8	783	4	US-09-252-991A-927	Sequence 927, App
C 275	16	1.8	601	4	US-09-949-016-59659	Sequence 59659, A	348	16	1.8	792	4	US-09-902-540-8438	Sequence 8438, Ap
C 276	16	1.8	601	4	US-09-949-016-59660	Sequence 59660, A	349	16	1.8	797	1	US-08-323-444A-3	Sequence 3, Appl1
C 277	16	1.8	601	4	US-09-949-016-66010	Sequence 66010, A	350	16	1.8	797	5	US-08-515-903A-3	Sequence 3, Appl1
C 278	16	1.8	601	4	US-09-949-016-66019	Sequence 66019, A	351	16	1.8	797	5	PCT-US95-12840-3	Sequence 3, Appl1
C 279	16	1.8	601	4	US-09-949-016-66020	Sequence 66020, A	352	16	1.8	801	4	US-09-902-540-7321	Sequence 7321, Ap
C 280	16	1.8	601	4	US-09-949-016-72408	Sequence 72408, A	353	16	1.8	803	1	US-08-323-444A-7	Sequence 7, Appl1
C 281	16	1.8	601	4	US-09-949-016-80891	Sequence 80891, A	354	16	1.8	803	1	US-08-515-903A-7	Sequence 7, Appl1
C 282	16	1.8	601	4	US-09-949-016-86867	Sequence 86867, A	355	16	1.8	803	5	PCT-US95-12840-7	Sequence 7, Appl1
C 283	16	1.8	601	4	US-09-949-016-95030	Sequence 95030, A	356	16	1.8	810	4	US-09-252-991A-1547	Sequence 1547, Ap
C 284	16	1.8	601	4	US-09-949-016-95142	Sequence 95142, A	357	16	1.8	816	4	US-09-252-991A-11434	Sequence 11434, A
C 285	16	1.8	601	4	US-09-949-016-134281	Sequence 134281, A	358	16	1.8	828	4	US-09-252-991A-1643	Sequence 1643, Ap
C 286	16	1.8	601	4	US-09-949-016-136139	Sequence 136139, A	C 359	16	1.8	831	1	US-07-882-328-1	Sequence 1, Appl1
C 287	16	1.8	601	4	US-09-949-016-136140	Sequence 136140, A	C 360	16	1.8	831	1	US-08-183-213-1	Sequence 1, Appl1
C 288	16	1.8	601	4	US-09-949-016-137594	Sequence 137594, A	361	16	1.8	831	4	US-09-252-991A-4529	Sequence 4529, Ap
C 289	16	1.8	601	4	US-09-949-016-137955	Sequence 137955, A	362	16	1.8	840	4	US-09-252-991A-13957	Sequence 13957, A
C 290	16	1.8	601	4	US-09-949-016-137955	Sequence 137955, A	363	16	1.8	852	4	US-09-893-737-151	Sequence 151, App
C 291	16	1.8	601	4	US-09-949-016-137956	Sequence 137956, A	364	16	1.8	852	4	US-09-893-737-297	Sequence 297, App
C 292	16	1.8	601	4	US-09-949-016-137957	Sequence 137957, A	C 365	16	1.8	855	4	US-09-252-991A-11001	Sequence 11001, A
C 293	16	1.8	601	4	US-09-949-016-141163	Sequence 141163, A	366	16	1.8	875	4	US-09-252-991A-3602	Sequence 3602, Ap
C 294	16	1.8	601	4	US-09-949-016-141164	Sequence 141164, A	C 367	16	1.8	891	4	US-09-252-991A-15782	Sequence 15782, A
C 295	16	1.8	601	4	US-09-949-016-151100	Sequence 151100, A	C 368	16	1.8	891	4	US-09-252-991A-13439	Sequence 13439, A
C 296	16	1.8	601	4	US-09-949-016-158367	Sequence 158367, A	369	16	1.8	897	4	US-09-252-991A-4427	Sequence 4427, Ap
C 297	16	1.8	601	4	US-09-949-016-158368	Sequence 158368, A	370	16	1.8	897	4	US-09-902-540-7446	Sequence 7446, Ap
C 298	16	1.8	601	4	US-09-949-016-158369	Sequence 158369, A	371	16	1.8	909	1	US-08-133-804-1	Sequence 1, Appl1
C 299	16	1.8	601	4	US-09-949-016-169025	Sequence 169025, A	372	16	1.8	909	1	US-08-461-184-7	Sequence 7, Appl1
C 300	16	1.8	601	4	US-09-949-016-172825	Sequence 172825, A	373	16	1.8	909	1	US-08-461-675-7	Sequence 7, Appl1
C 301	16	1.8	601	4	US-09-949-016-172826	Sequence 172826, A	374	16	1.8	909	1	US-08-461-683-1	Sequence 1, Appl1
C 302	16	1.8	601	4	US-09-949-016-181757	Sequence 181757, A	375	16	1.8	909	2	US-08-461-838-1	Sequence 1, Appl1
C 303	16	1.8	601	4	US-09-949-016-181975	Sequence 181975, A	376	16	1.8	909	2	US-08-461-386-1	Sequence 1, Appl1
C 304	16	1.8	601	4	US-09-949-016-181995	Sequence 181995, A	377	16	1.8	909	2	US-09-252-991A-11185	Sequence 11185, A
C 305	16	1.8	601	4	US-09-949-016-183042	Sequence 183042, A	378	16	1.8	918	4	US-09-902-540-7975	Sequence 7975, Ap
C 306	16	1.8	601	4	US-09-949-016-183043	Sequence 183043, A	379	16	1.8	924	4	US-09-252-991A-1483	Sequence 1483, Ap
C 307	16	1.8	601	4	US-09-949-016-185638	Sequence 185638, A	C 380	16	1.8	948	4	US-09-489-039A-3064	Sequence 3064, Ap
C 308	16	1.8	601	4	US-09-949-016-186975	Sequence 186975, A	C 381	16	1.8	951	4	US-09-902-540-5206	Sequence 5206, Ap
C 309	16	1.8	601	4	US-09-949-016-186977	Sequence 186977, A	382	16	1.8	960	4	US-09-902-540-7932	Sequence 7932, Ap
C 310	16	1.8	601	4	US-09-949-016-194578	Sequence 194578, A	383	16	1.8	966	4	US-09-252-991A-6602	Sequence 6602, Ap
C 311	16	1.8	601	4	US-09-949-016-194579	Sequence 194579, A	C 384	16	1.8	984	4	US-09-252-991A-1038	Sequence 1038, Ap
C 312	16	1.8	601	4	US-09-949-016-203219	Sequence 203219, A	385	16	1.8	1011	4	US-09-902-540-3195	Sequence 3195, Ap
C 313	16	1.8	601	4	US-09-949-016-203220	Sequence 203220, A	386	16	1.8	1079	2	US-09-135-121B-6	Sequence 6, Appl1
C 314	16	1.8	601	4	US-09-949-016-203279	Sequence 203279, A	387	16	1.8	1080	2	US-08-918-727-2	Sequence 2, Appl1
C 315	16	1.8	601	4	US-09-949-016-203580	Sequence 203580, A	388	16	1.8	1080	3	US-09-205-988A-2	Sequence 2, Appl1
C 316	16	1.8	601	4	US-09-949-016-206933	Sequence 206933, A	389	16	1.8	1080	4	US-09-252-991A-4554	Sequence 4554, Ap
C 317	16	1.8	606	3	US-09-064-414-1	Sequence 1, Appl1	390	16	1.8	1081	2	US-09-016-366A-22	Sequence 22, Appl
C 318	16	1.8	606	3	US-09-064-414-3	Sequence 3, Appl1	391	16	1.8	1081	2	US-08-978-404B-17	Sequence 17, Appl
C 319	16	1.8	609	4	US-09-621-976-1139	Sequence 1139, Ap	392	16	1.8	1081	4	US-09-917-254-50	Sequence 50, Appl

393	16	1.8	1083	4	US-09-489-039A-5884	Sequence 5884, Ap
394	16	1.8	1093	4	US-09-010-147B-1	Sequence 1, Appl1
395	16	1.8	1093	4	US-09-489-039A-3658	Sequence 3658, Ap
396	16	1.8	1098	4	US-09-252-991A-5384	Sequence 5384, Ap
397	16	1.8	1120	1	US-07-882-329-3	Sequence 3, Appl1
398	16	1.8	1120	1	US-08-183-213-3	Sequence 3, Appl1
399	16	1.8	1125	4	US-09-489-039A-5507	Sequence 5507, Ap
400	16	1.8	1128	2	US-09-016-366A-20	Sequence 20, Appl
401	16	1.8	1128	2	US-08-978-404B-15	Sequence 15, Appl
402	16	1.8	1137	2	US-09-016-366A-18	Sequence 18, Appl
403	16	1.8	1137	2	US-08-978-404B-13	Sequence 13, Appl
404	16	1.8	1154	2	US-09-016-366A-16	Sequence 16, Appl
405	16	1.8	1154	2	US-08-978-404B-11	Sequence 11, Appl
406	16	1.8	1159	4	US-09-665-189A-57	Sequence 57, Appl
407	16	1.8	1167	4	US-09-489-039A-5896	Sequence 5896, Ap
408	16	1.8	1170	4	US-09-489-039A-3821	Sequence 3821, Ap
409	16	1.8	1173	4	US-09-252-991A-5197	Sequence 5197, Ap
410	16	1.8	1173	4	US-09-902-540-7010	Sequence 7010, Ap
411	16	1.8	1176	4	US-09-252-991A-11843	Sequence 11843, A
412	16	1.8	1203	4	US-09-252-991A-6250	Sequence 6250, Ap
413	16	1.8	1205	4	US-09-620-312D-949	Sequence 949, App
414	16	1.8	1206	4	US-09-949-016-5866	Sequence 5866, Ap
415	16	1.8	1227	4	US-09-252-991A-5278	Sequence 5278, Ap
416	16	1.8	1250	4	US-09-270-767-13107	Sequence 13107, A
417	16	1.8	1254	4	US-09-252-991A-11478	Sequence 11478, A
418	16	1.8	1254	4	US-09-902-540-4234	Sequence 4234, Ap
419	16	1.8	1257	4	US-09-252-991A-16062	Sequence 16062, A
420	16	1.8	1275	4	US-09-252-991A-13638	Sequence 13638, A
421	16	1.8	1278	4	US-09-902-540-6294	Sequence 6294, A
422	16	1.8	1281	4	US-09-902-540-377	Sequence 377, App
423	16	1.8	1299	4	US-09-902-540-3581	Sequence 3581, Ap
424	16	1.8	1302	4	US-09-902-540-2306	Sequence 2306, Ap
425	16	1.8	1305	2	US-08-896-410-37	Sequence 37, Appl
426	16	1.8	1313	4	US-09-949-016-5475	Sequence 5475, Ap
427	16	1.8	1314	4	US-09-902-540-5877	Sequence 5877, Ap
428	16	1.8	1315	4	US-09-902-540-156	Sequence 156, App
429	16	1.8	1329	1	US-07-882-329-4	Sequence 4, Appl1
430	16	1.8	1329	1	US-08-183-213-4	Sequence 4, Appl1
431	16	1.8	1334	4	US-09-949-016-602	Sequence 602, App
432	16	1.8	1362	4	US-09-023-655-485	Sequence 485, App
433	16	1.8	1364	4	US-09-949-016-233	Sequence 233, App
434	16	1.8	1364	4	US-09-949-016-3758	Sequence 3758, Ap
435	16	1.8	1396	4	US-09-902-540-2206	Sequence 2206, Ap
436	16	1.8	1404	2	US-08-487-113D-119	Sequence 119, App
437	16	1.8	1419	4	US-08-720-420A-119	Sequence 119, App
438	16	1.8	1419	4	US-09-489-039A-5224	Sequence 5224, Ap
439	16	1.8	1440	4	US-09-902-540-8052	Sequence 8052, Ap
440	16	1.8	1452	4	US-09-252-991A-15812	Sequence 15812, A
441	16	1.8	1458	3	US-09-105-537-9	Sequence 9, Appl1
442	16	1.8	1458	3	US-09-489-039A-6655	Sequence 6655, Ap
443	16	1.8	1460	2	US-08-392-338A-18	Sequence 18, Appl
444	16	1.8	1460	3	US-09-166-750-18	Sequence 18, Appl
445	16	1.8	1460	3	US-09-166-093-18	Sequence 18, Appl
446	16	1.8	1460	3	US-09-172-019-18	Sequence 18, Appl
447	16	1.8	1460	3	US-09-166-094-18	Sequence 18, Appl
448	16	1.8	1460	4	US-09-443-213-18	Sequence 18, Appl
449	16	1.8	1473	4	US-09-252-991A-4196	Sequence 4196, Ap
450	16	1.8	1488	1	US-07-914-281-9	Sequence 9, Appl1
451	16	1.8	1488	1	US-08-393-246-9	Sequence 9, Appl1
452	16	1.8	1488	1	US-08-525-058A-9	Sequence 9, Appl1
453	16	1.8	1488	2	US-08-696-731-9	Sequence 9, Appl1
454	16	1.8	1488	2	US-09-042-531-9	Sequence 9, Appl1
455	16	1.8	1514	3	US-09-162-524-4	Sequence 4, Appl1
456	16	1.8	1515	4	US-09-252-991A-12935	Sequence 12935, A
457	16	1.8	1517	4	US-09-902-540-214	Sequence 214, App
458	16	1.8	1524	4	US-09-252-991A-11455	Sequence 11455, A
459	16	1.8	1533	4	US-09-252-991A-800	Sequence 800, App
460	16	1.8	1539	3	US-09-364-230-28	Sequence 29, Appl
461	16	1.8	1554	4	US-09-902-540-2897	Sequence 2897, Ap
462	16	1.8	1565	3	US-09-320-878-24	Sequence 24, Appl
463	16	1.8	1565	4	US-09-141-908-22	Sequence 22, Appl
464	16	1.8	1565	4	US-09-657-440-24	Sequence 24, Appl
465	16	1.8	1572	4	US-09-252-991A-15025	Sequence 15025, A
466	16	1.8	1581	4	US-09-902-540-3972	Sequence 3972, Ap
467	16	1.8	1583	3	US-09-370-838-224	Sequence 224, App
468	16	1.8	1583	4	US-09-854-133-224	Sequence 224, App
469	16	1.8	1587	4	US-09-489-039A-6670	Sequence 6670, Ap
470	16	1.8	1590	4	US-09-252-991A-2259	Sequence 2259, Ap
471	16	1.8	1617	4	US-09-620-312D-265	Sequence 265, App
472	16	1.8	1623	4	US-09-252-991A-15700	Sequence 15700, A
473	16	1.8	1632	4	US-09-252-991A-3859	Sequence 3859, Ap
474	16	1.8	1637	4	US-09-949-016-2339	Sequence 2339, Ap
475	16	1.8	1642	4	US-09-159-277A-1	Sequence 1, Appl
476	16	1.8	1642	4	US-09-623-655-1485	Sequence 1485, Ap
477	16	1.8	1642	4	US-08-844-681A-1	Sequence 1, Appl1
478	16	1.8	1644	4	US-09-252-991A-6420	Sequence 6420, Ap
479	16	1.8	1701	3	US-09-357-072-1	Sequence 1, Appl1
480	16	1.8	1701	3	US-08-983-502-1	Sequence 1, Appl1
481	16	1.8	1701	4	US-09-516-747-1	Sequence 1, Appl1
482	16	1.8	1701	4	US-09-933-814-1	Sequence 1, Appl1
483	16	1.8	1701	5	PCT-US95-16542-1	Sequence 1, Appl1
484	16	1.8	1701	5	PCT-US96-10521-1	Sequence 1, Appl1
485	16	1.8	1762	4	US-09-265-383-2	Sequence 2, Appl1
486	16	1.8	1762	4	US-09-252-991A-863	Sequence 863, App
487	16	1.8	1791	4	US-09-902-540-2785	Sequence 2785, Ap
488	16	1.8	1796	3	US-09-255-392-1	Sequence 1, Appl1
489	16	1.8	1797	4	US-09-270-767-13142	Sequence 13142, A
490	16	1.8	1824	4	US-09-799-451-301	Sequence 301, App
491	16	1.8	1860	4	US-09-902-540-6841	Sequence 6841, Ap
492	16	1.8	1866	3	US-09-224-048A-1	Sequence 1, Appl1
493	16	1.8	1869	2	US-08-356-786-15	Sequence 15, Appl1
494	16	1.8	1900	4	US-09-949-016-1941	Sequence 1941, Ap
495	16	1.8	1919	4	US-09-949-016-801	Sequence 801, App
496	16	1.8	1919	4	US-09-949-016-6034	Sequence 6034, Ap
497	16	1.8	1947	4	US-09-252-991A-14778	Sequence 14728, A
498	16	1.8	1958	4	US-09-620-312D-354	Sequence 354, App
499	16	1.8	1992	4	US-09-252-991A-15580	Sequence 15580, A
500	16	1.8	2005	2	US-08-484-200-1	Sequence 1, Appl1
501	16	1.8	2005	2	US-08-477-493-1	Sequence 1, Appl1
502	16	1.8	2005	3	US-08-465-375-1	Sequence 1, Appl1
503	16	1.8	2005	3	US-09-788-070-1	Sequence 1, Appl1
504	16	1.8	2005	4	US-10-142-373-1	Sequence 1, Appl1
505	16	1.8	2005	4	US-09-155-252A-1	Sequence 1, Appl1
506	16	1.8	2028	4	US-09-252-991A-11416	Sequence 11416, A
507	16	1.8	2037	4	US-09-252-991A-4499	Sequence 4499, Ap
508	16	1.8	2048	3	US-09-199-637A-136	Sequence 136, App
509	16	1.8	2097	3	US-09-002-567B-2	Sequence 2, Appl1
510	16	1.8	2097	3	US-09-571-347-2	Sequence 2, Appl1
511	16	1.8	2097	4	US-09-252-991A-885	Sequence 885, App
512	16	1.8	2097	4	US-09-949-016-5524	Sequence 5524, Ap
513	16	1.8	2097	4	US-09-902-540-7039	Sequence 7039, Ap
514	16	1.8	2100	4	US-09-949-016-530	Sequence 530, App
515	16	1.8	2103	4	US-09-252-991A-11773	Sequence 11773, A
516	16	1.8	2208	4	US-09-252-991A-13675	Sequence 13675, A
517	16	1.8	2208	4	US-09-252-991A-15669	Sequence 15669, A
518	16	1.8	2209	4	US-09-489-847-16	Sequence 16, Appl
519	16	1.8	2211	4	US-09-324-258-4	Sequence 4, Appl1
520	16	1.8	2218	2	US-08-845-988-5	Sequence 5, Appl1
521	16	1.8	2218	3	US-09-206-537-5	Sequence 5, Appl1
522	16	1.8	2218	3	US-09-430-854-5	Sequence 5, Appl1
523	16	1.8	2218	4	US-09-814-915A-4	Sequence 4, Appl1
524	16	1.8	2233	4	US-09-949-016-626	Sequence 526, App
525	16	1.8	2235	4	US-09-949-016-626	Sequence 526, App
526	16	1.8	2237	5	PCT-US93-08282-1	Sequence 4766, Ap
527	16	1.8	2254	4	US-09-620-312D-73	Sequence 73, Appl
528	16	1.8	2259	2	US-08-845-988-3	Sequence 3, Appl1
529	16	1.8	2259	3	US-09-206-537-3	Sequence 3, Appl1
530	16	1.8	2259	3	US-09-430-854-3	Sequence 3, Appl1
531	16	1.8	2274	4	US-09-252-991A-15970	Sequence 15970, A
532	16	1.8	2302	1	US-08-354-456A-1	Sequence 1, Appl1
533	16	1.8	2302	1	US-07-999-280A-1	Sequence 1, Appl1
534	16	1.8	2302	1	US-08-426-036-1	Sequence 1, Appl1
535	16	1.8	2302	1	US-08-426-279-1	Sequence 1, Appl1
536	16	1.8	2302	1	US-08-401-013-1	Sequence 1, Appl1
537	16	1.8	2302	3	US-08-426-570-1	Sequence 1, Appl1
538	16	1.8	2302	3	US-08-425-876-1	Sequence 1, Appl1

539	16	1.8	2302	3	US-08-426-243-1	Sequence 1, Appl1	C 612	16	1.8	5932	4	US-09-949-016-15500	Sequence 15500, A
540	16	1.8	2302	3	US-08-401-632-1	Sequence 1, Appl1	C 613	16	1.8	6063	4	US-09-902-540-807	Sequence 807, App
541	16	1.8	2327	3	US-08-868-435-1	Sequence 1, Appl1	C 614	16	1.8	6119	4	US-09-949-016-16794	Sequence 16794, A
542	16	1.8	2327	3	US-08-744-231-1	Sequence 1, Appl1	C 615	16	1.8	6567	4	US-09-902-540-769	Sequence 769, App
543	16	1.8	2327	4	US-09-635-504-1	Sequence 1, Appl1	C 616	16	1.8	6791	4	US-09-771-035A-1	Sequence 1, Appl1
544	16	1.8	2361	4	US-09-352-991A-13870	Sequence 13870, A	C 617	16	1.8	7460	4	US-09-949-016-12375	Sequence 12375, A
545	16	1.8	2376	4	US-09-352-991A-6630	Sequence 6630, Ap	C 618	16	1.8	7546	4	US-09-949-016-13384	Sequence 14384, A
546	16	1.8	2469	4	US-09-489-039A-6749	Sequence 6749, Ap	C 619	16	1.8	7462	4	US-09-902-540-801	Sequence 801, App
547	16	1.8	2493	4	US-09-352-991A-4346	Sequence 4346, Ap	C 620	16	1.8	7700	4	US-09-949-016-15619	Sequence 15619, A
548	16	1.8	2539	4	US-09-620-312D-454	Sequence 454, App	C 621	16	1.8	7898	3	US-08-984-709A-19	Sequence 49, Appl1
549	16	1.8	2535	3	US-09-077-354B-1	Sequence 1, Appl1	C 622	16	1.8	7858	4	US-09-949-016-15531	Sequence 16531, A
550	16	1.8	2592	4	US-09-352-991A-5260	Sequence 5260, Ap	C 623	16	1.8	8025	4	US-09-949-016-14081	Sequence 14081, A
551	16	1.8	2618	4	US-09-976-594-474	Sequence 474, App	C 624	16	1.8	8144	4	US-09-902-540-820	Sequence 820, App
552	16	1.8	2631	4	US-09-949-016-3148	Sequence 3148, Ap	C 625	16	1.8	8279	4	US-09-949-016-13478	Sequence 13478, A
553	16	1.8	2652	4	US-09-489-039A-5584	Sequence 5584, Ap	C 626	16	1.8	8371	4	US-09-065-027-1	Sequence 1, Appl1
554	16	1.8	2681	4	US-09-749-340-8	Sequence 8, Appl1	C 627	16	1.8	8831	4	US-09-949-016-17608	Sequence 17608, A
555	16	1.8	2687	4	US-09-949-016-4588	Sequence 4588, Ap	C 628	16	1.8	8817	4	US-09-902-540-887	Sequence 887, App
556	16	1.8	2688	4	US-09-749-340-5	Sequence 5, Appl1	C 629	16	1.8	8976	3	US-09-495-797-44	Sequence 44, Appl1
557	16	1.8	2714	4	US-09-949-016-1021	Sequence 1021, Ap	C 630	16	1.8	9146	4	US-09-902-540-930	Sequence 930, App
558	16	1.8	2715	4	US-09-352-991A-12548	Sequence 12548, A	C 631	16	1.8	9382	4	US-09-949-016-15306	Sequence 15306, A
559	16	1.8	2793	1	US-08-458-298-1	Sequence 1, Appl1	C 632	16	1.8	9960	3	US-08-822-586-46	Sequence 46, Appl1
560	16	1.8	2793	1	US-08-651-658-4	Sequence 1, Appl1	C 633	16	1.8	10380	3	US-09-077-354B-3	Sequence 3, Appl1
561	16	1.8	2805	3	US-09-650-855-4	Sequence 1, Appl1	C 634	16	1.8	10391	4	US-09-902-540-998	Sequence 958, App
562	16	1.8	2805	3	US-09-650-855-4	Sequence 4, Appl1	C 635	16	1.8	10396	4	US-09-949-016-15573	Sequence 15573, A
563	16	1.8	2841	4	US-09-302-540-9681	Sequence 9681, Ap	C 636	16	1.8	11652	4	US-09-949-016-15560	Sequence 15560, A
564	16	1.8	2862	4	US-09-302-540-7749	Sequence 7749, Ap	C 637	16	1.8	11854	4	US-09-902-540-1037	Sequence 1037, Ap
565	16	1.8	2862	4	US-09-949-016-3998	Sequence 3998, Ap	C 638	16	1.8	12824	4	US-09-902-540-993	Sequence 993, App
566	16	1.8	2871	4	US-08-457-176-1	Sequence 1, Appl1	C 639	16	1.8	12715	4	US-09-949-016-11718	Sequence 17148, A
567	16	1.8	2947	1	US-08-457-175-1	Sequence 1, Appl1	C 640	16	1.8	13426	4	US-09-902-540-1132	Sequence 1132, Ap
568	16	1.8	2947	1	US-08-457-175-1	Sequence 1, Appl1	C 641	16	1.8	13426	4	US-09-949-016-13683	Sequence 13683, A
569	16	1.8	2976	4	US-09-220-132-8	Sequence 8, Appl1	C 642	16	1.8	13637	3	US-09-105-537-3	Sequence 3, Appl1
570	16	1.8	2976	4	US-09-302-540-554	Sequence 554, App	C 643	16	1.8	13637	4	US-09-902-540-1097	Sequence 1097, Ap
571	16	1.8	2980	4	US-09-352-991A-13468	Sequence 13468, A	C 644	16	1.8	13644	4	US-09-949-016-13054	Sequence 13054, A
572	16	1.8	3027	4	US-09-799-451-652	Sequence 5268, Ap	C 645	16	1.8	15445	4	US-09-949-016-11271	Sequence 17271, A
573	16	1.8	3070	4	US-09-949-016-3877	Sequence 3877, Ap	C 646	16	1.8	17247	4	US-09-902-540-1185	Sequence 1185, Ap
574	16	1.8	3105	4	US-09-352-991A-4398	Sequence 4398, Ap	C 647	16	1.8	17662	4	US-09-902-540-1146	Sequence 1146, Ap
575	16	1.8	3145	4	US-09-788-657-9	Sequence 9, Appl1	C 648	16	1.8	18324	4	US-09-902-540-1196	Sequence 1196, Ap
576	16	1.8	3145	4	US-09-712-691-12	Sequence 12, Appl1	C 649	16	1.8	19662	4	US-09-949-016-14877	Sequence 14877, A
577	16	1.8	3145	4	US-09-707-468C-12	Sequence 12, Appl1	C 650	16	1.8	19112	4	US-09-902-540-1181	Sequence 1181, Ap
578	16	1.8	3153	4	US-09-922-501-13	Sequence 13, Appl1	C 651	16	1.8	19598	4	US-09-902-540-1143	Sequence 1143, Ap
579	16	1.8	3458	4	US-09-105-470B-8	Sequence 7, Appl1	C 652	16	1.8	20740	4	US-09-902-540-1223	Sequence 1223, Ap
580	16	1.8	3512	4	US-09-749-340-7	Sequence 674, App	C 653	16	1.8	22311	4	US-09-949-016-12344	Sequence 12344, A
581	16	1.8	3512	4	US-09-949-016-3877	Sequence 3877, Ap	C 654	16	1.8	22327	4	US-09-949-016-11217	Sequence 17217, A
582	16	1.8	3641	4	US-09-949-016-3877	Sequence 3877, Ap	C 655	16	1.8	22927	4	US-09-949-016-11849	Sequence 11849, A
583	16	1.8	3650	4	US-09-620-312D-30	Sequence 30, Appl1	C 656	16	1.8	22927	4	US-09-949-016-13071	Sequence 13071, A
584	16	1.8	3657	4	US-09-976-451-10	Sequence 10, Appl1	C 657	16	1.8	23257	4	US-09-949-016-12894	Sequence 12894, A
585	16	1.8	3657	4	US-09-976-451-10	Sequence 10, Appl1	C 658	16	1.8	23260	4	US-09-949-016-13300	Sequence 13300, A
586	16	1.8	3675	4	US-09-352-991A-16309	Sequence 16309, A	C 659	16	1.8	23560	4	US-09-949-016-13364	Sequence 13364, A
587	16	1.8	3699	4	US-09-302-540-3731	Sequence 3731, Ap	C 660	16	1.8	25404	4	US-09-949-016-13416	Sequence 13416, A
588	16	1.8	3867	4	US-09-302-540-572	Sequence 572, App	C 661	16	1.8	26289	4	US-09-902-540-1210	Sequence 1210, Ap
589	16	1.8	3924	4	US-09-023-655-1168	Sequence 1168, Ap	C 662	16	1.8	26289	4	US-09-902-540-1210	Sequence 1210, Ap
590	16	1.8	3924	4	US-09-762-195-2	Sequence 2, Appl1	C 663	16	1.8	27908	4	US-09-949-016-12397	Sequence 12397, A
591	16	1.8	4018	4	US-09-302-540-616	Sequence 616, App	C 664	16	1.8	27909	4	US-09-949-016-11082	Sequence 17082, A
592	16	1.8	4175	4	US-09-302-540-609	Sequence 609, App	C 665	16	1.8	29667	4	US-09-949-016-12535	Sequence 12535, A
593	16	1.8	4175	4	US-09-749-340-3	Sequence 3, Appl1	C 666	16	1.8	29993	4	US-09-949-016-17476	Sequence 17476, A
594	16	1.8	4195	4	US-09-302-540-695	Sequence 695, App	C 667	16	1.8	29993	4	US-09-949-016-15740	Sequence 15740, A
595	16	1.8	4279	4	US-09-672-725C-1	Sequence 1, Appl1	C 668	16	1.8	29885	4	US-09-785-381-6	Sequence 6, Appl1
596	16	1.8	4279	4	US-09-672-725C-22	Sequence 22, Appl1	C 669	16	1.8	29885	4	US-09-949-016-13682	Sequence 13682, A
597	16	1.8	4279	4	US-09-672-725C-24	Sequence 24, Appl1	C 670	16	1.8	30336	4	US-09-949-016-12268	Sequence 12268, A
598	16	1.8	4279	4	US-09-672-725C-26	Sequence 26, Appl1	C 671	16	1.8	30337	4	US-09-949-016-15508	Sequence 16508, A
599	16	1.8	4317	4	US-09-672-725C-3	Sequence 3, Appl1	C 672	16	1.8	31035	4	US-09-949-016-12272	Sequence 12272, A
600	16	1.8	4317	4	US-10-044-671-1	Sequence 1, Appl1	C 673	16	1.8	31035	4	US-09-949-016-17266	Sequence 17266, A
601	16	1.8	4663	4	US-09-949-016-2387	Sequence 2387, Ap	C 674	16	1.8	31440	4	US-09-949-016-12578	Sequence 12578, A
602	16	1.8	4991	4	US-09-902-540-719	Sequence 719, App	C 675	16	1.8	31444	4	US-09-949-016-15400	Sequence 16400, A
603	16	1.8	5102	1	US-08-94A-168-1	Sequence 1, Appl1	C 676	16	1.8	34312	4	US-09-949-016-13352	Sequence 12352, A
604	16	1.8	5184	4	US-09-845-583A-9	Sequence 9, Appl1	C 677	16	1.8	35081	2	US-08-752-760A-1	Sequence 1, Appl1
605	16	1.8	5184	4	US-09-561-709B-4	Sequence 4, Appl1	C 678	16	1.8	36387	4	US-09-949-016-13370	Sequence 12370, A
606	16	1.8	5570	4	US-09-302-540-623	Sequence 623, App	C 679	16	1.8	36387	4	US-09-949-016-12543	Sequence 12543, A
607	16	1.8	5610	4	US-09-262-537-57	Sequence 57, Appl1	C 680	16	1.8	37068	4	US-09-949-016-11376	Sequence 17376, A
608	16	1.8	5931	3	US-08-783-774-1	Sequence 1, Appl1	C 681	16	1.8	37068	4	US-09-949-016-11376	Sequence 17376, A
609	16	1.8	5931	3	US-09-556-706B-1	Sequence 1, Appl1	C 682	16	1.8	38653	4	US-09-922-445-1	Sequence 1, Appl1
610	16	1.8	5931	4	US-09-724-418A-1	Sequence 1, Appl1	C 683	16	1.8	39113	4	US-09-949-016-15634	Sequence 15634, A
611	16	1.8	5931	4	US-09-949-016-11975	Sequence 11975, A	C 684	16	1.8	40429	4	US-08-311-731A-125	Sequence 125, App

665	16	1.8	41937	4	US-09-902-540-1268	Sequence 1268, Ap	758	16	1.8	156895	4	US-09-949-016-16958	Sequence 1658, A
C 666	16	1.8	44377	2	US-08-804-227C-7	Sequence 7, Appl	759	16	1.8	156895	4	US-09-949-016-16959	Sequence 1659, A
C 687	16	1.8	44377	2	US-08-804-199-1	Sequence 1, Appl	760	16	1.8	156895	4	US-09-497-855A-40	Sequence 40, Appl
C 688	16	1.8	47727	4	US-09-949-016-12904	Sequence 12904, A	761	16	1.8	177669	4	US-09-949-016-13713	Sequence 13713, A
C 689	16	1.8	50937	3	US-09-428-517-1	Sequence 1, Appl	762	16	1.8	177669	4	US-09-949-016-13713	Sequence 12733, A
C 690	16	1.8	51849	4	US-09-949-016-15433	Sequence 15433, A	763	16	1.8	178884	4	US-09-949-016-13039	Sequence 13039, A
C 691	16	1.8	52199	4	US-09-949-016-12763	Sequence 12763, A	764	16	1.8	183202	4	US-09-949-016-13614	Sequence 13614, A
C 692	16	1.8	52203	4	US-09-949-016-16330	Sequence 16330, A	765	16	1.8	187848	4	US-09-949-016-12111	Sequence 12111, A
C 693	16	1.8	61199	4	US-09-949-016-14386	Sequence 14386, A	766	16	1.8	187916	4	US-09-949-016-12980	Sequence 12980, A
C 694	16	1.8	61961	4	US-09-949-016-16419	Sequence 16419, A	767	16	1.8	236964	4	US-09-949-016-15753	Sequence 15753, A
C 695	16	1.8	61923	4	US-09-949-016-15338	Sequence 15338, A	768	16	1.8	239527	4	US-09-949-016-15980	Sequence 15980, A
C 696	16	1.8	61922	4	US-09-949-016-11772	Sequence 11772, A	769	16	1.8	247781	4	US-09-949-016-14193	Sequence 14193, A
C 697	16	1.8	62386	4	US-09-949-016-12823	Sequence 12823, A	C 770	16	1.8	390890	4	US-09-949-016-14720	Sequence 14720, A
C 698	16	1.8	62386	4	US-09-949-016-12539	Sequence 12539, A	771	16	1.8	784019	4	US-09-949-016-14033	Sequence 14033, A
C 699	16	1.8	63428	4	US-09-949-016-12426	Sequence 12426, A	772	16	1.8	828152	4	US-09-949-016-12777	Sequence 12777, A
C 700	16	1.8	67745	4	US-09-949-016-17251	Sequence 17251, A	773	16	1.8	1664976	4	US-08-916-421B-1	Sequence 1, Appl
C 701	16	1.8	69924	4	US-09-949-016-15367	Sequence 15367, A	C 774	16	1.8	1664976	4	US-08-916-421B-1	Sequence 1, Appl
C 702	16	1.8	70828	4	US-09-949-016-13122	Sequence 13122, A	C 775	16	1.8	1664976	4	US-09-692-570-1	Sequence 1, Appl
C 703	16	1.8	72742	4	US-09-949-016-16161	Sequence 16161, A	C 776	16	1.8	1664976	4	US-09-692-570-1	Sequence 1, Appl
C 704	16	1.8	76610	4	US-09-949-016-15521	Sequence 15521, A	777	15	1.7	21	4	US-09-778-510-14	Sequence 14, Appl
C 705	16	1.8	77626	4	US-09-949-016-11941	Sequence 11941, A	C 778	15	1.7	25	4	US-09-396-196G-36122	Sequence 36122, A
C 706	16	1.8	81433	4	US-09-949-016-11608	Sequence 11608, A	779	15	1.7	25	4	US-09-396-196G-56577	Sequence 56577, A
C 707	16	1.8	84237	4	US-09-949-016-17374	Sequence 17374, A	780	15	1.7	25	4	US-09-396-196G-76630	Sequence 76630, A
C 708	16	1.8	84875	4	US-09-949-016-17334	Sequence 17334, A	C 781	15	1.7	76	4	US-09-270-767-4890	Sequence 4890, Ap
C 709	16	1.8	84875	4	US-09-949-016-17335	Sequence 17335, A	C 782	15	1.7	76	4	US-09-270-767-20172	Sequence 20172, A
C 710	16	1.8	84875	4	US-09-949-016-17336	Sequence 17336, A	C 783	15	1.7	81	2	US-07-814-220-34	Sequence 34, Appl
C 711	16	1.8	84875	4	US-09-949-016-17337	Sequence 17337, A	C 784	15	1.7	81	2	US-07-814-220-31	Sequence 31, Appl
C 712	16	1.8	85152	4	US-09-949-016-12666	Sequence 12666, A	C 785	15	1.7	82	2	US-07-814-220-31	Sequence 31, Appl
C 713	16	1.8	85152	4	US-09-949-016-12666	Sequence 12666, A	C 786	15	1.7	82	2	US-07-814-220-31	Sequence 31, Appl
C 714	16	1.8	85152	4	US-09-949-016-12667	Sequence 12667, A	C 787	15	1.7	89	2	US-07-814-220-35	Sequence 35, Appl
C 715	16	1.8	85152	4	US-09-949-016-12668	Sequence 12668, A	788	15	1.7	89	2	US-07-814-220-35	Sequence 35, Appl
C 716	16	1.8	86127	4	US-09-949-016-12209	Sequence 12209, A	789	15	1.7	90	2	US-07-814-220-32	Sequence 32, Appl
C 717	16	1.8	86127	4	US-09-949-016-12209	Sequence 12209, A	790	15	1.7	90	2	US-07-814-220-32	Sequence 32, Appl
C 718	16	1.8	87563	3	US-09-949-016-15608	Sequence 15608, A	791	15	1.7	138	4	US-09-902-540-5103	Sequence 5103, Ap
C 719	16	1.8	89210	4	US-09-949-016-16988	Sequence 16988, A	792	15	1.7	150	3	US-09-495-052-39	Sequence 39, Appl
C 720	16	1.8	92227	4	US-09-949-016-11929	Sequence 11929, A	793	15	1.7	156	3	US-09-277-078-45	Sequence 45, Appl
C 721	16	1.8	92232	4	US-09-949-016-15421	Sequence 15421, A	794	15	1.7	156	4	US-09-621-976-9095	Sequence 9095, Ap
C 722	16	1.8	93364	4	US-09-949-016-14890	Sequence 14890, A	795	15	1.7	164	4	US-09-313-294A-6924	Sequence 6924, Ap
C 723	16	1.8	98828	4	US-09-949-016-16300	Sequence 16300, A	796	15	1.7	166	4	US-09-513-999C-29205	Sequence 29205, A
C 724	16	1.8	104428	4	US-09-949-016-12737	Sequence 12737, A	C 797	15	1.7	173	4	US-09-513-999C-14602	Sequence 14602, A
C 725	16	1.8	104428	4	US-09-949-016-12737	Sequence 12737, A	798	15	1.7	177	1	US-08-470-179-84	Sequence 84, Appl
C 726	16	1.8	113966	4	US-09-949-016-12277	Sequence 12277, A	799	15	1.7	181	4	US-09-270-767-1608	Sequence 1608, Ap
C 727	16	1.8	113966	4	US-09-949-016-12277	Sequence 12277, A	800	15	1.7	181	4	US-09-270-767-19890	Sequence 19890, A
C 728	16	1.8	117807	4	US-09-949-016-17051	Sequence 17051, A	801	15	1.7	183	4	US-09-583-110-713	Sequence 713, App
C 729	16	1.8	118143	4	US-09-949-016-11525	Sequence 11525, A	802	15	1.7	184	4	US-09-513-999C-28288	Sequence 28288, A
C 730	16	1.8	118143	4	US-09-949-016-11525	Sequence 11525, A	803	15	1.7	186	4	US-09-583-110-2405	Sequence 2405, Ap
C 731	16	1.8	119032	4	US-09-949-016-11268	Sequence 11268, A	804	15	1.7	186	4	US-09-248-796A-11182	Sequence 11182, A
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ALIGNMENTS

RESULT 1

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; Sequence 853, Application US/09620312D
; Patent No. 6569662

; GENERAL INFORMATION:

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; TYPE: DNA

; ORGANISM: Homo sapiens

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; LOCATION: (151) .. (984)

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Query Match 30.9%; Score 281; DB 4; Length 1067;
Best Local Similarity 99.3%; Pred. No. 2.2e-122;

Matches 431; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 211 TACGGAGTCTGCTGCTTACCCGATATGTTGAGTGTGTGGCGGGCACTGACGAGTGC 270

QY 121 GAGCTGAGCTCTCGGCTTCTGCTGATAGAGCTCTGAGCGCGCGGAGGCTTACG 180

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QY 271 GAGCTGAGCTCTCGGCTTCTGCTGATAGAGCTCTGAGCGCGCGGAGGCTTATCC 330

Db 271 GAGCTGAGCTCTCGGCTTCTGCTGATAGAGCTCTGAGCGCGCGGAGGCTTATCC 330

QY 181 CGGGCCGACGCGGCTTACGCTCTGCTGAGTGTGAGCGCGCGGCACTGCTGCTGCG 240

Db 331 CGGGCCGACGCGGCTTACGCTCTGCTGAGTGTGAGCGCGCGGCACTGCTGCTGCG 240

QY 241 AGCAACTGCGGCTGCTGCTGCGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCG 300

Db 391 AGCAACTGCGGCTGCTGCTGCGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCG 300

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Db 571 AATTCTCAGCAGGG 584

RESULT 2
US-09-252-991A-2993/c
; Sequence 2993, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 2993
; LENGTH: 2673
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-2993

Query Match

2.2%; Score 20; DB 4; Length 2673;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 308 CGCGCAAGCGCGCGCGCA 327

Db 1472 CGCGCAAGCGCGCGCGCA 1453

RESULT 3
US-09-252-991A-2686
; Sequence 2686, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS


```
/ TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ CURRENT FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 2686
/ LENGTH: 2715
/ TYPE: DNA
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2686

Query Match      2.2%; Score 20; DB 4; Length 2715;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      308 CGCGCAAGCGCGCGCGCA 327
      |||||
DB      1313 CGCGCAAGCGCGCGCGCA 1332

RESULT 4
US-09-252-991A-2875
/ Sequence 2875, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ CURRENT FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 2875
/ LENGTH: 2814
/ TYPE: DNA
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2875

Query Match      2.2%; Score 20; DB 4; Length 2814;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      308 CGCGCAAGCGCGCGCGCA 327
      |||||
DB      1371 CGCGCAAGCGCGCGCGCA 1390

RESULT 5
US-09-949-016-21931/C
/ Sequence 21931, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ TYPE: DNA
/ ORGANISM: Human
```

```
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 21931
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-21931

Query Match      2.1%; Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      362 GCTCTCAAGAGACAGA 380
      |||||
DB      584 GCTCTCAAGAGACAGA 566

RESULT 6
US-09-949-016-21932/C
/ Sequence 21932, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 21932
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-21932

Query Match      2.1%; Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      362 GCTCTCAAGAGACAGA 380
      |||||
DB      233 GCTCTCAAGAGACAGA 215

RESULT 7
US-09-949-016-21933/C
/ Sequence 21933, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 21933
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
```


US-09-949-016-21933

Query Match 2.1%; Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 GCTCTTCAAGAGACAGA 380
DB 93 GCTCTTCAAGAGACAGA 75

RESULT 8
US-09-949-016-21934/C
; Sequence 21934, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21934
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-21934

Query Match 2.1%; Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 GCTCTTCAAGAGACAGA 380
DB 77 GCTCTTCAAGAGACAGA 59

RESULT 9
US-09-949-016-21935/C
; Sequence 21935, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21935
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-21935

Query Match 2.1%; Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 GCTCTTCAAGAGACAGA 380
DB 30 GCTCTTCAAGAGACAGA 12

RESULT 10
US-09-949-016-84252/C
; Sequence 84252, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84252
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-84252

Query Match 2.1%; Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 GCTCTTCAAGAGACAGA 380
DB 584 GCTCTTCAAGAGACAGA 566

RESULT 11
US-09-949-016-84253/C
; Sequence 84253, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84253
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-84253

Query Match 2.1%; Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 GCTCTTCAAGAGACAGA 380
DB 233 GCTCTTCAAGAGACAGA 215


```
RESULT 12
US-09-949-016-84254/C
; Sequence 84254, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84254
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-84254
```

```
Query Match          2.1% Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      362 GCTCTTCAAGAGACAGA 380
DB      93 GCTCTTCAAGAGACAGA 75
```

```
RESULT 13
US-09-949-016-84255/C
; Sequence 84255, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84255
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-84255
```

```
Query Match          2.1% Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      362 GCTCTTCAAGAGACAGA 380
DB      77 GCTCTTCAAGAGACAGA 59
```

```
RESULT 14
US-09-949-016-84256/C
; Sequence 84256, Application US/09949016
; Patent No. 6812339
```

```
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84256
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-84256
```

```
Query Match          2.1% Score 19; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      362 GCTCTTCAAGAGACAGA 380
DB      30 GCTCTTCAAGAGACAGA 12
```

```
RESULT 15
US-09-270-767-27566
; Sequence 27566, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27566
; LENGTH: 878
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-27566
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Query Match          2.1% Score 19; DB 4; Length 878;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      123 GCTGAGCTCTGCGCTTT 141
DB      388 GCTGAGCTCTGCGCTTT 406
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Search completed: February 12, 2005, 15:26:52
Job time : 181 secs
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Qy	61	TACGGATGCTGTCGGCTTACCGTATGTTCAAGAGTGAGGGCCGAGCAATCAACGAATGC	120
Db	211	TACGGATGCTGTCGGCTTACCGTATGTTCAAGAGTGAGGGCCGAGCAATCAACGAATGC	270
Qy	121	GACCTGAGGCTCTGGCCCTTTCTGCTGATGATGAGGCTCTCGGCGCCGCGAGCTTAGCC	180
Db	271	GACCTGAGGCTCTGGCCCTTTCTGCTGATGATGAGGCTCTCGGCGCCGCGAGCTTAGCC	330
Qy	181	CGGACCGCGAGCGGCTTAGAGCTCTGCTGAGAGCTGAGACCGCGCGGGCAATGCGGAG	240
Db	331	CGGACCGCGAGCGGCTTAGAGCTCTGCTGAGAGCTGAGACCGCGCGGGCAATGCGGAG	390
Qy	241	AGCAACTGCGGCTGCTGCGGCACTCTGCGCGTGTGG-CCCGCACGACTGTGCGG	300
Db	391	AGCAACTGCGGCTGCTGCGGCACTCTGCGCGTGTGG-CCCGCACGACTGTGCGG	450
Qy	301	CACCTGACGCGCAAGCGGCGCGCGCAAGTGTCCAGAAAGCTTAGCTTAGGCACTCC	360
Db	451	CACCTGACGCGCAAGCGGCGCGCGCAAGTGTGTCCAGAAAGCTTAGCTTAGGCACTCC	510
Qy	361	AGCTCTTCAAGAGGACAGAGGATAGCTGCGCGCTGCGGAGTCAAGCAATGTTGCA	420
Db	511	AGCTCTTCAAGAGGACAGAGGATAGCTGCGCGCTGCGGAGTCAAGCAATGTTGCA	570
Qy	421	AATTCTCAGAGGGTCAGTGGGAGACAGGCTCCCCCAACAAGCGGCAAGCGGCGAGT	480
Db	571	AATTCTCAGAGG-----GGCTTCCCCCAACAAGCGGCAAGCGGCGAGT	615
Qy	481	CGGGGCGCGCCCAAGTGTGTGCCAGACCGCGCGAGAGGGGCCAGCGCACCCAG	540
Db	616	CGGGGCGCGCCCAAGTGTGTGTCAGACCGCGCGGAGAGGGGCCAGCGCACCCAG	675
Qy	541	CACCACTCAGAGCGCGCGCACCTTCTCTAAGCAAAAGGACCTGTGACATCCG	597
Db	676	CACCACTCAGAGCGCGCGCACCTTCTCTAAGCAAAAGGACCAACACCACTG	732

RESULT 2
US-09-733-167A-2
; Sequence 2, Application US/09733167A
; Datafile: 550CF47

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? APPLICANT: Peter, Marcus
? APPLICANT: Krammer, Peter
? TITLE OF INVENTION: Protein for Regulation of Apoptosis
? FILE REFERENCE: 4121-120
? CURRENT APPLICATION NUMBER: US/09/733,167A
? CURRENT FILING DATE: 2000-12-08
? PRIOR APPLICATION NUMBER: PCT/DE99/01712
? PRIOR FILING DATE: 1999-06-08
? PRIOR APPLICATION NUMBER: German Patent Application No. 6696547
? PRIOR FILING DATE: 1998-06-08
? NUMBER OF SEQ ID NOS: 10
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 2

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? LENGTH: 1142
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: (1042)..(1042)
? OTHER INFORMATION: n represents any one of a, c, t, and g
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: (1043)..(1043)
? OTHER INFORMATION: n represents any one of a, c, t, and g
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: (1114)..(1114)
? OTHER INFORMATION: n represents any one of a, c, t, and g
US-09-733-167A-2

```

Query Match 21.3%; Score 193.8; DB 4; Length 1142;

Best Local Similarity	52.9%;	Pred. NO. 1.7e-34;					
Matches 467;	Conservative	0;	Mismatches 407;	Indels	9;	Gaps	2

QY	27	CCGCTCTGGAGAGAGATAGTCCTGGACTATCTACGGAATGCTGTGCTTCACCGTAT	86
Db	54	CGAGGTGTCCAGAAAGCATGTGTGACAGGAACCGGGCTTACACAGCTCCACCGCAT	113
QY	87	GTTTCAGGTGTGGCGGGCAACTGACCGAGTGCAGCTGAGGCTCTTGCT	146
Db	114	GTTTGACATCGGGGCACTCATCTGACACAGAGATGTGGCGCTTTCTTCCCTT	173
QY	147	GGATGAGGCTCCCGGGCGCCCGAGAGGTTAGCCCGGGCCCGCAGGGCCCTAGAGCTT	206
Db	174	TGTTGATGTCAATTGATGACACAGACGGTGACTCTA---CCGAATGAGTGACTTCTT	230
QY	207	GCTGAGCTGAGAGCGCCGGGCACTGTGGGAGAGCAACTGTGGCTGTGGGGCACT	266
Db	231	ATTGGCACTGAGCGCAGGGCCGCTGTGATGAAATGATCTTTTGCCAGGTGTGAGCT	290
QY	267	CTGTCCCGGTGTGGCCCGCAGACCTGTCTCCGCACTGTGGCGGCAAGCGCGCGCC	326
Db	291	GCTGCGCATATCACTGTCCAGACACTGTCTCCTTAAGTCACTTCAAGAGAGACGGCG	350
QY	327	AGGTGTCCAGAACGCTATAGCTATGTGACCTCCAGCTCTTCAAGAGAGACAGGGTAG	386
Db	351	TGTGTCCCTGTATCTTTGAGCAAGTATCTGGAGAGACATCAATTGCTATGTGACCC	410
QY	387	CTGCGCTGCGCCGTGGCAGTCAAGCATTTCTGCAATTTCTGACAGGGTCAGTGGAGAC	446
Db	411	CAGAGCCTCAGTGATTCAGAACCAAGGCC-----TCCCGAGCCTCTTAAACAGTGGC	464
QY	447	AGGCTCCCCCAACCAAGCGGACGGCGGAGTCCGGGGCCGGCCAGTGTGTGCGACG	506
Db	465	TCCCCACTATCTGTGTGTGTGTGTGCTCCACTTCGGGTCTTCAGATGTGTAGCAAGCGCC	524
QY	507	ACGGCGGCGAGAGGGGCCCAAGCCGACCCCAAGACAGTCAAGGCCCGCAGACTTTC	566
Db	525	AGCCCGAGGGAGAGCCACACTTGGGAGCGACGAAACGCCGGAAGTCAGTGACACAGA	584
QY	567	CTCTGAAGGCAAAGTGAAGCTGTGACATTCGGGCTCCGGGTTGAGACAGATGCTGCGACG	626
Db	585	TCCAAAGGAAAGCAGACATGTGAATCAGCTCGGGTTTCGGCTGAAATACGACAGA	644
QY	627	TGGGCAAGCTTTGAGAGAGGGCGTGGCATCCCGCGGCCCAAGAGCGCTGCGCGGAGCT	686
Db	645	TGAGACTGTCTCGAGGGGCAATGTCTTCTTCAACACAGAGCCCATTTGAGCGCAAGTT	704
QY	687	GGAAGTGTTTGGGCGAGGCCACCGCAGTGTGTGCGCTCAAGGACCTTGAGCTTGTGTTTG	746
Db	705	TGAGCGCTTTTAAACAGGGCCAAACACATCTCTCAATCCCGGAACTTGGGCTTCATCTCTG	764
QY	747	TGACATCAAGTTCTCAGAGCTCTCCATCTGGAAGCCTTCTGGGGGCACTACCTGAGTGG	806
Db	765	TGACATCAAGTTCTCTGAGCTCACCTTACTTGATGCAATTTGGCGTGAATCATATGG	824
QY	807	CGCGCTGTGACAGCGCTGCGGGCGTGTCTTGACTGAGGCCCTGCGAGGCTGTGGG	866
Db	825	CTCTTATTAGAGGCACTTAAAGGTGCTTCATACAGACTCCCTCAAGCAACTGTGGG	884
QY	867	CGGGAGAGCTGTTCCGCTGTGCTGTCAAGTGTGAAGAGGCTGAC	909
Db	885	CCATGAGCCATCAAGCTGTGTGTAATGTAGACAGAGAGAGC	927

RESULT 3
US-08-859-167-3

Sequence 3 Application US/08859167
Patent No. 6037461
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandez-Alnemri, Teresa
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS

TITLE OF INVENTION: OF MAKING THE SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESS: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461115
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,167
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1045 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 88..1044
US-08-859-167-3

Query Match 21.1%; Score 192.2; DB 3; Length 1045;
Best Local Similarity 52.8%; Pred No. 3.8e-34;
Matches 466; Conservative 0; Mismatches 408; Indels 9; Gaps 2;

QY 27 CCCGCTGCTGGAGAGAGTAGTGCCTTGACTACTAGCGGAGTCTGCTTACCCGAT 86
DB 114 CCAAGTGTGGCCAGAAAGAGATGTAGAGAGAAACATGGGCTGTACAGCTGCACCGCAT 173
QY 87 GTTCAGAGTGTGGGCGGCACTGACCGAGTCCAGAGCTGTGCTCTTCTGCT 146
DB 174 GTTGCATCGGGCAGCTCATCTGACACACAGATGTGCGCGTCTTCTTCTCTT 233
QY 147 GGATAGAGCTCTGGGCGCGCGGAGGCTTACCGCGGCGCGAGCGGCTAGAGCTCCT 206
DB 234 TGTTCATGTCTATTGATGACACGAGCGTGTGACTC---ATCCAAATGACGTGACTTCTT 290
QY 207 GCTGAGCTGAGCGCCGCGGAGTGTGCGGCGAGAGCAACTCTGCGGCTGCTGGGCACT 266
DB 291 ATTGCACCTGAGCGCCAGGCGCGCTGTGATGAAAGTAACTTTCGAGGTGCTGAGCT 350
QY 267 CCTGCGGCTGTGGCGCCGACGACTGTGCTGCGCACTGTGGCGGCGAGCGCGCGGCG 326
DB 351 GCTGGGCACTCATCTGCGCAGAGCTGTGCTGCTTACGTCACCTCAAGAGAGAGCGGCG 410
QY 327 AGTGTCTCAGAAAGCTATAGCTATGAGCACTCCAGCTTCAAAAGAGAGAGAGGTG 386
DB 411 TGTGTGCTCTGATCTTTGTAGACAGATGTGAGAGAGACATCAATTCGCTATGTGACCCC 470
QY 387 CTGCGGTGCGCGTGTGAGCACTGAGCACTTCTCAAAATTCAGCAAGGCTCAGTGGAGAC 446
DB 471 CAGAGCCCTCAGTGTATCCAGAACAAAGGCG-----TCCGAGCGCCCTTAATAACAGTGC 524
QY 447 AGGCTTCCCCCAACCAAGCGGAGCGGCGGAGTGTGGGCGCGCCCACTGTGTGTCCAG 506
DB 525 TCCCACTATCTGTGTGTGTGTGCCCCCACTTGGGTCTCTCAGATGTGTAGCAAGCGGCG 584

QY 507 ACGCGCGGAGAGAGGCGCCAGCGGACCCAGAGAGTCAAGCCCGCAGACTTC 566
DB 585 AGCCGAGAGAGGACCACTTGGAGGCGAGGAAAGCGCGGAAGTCACTGAGACACAGA 644
QY 567 CTGGAAGCAAGTACCTGTGACATCCGGCTCCGGGTTGAGAGAGTACTGAGACA 626
DB 645 TCCCAAGAGAGAGAGAGATGTGACATGACATGCGGGGTTGGGCTGTAATCTGCACGA 704
QY 627 TGGGCGAGCTTGGAGAGGCGGTGAGCATCCCGGCGGCCAGAGGCGCTGGCGGCGACT 686
DB 705 TGAGCTCTCTGAGGCGCAATGTCTTCTTAACAGAGAGAGACCACTTGAAGCGCAATT 764
QY 687 GGACGTGTTTGGGCGGACCGGAGTGTGCTGCTCAAGAGAGACTGTGTGTTG 746
DB 765 TGAAGGCTTAAACAGGCGCAACACATCTCAAGTCCGGGAGCTGGGCTCATCATCTG 824
QY 747 TGACATCAAGTTCTCAGAGCTCTCTATCTGAGAGCGCTTGTGGGCGACTACCTGAGTGG 806
DB 825 TGACATCAAGTTCTCTGAGCTCACTACCTGATGATCTTGGCGGTGACTATCATATGG 884
QY 807 CGCCCTGTGAGAGCGCCGCGGGGCGGTCTCTGCTGAGAGCGCTGAGAGAGAGCTGTGGG 866
DB 885 CTCTTATTAGAGCACTTAAAGTGTCTTCAATCAAGACTCTCTCAAGCAAGCTGTGGG 944
QY 867 CCGGAGGCTGTTCGCTGTGCTGATGATGATGAGGCTGAC 909
DB 945 CCATGAGCCATCAAGCTGTGTGTAATGTAGAGAGAGAGAC 987

RESULT 4
US-09-109-273-3
Sequence 3, Application US/09109273
Patent No. 6063760
GENERAL INFORMATION:
APPLICANT: Alnemti, Emad S.
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESS: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760115
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,273
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,167
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1045 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: CDNA


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FEATURE:
; NAME/KEY: CDS
; LOCATION: 88..1044
US-09-109-273-3

Query Match      21.1%; Score 192.2; DB 3; Length 1045;
Best Local Similarity 52.8%; Pred. No. 3.8e-34;
Matches 466; Conservative 0; Mismatches 408; Indels 9; Gaps 2;

Oy 27 CCCGTGCTGGAGAGAGATGAGTGCCTGACTACTACGAGATGCTGCTTCAACCGTAT 86
Db 114 CCAGGTGTGGCCAGAAAGACATGTGTAGAGAGACATGGGCTGTACAGCTTGACCGCAT 173
Oy 87 GTTCAGAGTGTGGGCGGCGCACTGACCGAGTGCAGCTGCGACTCTGCGCTTTCTGCT 146
Db 174 GTTTGACATCGTGGGCACTCATCTGACACACAGAGATGTGCGCGTCTTTCTTCTCTT 233
Oy 147 GGATGAGGCTCCTGGCGCGCGGAGGCTTACCGCGGCGCGACGCGCTAGACTCCT 206
Db 234 TGTTCATGTCAATTGATGACACAGAGCGTGTGACTC--ATCCGAAATGACGTGACTTCTT 290
Oy 207 GCTGAGCTGAGAGCGCGCGGCGGAGTGGCGGCGAGAGACAACTGCGGCTGTGGGCAACT 266
Db 291 ATTGGCACTGAGAGCGCGCGGCGGCTGTGTATGAAAGTAACTTTCCGCAAGTGTCTGAGCT 350
Oy 267 CCTGCGCTGTGCGCGCGCGACGACTTGTCTGCGCACTGCGCGGCGAGCGCGCGCC 326
Db 351 GCTGGCATCATCACTGCGCGACGACCTGCTGCTTACGTCACCTCAAGAGAGAGACGCGGC 410
Oy 327 AGTGTCTCCAGAAAGCTATAGCTATGAGCACTCCAGCTCTTCAAGAGAGACAGAGGTAG 386
Db 411 TGTGTGCTCTGATCTTTGTAGACATATCTGGAGAGACATTAATTCGTATGTACCCC 470
Oy 387 CTGCGGTGCGCGTGGCGAGTCAAGCAATTTCTGCAAGAGGTCTAGTGGAGAC 446
Db 471 CAGAGCCCTCAGTATCCAGAACAAAGGC-----TCCGAGCCCTCTAAAGAGTGC 524
Oy 447 AGGCTCCCCCAACCAAGCGGCGAGCGGAGTGGGGCGGCGGCAAGTGTGTGCTGCG 506
Db 525 TCCCATCATCTGTGTGTGTGTGCGCCCACTTCGCGGTCTCTAGATGTGTAGCAGCGGC 584
Oy 507 ACGGCGGAGAGAGAGGCGCGGCGGACCCGAGAGAGTCAAGAGCGCGCGACGCTTC 566
Db 585 AGCCGAGAGAGAGAGCACTTTGGAGCGGAGGAAACCGCGAATGTACATGACACGAGA 644
Oy 567 CTCTGAAGGCAAAAGTACCTGTGATCCGCTCCGAGTTGAGCAGAGTACTGCGACA 626
Db 645 TCCCAAGAGAGAGAGCATGTGATCATGACTGGGGTTGGGCTGTAATCTGCGACACA 704
Oy 627 TGGGCGAGCTTTGAGAGAGGCGGTGGCATCCGCGCGCGCCGAGGCGCTGGCGCGGAGCT 686
Db 705 TGAAGCTGCTCTGCAAGGCAATGTCTTCTTAAACAAGAGAGACCACTTGAAGCGCACTT 764
Oy 687 GAGCGTGTGGGCGGCGGCGGAGCTGTGCGCTCAAGGAGCGTGGGCTGTGGTTG 746
Db 765 TGAAGGCTTTAAACAGGCGCAACATCTCAAGTCCGCGAAGCTGGGCTCATATCTG 824
Oy 747 TGAATCAAGTTCTCAGAGCTCTCTTATCTGAGCGCTTCTGGGCGCATCTAGTGTG 806
Db 825 TGAATCAAGTTCTCTGAGCTCACTTACCTGATTCATTTGGCGGTGACTATCATATG 884
Oy 807 CGCCCTGTGAGAGCGCTGGCGGCGGTGTCTCTGACTAGAGCGCTGGCAGAGGCTGTGG 866
Db 885 CTCTTATTTAAGGAGACTTAAAGGTGTCTTATCAACAACTCCCTCAAGAGGCTGTGG 944
Oy 867 CCGGAGAGCTGTGCGCTGTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 909
Db 945 CCAATGAAGCATCAAGCTGTGTGTATGTATGTATGTATGTATGTATGTATGTATGTATG 987
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RESULT 5
US-09-276-993-3
; Sequence 3, Application US/09276993

```
; Patent No. 6207801
; GENERAL INFORMATION:
; APPLICANT: Alnemuri, Emad S.
; APPLICANT: Fernandez-Alnemuri, Teresa
; TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
; TITLE OF INVENTION: OF MAKING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801x18
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/276,993
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,167
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TCU-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1045 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 88..1044
US-09-276-993-3

Query Match      21.1%; Score 192.2; DB 3; Length 1045;
Best Local Similarity 52.8%; Pred. No. 3.8e-34;
Matches 466; Conservative 0; Mismatches 408; Indels 9; Gaps 2;

Oy 27 CCCGTGCTGGAGAGAGATGAGTGCCTGACTACTACGAGATGCTGCTTCAACCGTAT 86
Db 114 CCAGGTGTGGCCAGAAAGACATGTGTAGAGAGACATGGGCTGTACAGCTTGACCGCAT 173
Oy 87 GTTCAGAGTGTGGGCGGCGCACTGACCGAGTGCAGCTGCGACTCTGCGCTTTCTGCT 146
Db 174 GTTTGACATCGTGGGCACTCATCTGACACACAGAGATGTGCGCGTCTTTCTTCTCTT 233
Oy 147 GGATGAGGCTCCTGGCGCGCGGAGGCTTACCGCGGCGCGACGCGCTAGACTCCT 206
Db 234 TGTTCATGTCAATTGATGACACAGAGCGTGTGACTC--ATCCGAAATGACGTGACTTCTT 290
Oy 207 GCTGAGCTGAGAGCGCGCGGCGGAGTGGCGGCGAGAGACAACTGCGGCTGTGGGCAACT 266
Db 291 ATTGGCACTGAGAGCGCGCGGCGGCTGTGTATGAAAGTAACTTTCCGCAAGTGTCTGAGCT 350
Oy 267 CCTGCGCTGTGCGCGCGCGACGACTTGTCTGCGCACTGCGCGGCGAGCGCGCGCC 326
Db 351 GCTGCGATCATCACTGCGCGACGACCTGCTGCTTACGTCACCTCAAGAGAGACGCGGC 410
Oy 327 AGTGTCTCCAGAAAGCTATAGCTATGAGCACTCCAGCTCTTCAAGAGAGACAGAGGTAG 386
Db 411 TGTGTGCTCTGATCTTTGTAGACATATCTGGAGAGACATTAATTCGTATGTACCCC 470
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NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 1142
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; US-09-733-167A-4

Query Match 21.0%; Score 190.6; DB 4; Length 1142;
 Best Local Similarity 52.7%; Pred. No. 8.9e-34;
 Matches 465; Conservative 0; Mismatches 409; Indels 9; Gaps 2;

27 CCCGCTGCTGAGAGAGATGAGTGCCTGACTACTACGGAGTCTGTGCTTACCGTAT 86
 54 CCAAGTGTGGCCCGAAGAGCCGTGGAGACCAAAATGGGCTCTACAGCTTCCACCGCAT 113
 87 GTTGAGAGTGTGGGCGGCAACTGACCGAGTGGAGGCTGCTGCTTCTCTCT 146
 114 GTTGACATCTGTGGGACCCCACTTAACACAGAGATGTCGAGTCTTCTTCTTCTT 173
 147 GATGAGGCTCTGTGGCGCCGCGAGGCTTAAGCCCGGCGCGACGCGCTTAGAGCTCT 206
 174 TGTGATGTATATGATGACATGAACG--TGACTCATCCGAATGAGCGTGACTTCTT 230
 207 GCTGAGCTGAGAGCGCCCGGCGAGTGGGAGAGCAACTGCGGCTGTGGGCAACT 266
 231 ATTGCACTGAGAGCGCCAGGCGCGCTGTGAGAGTAACTTCCCGAGTGTGCAACT 290
 267 CCTGGCGCTGTGGCGCCGCGACGACCTGTGCGGAGCTGGGCGCGCAAGCGCGCGCC 326
 291 GCTGGCATCATCATCTGCGCATGACTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTT 350
 327 AGTGTCTTCAGAAAGCTATAGCTATAGCACTTCCAGCTTTTCAAGAGAGAGAGGTAG 386
 351 TGTGGCCCTGATCTTTAGACAAGATATCTGGAGAGAAATCAATTCCTATATGACCCC 410
 387 CTGCGCTGCGCGCGAGTCAAGACATTTCTGCAAGAGGTCTAGTGGAGAC 446
 411 CAGAGCCTCAAGTACCAAGAACGAGGCGC-----TCCCAAGCCTCTTAAACAGTGC 464
 447 AGGCTCCCCCAACCAAGCGGAGCGGAGGTGGGCGCGCGCCCAATGTGTGTGCGAG 506
 465 TCCCACTATCTGT 524
 507 AGCGCGCGAGAGAGGCGCGCGAGCGCGACCCAGACAGATCAGAGCCCGCAGACTTC 566
 525 AGCCGAGGAGAGAACCAACTTGGAGGCGAGCAAAAGCGGAGATGTGTGTGTGTGTGT 584
 567 CTCTGAAGGCAAAATGACCTGTGACATCCGCTCCGGTTTGGAGCAGATCTGTGAGCA 626
 585 CCCAAGGAAAAAGACAGATGTGATTCAGGCTCGAGTTTGGGCGGAAATCTGCGCAGCA 644
 627 TGGGCGAGCTTGGAGCAGGCGTGGCATCCCGGCGCGCCAGGCGCTGGGCGGCGAGCT 686
 645 TGAACCGCTTGCAGAGCAATGTCTTCCAAATAGCAGACCCACTTGTGAGCGCAATT 704
 687 GAGAGTGTGGGAGGCGACCGAGTGTGCTGCTCAAGAGACCTGGGCTGTGTGTGTG 746
 705 TGAACGCTTAAACAGGCGCAACATATCTCAAGTCCCGGAGCCTGGGCTTCATCATCTG 764
 747 TGAATCAAGTTCACAGCTCTCTTATCTGAGAGCGCTTCTGGGCGCACTACAGATGG 806
 765 TGAATCAAGTTCCTGAGCTCACTTACCTTGAAGCAATTTGGGAGACTACATTAATGG 824
 807 CGGCTCTGTGAGGCGCTGCGGCGGTGTTCCTGCTGAGGCGCTGGAGAGAGGCTGTGG 866
 825 CTGATATTAAGAGCACTGAAGGTGTCTTATACAGACTCTTCAAGCAAGCTGTGGG 884
 867 CCGGAGAGCTGTGCTGT 909
 885 CAAATGAACCATCAAGCTGT 927

RESULT 8

US-08-859-167-5

Sequence 5, Application US/08859167

Patent No. 6037461

GENERAL INFORMATION:

APPLICANT: Alnemri, Emad S.

APPLICANT: Fernandez-Alnemri, Teresa

TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF

TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS

TITLE OF INVENTION: OF MAKING THE SAME

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESS: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6037461iris

STREET: One Liberty Place, 46th floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: WINDOWS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/859,167

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Deluca, Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TUN-

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1200 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: both

MOLECULE TYPE: cdna

FEATURE:

NAME/KEY: CDS

LOCATION: 32..988

US-08-859-167-5

Query Match 21.0%; Score 190.6; DB 3; Length 1200;
 Best Local Similarity 52.7%; Pred. No. 9e-34;
 Matches 465; Conservative 0; Mismatches 409; Indels 9; Gaps 2;

27 CCCGCTGCTGAGAGAGATGAGTGCCTGACTACTACGGAGTCTGTGCTTACCGTAT 86
 58 CCAAGTGTGGCCCGAAGAGCCGTGGAGAGCAAAATGGGCTCTACAGCTTCCACCGCAT 117
 87 GTTGAGAGTGTGGGCGGCAACTGACCGAGTGGAGGCTGCTGCTTCTTCTGCT 146
 118 GTTGACATCTGTGGGACCCCACTTAACACAGAGATGTCGAGTCTTCTTCTTCTT 177
 147 GATGAGGCTCTGTGGCGCCCGCGAGGCTTAAGCCCGGCGCGACGCGCTTAGAGCTCT 206
 178 TGTGATGTATATGATGACATGAACG--TGACTCATCCGAATGAGAGCTGTGACTTCT 234
 207 GCTGAGACTGAGAGCGCGCGGCGAGTGGCGAGAGCAACTGTGGGCTGTGGGCAACT 266
 235 ATTGGCACTGAGAGGCGGAGGCGCGCTGTGACAGAGTAACTTTGCGAGGTGTGCAACT 294
 267 CTGCGGCTGTGAGCGCCGCGACGACTGTGCGGACCTGAGCGGCAAGCGGCGCGGCC 326
 295 GCTGGCATCATCACTGCGCATGACTGTGCTGCTTACTTCTTCAAGAAAGAGAGCAGC 354
 327 AGTGTCTCCAGAAAGCTATAGCTATAGGCACTTCAAGTCTTCAAGAGAGAGAGGTAG 386
 355 TGTGTGCTGTATCTTGTAGACAAGTATCTGAGAGAAATCAATTCGCTATGTGACCCC 414

US-09-723-450-5

Query Match 21.0%; Score 190.6; DB 4; Length 1200;
 Best Local Similarity 52.7%; Pred. No. 98-34; Indels 9; Gaps 2;
 Matches 465; Conservative 0; Mismatches 409;

27 CCCGCTGGGAGAGATGAGTGCCTGACTACTACGAGATGCTGCTTACCGTAT 86
 58 CCAAGTGTGGCCGAGAGCGTGGGAGCAAAACATGGGCTCTACAGCTCCACGGAT 117
 87 GTTCAGAGTGTGGGCGGCAACTGACGAGTGCAGCTGAGCTCTGGCTTTCTGCT 146
 118 GTTCACATCTGGGCGACCCCACTTAACAACAGATGTCCAGTGTCTTCTCTCTTT 177
 147 GGATGAGCTCCTGGGCGCGCGGAGGCTTAGCCGGGCGGAGGCGCTAGACTCCT 206
 178 TGTGTATTTATTGATGACATGAACG--TGAATCATTCGAAATGAGCGTGAATCTT 234
 207 GCTGAGCTGAGAGCCCGCGGAGTGCAGGAGAGCAACTGCGGCTGCTGGGCACT 266
 225 ATTGCACTGAGAGCCCGCGGAGTGCAGGAGTGAATCTTCCGCAAGTCTGCACT 294
 267 CCTGCGCTGCTGCGCGCGGAGTGCAGTGTGCGCACTGCGCGCAAGCGCGCGCC 326
 295 GCTGCGCATCATCACTGCGCATGACTGTGCTGCTTACTCTCAAGAAAGACGAGC 354
 327 AGTGTCTCAGAAAGCTATAGCTATAGCACTCCAGCTCTTCAAGAGAGACAGAGTAT 386
 355 TGTGTGCTCTGATCTTTGATGACATGATCTGAGAGAAACATTAATTCGTATGATACCC 414
 387 CTGCGCTGCGCGCGGAGTGCAGGAGTCTGCAATTTCTCAGCAGAGGCTCAGTGGAGAC 446
 415 CAGAGCCCTCACTGACCCGAGAACGAGAGC-----TCCGAGCCCTCTAAAGAGTGC 468
 447 AAGCTTCCCCCAACAGCGGAGCGGAGTGCAGGCGCGCGCGCGCGCGCGCGCG 506
 469 TCCCACTATCTGTGTGTGTGTGTGCTGCGCCCACTTCCGGTTCTCAATGTGATGACGCGC 528
 507 ACGGCGGAGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 566
 529 AGCCGAGAGAGAACCAACTTGGAGCGCGAGAAACCGCGGAGTCCGTGACACGAGA 588
 567 CTCTGAGGCAAGTGAAGCTGTGACATCCGCTCCGCGTTTCGAGAGAGTACTGAGAGA 626
 589 CCGGAGAGAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATG 648
 627 TGGGCAAGCTTGAAGCAGGCGGTGAGCATCCGCGCGCGCGCGCGCGCGCGCG 686
 649 TGAGACGCGCTGTGAGAGGCAATGTCTTCTCAATAAGCAGAGCCCACTTGAAGCGCAGTT 708
 687 GGAAGCTTTTGGGCGAGCGCGAGTGTGCGCTCAAGGAGCTGAGGCTCTGTGGTTTG 746
 709 TGAGGCGCTTAAACAGGCGCAACTATCTCAAGTCCGCGGAGCTGAGGCTCAATCATCTG 768
 747 TGACATCAAGTCTGAGAGCTCTCTATCTGAGAGCGCTTCTGAGGCGCACTACTGAGTGG 806
 769 TGACATCAAGTCTCTGAGCTCACTCACTCACTCACTCACTCACTCACTCACTCACT 828
 807 CGCCCTGTGAGAGCGCGCGGCGGTGTTCTGACTGAGGCGCTGCGAGAGCGTGTGG 866
 829 CTCATTATTAAGAGCACTGAAAGGTGTCTTCAATCAAGAGCTCTCAACCAAGCTGTGG 888
 867 CCGGAGAGCTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 909
 889 CCATGAAGCATCAAGCTGCTGTGTGAAGTGTGATGAGGAGAC 931

RESULT 12
 US-09-733-167A-8
 ; Sequence 8, Application US/09733167A
 ; Patent No. 6696547
 ; GENERAL INFORMATION:
 ; APPLICANT: Peter, Marcus

APPLICANT: Krammer, Peter
 TITLE OF INVENTION: Protein for Regulation of Apoptosis
 FILE REFERENCE: 4121-120
 CURRENT APPLICATION NUMBER: US/09/733,167A
 CURRENT FILING DATE: 2000-12-08
 PRIOR APPLICATION NUMBER: PCT/DE99/01712
 PRIOR FILING DATE: 1999-06-08
 PRIOR APPLICATION NUMBER: German Patent Application No. 6696547 198 25 621.3
 PRIOR FILING DATE: 1998-06-08
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 8
 LENGTH: 630
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Truncated segment of the DNA sequence encoding human DEBD, compri
 US-09-733-167A-8

Query Match 16.1%; Score 146.2; DB 4; Length 630;
 Best Local Similarity 60.4%; Pred. No. 88-24; Indels 0; Gaps 0;
 Matches 241; Conservative 0; Mismatches 158;

511 CGGCGAGAGGCG 570
 178 CGAGGAGAGGCGCACTTGGGAGCGGAGAAAGCGCGGAGTGAATGATGATGATGATG 237
 571 GAAGGCAAGTGAAGCTGTGACATCCGCTCCGCGTTTCGAGAGAGTACTGCGAGATGG 630
 238 AAGGAG 297
 631 CGAGCTTGGAGAGAGGCGGCGGAGTGCAGTCCGCGCGCGCGCGCGCGCGCGCGCG 690
 298 ACTGCTGCGAGGCGAGATGTCTTCTTAACAAGAGAGAGAGAGAGAGAGAGAGAGAG 357
 691 GTGTTGGGAGAGGCG 750
 358 CGCTTAAACAGGCGCAACATCTCAAGTCCGCGAGCTGGGCTCCATCATCTGTGAC 417
 751 ATCAAGTCTCAAGAGCTCTCTATCTGAGAGCGCTTCTGAGGCGAGTACTGAGTGGCG 810
 418 ATCAAGTCTGAGAGCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 477
 811 CTGCTGAGAGCG 870
 478 TTATTAGAGGCACTTAAAGGTGTCTTCAATCAAGAGCTCCCTCAAGCAAGCTGTGGCAT 537
 871 GAGGCTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 909
 538 GAGGCAATCAAGCTGCTGTGTAATGTGATGAGAGAGAGAC 576

RESULT 13
 US-09-733-167A-7
 ; Sequence 7, Application US/09733167A
 ; Patent No. 6696547
 ; GENERAL INFORMATION:
 ; APPLICANT: Peter, Marcus
 ; APPLICANT: Krammer, Peter
 ; TITLE OF INVENTION: Protein for Regulation of Apoptosis
 ; FILE REFERENCE: 4121-120
 ; CURRENT APPLICATION NUMBER: US/09/733,167A
 ; CURRENT FILING DATE: 2000-12-08
 ; PRIOR APPLICATION NUMBER: PCT/DE99/01712
 ; PRIOR FILING DATE: 1999-06-08
 ; PRIOR APPLICATION NUMBER: German Patent Application No. 6696547 198 25 621.3
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 342
 ; TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Truncated segment of the DNA sequence encoding human DEPD, compr
OTHER INFORMATION: sing nucleotides 28-369 of SEQ ID NO 2.
US-09-733-167A-7

Query Match 9.7%; Score 88.4; DB 4; Length 342;
Best Local Similarity 57.3%; Pred. No. 7.5e-11;
Matches 180; Conservative 0; Mismatches 131; Indels 3; Gaps 1;

QY 27 CCCGCTGAGGAGAGATGAGTGCCTGACTACTACGGAGTCTGTGCTTACCGTAT 86
DB 27 CCAGGTGTGCGCCAGAGACATGTGAGCAGAAACAGGCTGTACAGCTTCCACCGCAT 86
QY 87 GTTCGAGGTGTGCGCGGCACTGACCGAGTGCAGTGTGAGCTCTGTGCTTCTGCT 146
DB 87 GTTTACATGTGCGCAGCTCATCTGACACAGAGATGTGGCGTCTTCTTCTCTCT 146
QY 147 GGATGAGCTCTGTGCGCGCGGAGGCTTACCCGGGCGCGACGGCTTAGAGCTCT 206
DB 147 TGTGTATGTTCATGTATGACACAGAGCTGACTCAT--CCGAAATGAGACGTGACTTCT 203
QY 207 GCTGAGCTGAGACCGCGCGGAGTGTGCGGAGAGCAACCTGTGCTGGGCACT 266
DB 204 ATTGCACTGAGAGCGCCAGGCGCTGTGATGAAGTAACTTTCCGCGAGTCTGCACT 263
QY 267 CTTGCGGTGTGCTGCGCGCCAGACCTGTGCGGACCTGTGGCGCAAGCGCGCGCC 326
DB 264 GCTGCGCATTCATCTCGCCAGACCTGTGCTGCTTACGTACCTTCAAGAGAGAGCGG 323
QY 327 AGTGTCTCCAGAAC 340
DB 324 TGTGTGCTCTGATC 337

RESULT 14

US-07-704-288C-2

; Sequence 2, Application US/07704288C
; Patent No. 539680
; GENERAL INFORMATION:
; APPLICANT: LAMB, CHRISTOPHER J.
; APPLICANT: ZHU, QUN
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY
; TITLE OF INVENTION: ELEMENTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGEMANN & CLARK
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07704.288C
; FILING DATE: 22-MAY-1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 8899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 546-4737
; TELEFAX: (619) 546-9392
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1151 base pairs
; TYPE: nucleic acid

; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 55..1062
; US-07-704-288C-2

Query Match 5.6%; Score 50.8; DB 1; Length 1151;
Best Local Similarity 57.6%; Pred. No. 0.03;
Matches 91; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 159 TGGCGCGCCGAGGCTTACCGCGGCGCGACGCGCTTACGCTCTGTGAGCTGGA 218
DB 71 TGTGTGCGCATGTGTGCGCGGCGGCTTCTGCGGCGCGCTGATGCGAGCAGTGGCGCA 130
QY 219 GCGCGCGGAGTGTGCGCGGAGAGCACTGCGGCTGTGAGGGAACCTTGGCGTCT 278
DB 131 GCGAGCGCGGCGGCGGAGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 190
QY 279 GCGCGCGCAGCACTGTGCGGCGCACTGCGCGGCGGCGGCGGCGGCGGCGGCGG 316
DB 191 GCTCCACTCCGACTACTGCGGCGCGCGGATGCGAGAGC 228

RESULT 15

US-08-093-372-1

; Sequence 1, Application US/08093372
; Patent No. 5530187
; GENERAL INFORMATION:
; APPLICANT: Lamb, Christopher J.
; APPLICANT: Zhu, Qun
; APPLICANT: Maher, Eileen A.
; APPLICANT: Dixon, Richard A.
; TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING MULTIPLE
; TITLE OF INVENTION: DISEASE RESISTANCE GENES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 90071-2921
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/093.372
; FILING DATE: 16-JUL-1993
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9391
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1151 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 55..1062
; OTHER INFORMATION: /product= "RICE CHITINASE"
; US-08-093-372-1

Query Match 5.6%; Score 50.8; DB 1; Length 1151;
 Best Local Similarity 57.6%; Pred. No. 0.03;
 Matches 91; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

```

Oy 159 TGGCGCCGCGGAGCTTAGCCCGGAGCCCGCAGCGCCTTAGAGCTTCCTGGAGCTGGA 218
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 71 TGGTGGCCATGGTGGCCAGGCCCCCTTCCTCGCGCGCGCCCGTCATGCGCAGTGGCGCA 130
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 219 GCGCGCGGCGGAGTGGCGGAGAGCAACCTGCGGCTGTGGGCAACTCTGCGGCTGCT 278
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 131 GCCAGGCCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 190
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy 279 GCGCGCGCAGACCTGTGCGCGCACCTGCGCGCGCAAGC 316
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 191 GCTCCACCTCCGACTACTGCGCGCGCGGATGCCAGAGC 228
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    
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Search completed: February 12, 2005, 12:44:46
 Job time : 151 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 10:58:57 ; Search time 424 Seconds
(without alignments)
12691.144 Million cell updates/sec

Title: US-10-030-271-1

Perfect score: 909
Sequence: 1 atgscgtctatccggctgcac.....tcagtctgagatgagctgac 909

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980a:*
2: geneseqn1990a:*
3: geneseqn2000a:*
4: geneseqn2001a:*
5: geneseqn2001b:*
6: geneseqn2002a:*
7: geneseqn2002b:*
8: geneseqn2003a:*
9: geneseqn2003b:*
10: geneseqn2003c:*
11: geneseqn2003d:*
12: geneseqn2004a:*
13: geneseqn2004b:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	909	100.0	909	5	AAf27407 Human apo
2	909	100.0	1883	5	AAf27408 Human apo
3	907.4	99.8	981	10	ADc79259 Human DED
4	907.4	99.8	1230	6	ABa94362 Human APR
5	907.4	99.8	1924	6	AAa00080 Human DED
6	907.4	99.8	1924	6	AAa00080 Human DED
7	907.4	99.8	1979	12	AAa00080 Human DED
8	907.4	99.8	2045	3	AAa00080 Human DED
9	907.4	99.8	2045	3	AAa00080 Human DED
10	895.4	98.5	2044	3	AAf18296 Human col
11	825.8	90.8	1084	6	ABU39692 Human NS
12	825.8	90.8	1106	6	ABU39692 Human NS
13	799.4	87.9	1966	6	AAa62603 cDNA sequ
14	581.2	63.9	1570	4	AAa99646 Human pro
15	541	59.5	1067	4	AAa158961 Human pol
16	541	59.5	1067	5	ADa99183 DNA encod
17	541	59.5	1067	5	ADa848943 Novel hum
18	529	58.2	1042	4	AAa160747 Human pol
19	528	58.1	626	4	AAaH07925 Human cDN
20	346.2	38.1	603	5	AAaF93937 Primer sp

C	21	326.6	35.9	111084	12	ADQ18808	AdQ18808 Human sof
	22	301.4	33.2	303	6	AAaD40075	AAaD40075 Human DED
	23	301.4	33.2	303	6	AAaD59057	AAaD59057 Human DED
	24	193.8	21.3	1139	3	AAaZ43923	AAaZ43923 Human DED
	25	193.8	21.3	1830	4	AAa15765	AAa15765 Human cDN
	26	193.8	21.3	2261	4	AAa14367	AAa14367 Human cDN
	27	193.8	21.3	2261	6	ABaK46133	ABaK46133 cDNA enco
	28	192.2	21.1	1045	5	AAaV74137	AAaV74137 Human FLA
	29	192.2	21.1	1045	5	AAaD43203	AAaD43203 Human FLA
	30	192.2	21.1	2079	5	ABaV24761	ABaV24761 Human pro
	31	190.6	21.0	1142	3	AAaZ43924	AAaZ43924 Murine DE
	32	190.6	21.0	1200	2	AAaV74138	AAaV74138 Mouse FLA
	33	190.6	21.0	1200	6	AAaV43204	AAaV43204 Mouse FLA
	34	157.2	17.3	484	9	ACH25056	ACH25056 Human adu
	35	152.4	16.8	451	9	ACH41209	ACH41209 Human foe
C	36	119.2	13.1	769	10	ADaD34431	ADaD34431 Mouse mit
	37	114.6	12.6	525	10	ADaD34432	ADaD34432 Mouse mit
	38	112	12.3	553	9	ACH23692	ACH23692 Human adu
	39	111	12.2	278	11	ADT94498	ADT94498 Colon can
	40	111	12.2	422	8	ABa18661	ABa18661 Group III
	41	86.8	9.5	669	4	AAaH05181	AAaH05181 Human cDN
	42	83.8	9.2	523	4	AAaH06261	AAaH06261 Human cDN
	43	56.6	6.2	114955	2	AAaX53491	AAaX53491 Human ade
	44	54.8	6.0	980	8	ADaV71128	ADaV71128 Rice gene
	45	52.8	5.8	2073	8	ACC42664	ACC42664 Human Lp3

ALIGNMENTS

RESULT 1	AAf27407	standard; cDNA; 909 BP.
ID	AAf27407	standard; cDNA; 909 BP.
XX		
AC	AAf27407;	
XX		
DT	24-APR-2001	(first entry)
XX		
DE	Human apoptosis-associated factor NT2RM1000558 partial cDNA, SEQ ID NO.1.	
XX		
KW	Human; apoptosis-associated factor; NT2RM1000558; death effector domain;	
KW	DED; caspase family cleavage domain; pro-apoptotic; drug screening;	
KW	cell proliferation; ischaemic disease; chronic viral disease; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	MO200104300-A1.	
XX		
PD	18-JAN-2001.	
XX		
PF	06-JUL-2000; 2000WO-JP004516.	
XX		
PR	08-JUL-1999; 99JP-00194179.	
XX		
PR	18-OCT-1999; 99US-0159586P.	
XX		
PA	(HELI-) HELIX RES INST.	
XX		
PI	Ota T, Isogai T, Nishikawa T, Kawai Y, Miyoshi S, Satoh S;	
XX		
DR	WPI; 2001-138348/14.	
XX		
F-PSDB; AAB60386.		
PT	Poly-nucleotide encoding an apoptosis-associated factor protein with death	
PT	effector domain and caspase family-cleavage domain, useful in regulating	
PT	diseases with cell proliferation.	
XX		
PS	Claim 1; Page 41-43; 53pp; Japanese.	
XX		
CC	The invention relates to a novel human apoptosis-associated factor	
CC	(AAB60386, AAB60387), designated NT2RM1000558, which contains a death	
CC	effector domain (DED) and a caspase family cleavage domain and is capable	
CC	of inducing apoptosis in cells. The invention also relates to nucleic	
CC	acids encoding the protein (AAf27407, AAf27408); variants of the protein	


```

QY 61 TACGGAGATGCTGCTTCAACCGTATGTTGAGAGTGTGGGCGGCACTGACCGAGTGC 120
DB 184 TACGGAGATGCTGCTTCAACCGTATGTTGAGAGTGTGGGCGGCACTGACCGAGTGC 243
QY 121 GAGCTGAGAGCTCTGAGCTTTTCTGCTGATGAGGCTCTGAGGCGGCGGAGGCTTAAAGC 180
DB 244 GAGCTGAGAGCTCTGAGCTTTTCTGCTGATGAGGCTCTGAGGCGGCGGAGGCTTAAAGC 303
QY 181 CGGGGCGGAGGCGCTAGAGCTCTGCTGAGGCTGAGGCGGCGGAGGCTGAGGCGGAG 240
DB 304 CGGGGCGGAGGCGCTAGAGCTCTGCTGAGGCTGAGGCGGCGGAGGCTGAGGCGGAG 363
QY 241 AGCAACTGCTGCTGCTGAGGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 364 AGCAACTGCTGCTGCTGAGGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 423
QY 301 CACTGAGGCGGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 360
DB 424 CACTGAGGCGGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 483
QY 361 AGCTCTTCAAGAGGAGCAGAGGGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 484 AGCTCTTCAAGAGGAGCAGAGGGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 543
QY 421 AATTCTCAGCAGAGGTCAGTGGAGAGCAGGCTCCCGCCCAACAGCGGCGGCGGCGGAGT 480
DB 544 AATTCTCAGCAGAGGTCAGTGGAGAGCAGGCTCCCGCCCAACAGCGGCGGCGGCGGAGT 603
QY 481 CGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
DB 604 CGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 663
QY 541 CAGCAGTCAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 600
DB 664 CAGCAGTCAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 723
QY 601 CGGGTTCAGCAGAGTACTGTCAGAGCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCG 660
DB 724 CGGGTTCAGCAGAGTACTGTCAGAGCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCG 783
QY 661 CGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
DB 784 CGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 843
QY 721 TCAAGGAGCCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 844 TCAAGGAGCCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 903
QY 781 GCTTCTGAGGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB 904 GCTTCTGAGGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 963
QY 841 ACTGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB 964 ACTGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1023
QY 901 GAGGCTGAC 909
DB 1024 GAGGCTGAC 1032

```

RESULT 3
ADCT9259 standard; cDNA; 981 BP.

ADCT9259;

01-JAN-2004 (first entry)

Human DEDD2 encoding cDNA SEQ ID NO:1.

human; death effector domains containing DNA-binding protein;

DE human; death effector domains containing DNA-binding protein; DEDD2; cell death; gene therapy;

```

KW cytosolic; cancer; chronic myeloid leukaemia; gene; ss.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH 1..981
FT CDS /tag= a
FT FT /product= "DEDD2"
XX
XX MO2003054195-A1.
XX
XX 03-JUL-2003.
XX
XX 20-DEC-2002; 2002MO-JP013371.
XX
XX 20-DEC-2001; 2001JP-00387854.
XX
XX 18-JUL-2002; 2002JP-00209458.
XX
XX (MORG ) MORINAGA MILK IND CO LTD.
XX
XX Suzu S, Hageshita H, Nomaguchi K, Yamada M, Hayasawa H;
XX WPI; 2003-569246/53.
XX
XX P-PSDB; ADC79260.
XX
XX DNA encoding cell death proteins for treatment of kidney, large intestine
XX and prostate cancers and leukemia.
XX
XX Claim 2; Page 18-20; 26pp; Japanese.
XX
XX The present sequence encodes a human death effector domains (DED)
XX containing DNA-binding protein (DEDD) protein, designated DEDD2, that
XX causes cell death. Also described: (1) primer and probe for investigation
XX of the DEDD2 gene; and (2) reagents for gene therapy. DEDD2 has
XX cytostatic activity. DEDD2 can be used in the diagnosis and treatment of
XX cancers of the kidney, large intestine and prostate, and acute and
XX chronic myeloid leukaemia.
XX
XX Sequence 981 BP; 151 A; 303 C; 363 G; 164 T; 0 U; 0 Other;
SQ
Query Match 99.8%; Score 907.4; DB 10; Length 981;
Best Local Similarity 99.8%; Pred. No. 4,4e-171;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGGGAGTATCCGGGTCGACCCCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
DB 1 ATGGGAGTATCCGGGTCGACCCCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
QY 61 TACGGAGATGCTGCTTCAACCGTATGTTGAGAGTGTGGGCGGCACTGACCGAGTGC 120
DB 61 TACGGAGATGCTGCTTCAACCGTATGTTGAGAGTGTGGGCGGCACTGACCGAGTGC 120
QY 121 GAGCTGAGAGCTCTGAGCTTTTCTGCTGATGAGGCTCTGAGGCGGCGGAGGCTTAAAGC 180
DB 121 GAGCTGAGAGCTCTGAGCTTTTCTGCTGATGAGGCTCTGAGGCGGCGGAGGCTTAAAGC 180
QY 181 CGGGGCGGAGGCGCTAGAGCTCTGCTGAGGCTGAGGCGGCGGCGGCGGCGGCGGCGGAG 240
DB 181 CGGGGCGGAGGCGCTAGAGCTCTGCTGAGGCTGAGGCGGCGGCGGCGGCGGCGGCGGAG 240
QY 241 AGCAACTGCTGCTGCTGAGGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 241 AGCAACTGCTGCTGCTGAGGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 301 CACTGAGGCGGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
DB 301 CACTGAGGCGGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
QY 361 AGCTCTTCAAGAGGAGCAGAGGGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 361 AGCTCTTCAAGAGGAGCAGAGGGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 421 AATTCTCAGCAGAGGTCAGTGGAGAGCAGGCTCCCGCCCAACAGCGGCGGCGGAGT 480

```



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Db 421 AATTTCTGACGAGGTCTGTTGAGAGACAGGCTCTCCCCCAACCAAGCGAGCGGAGT 480
Qy 481 CGGGGCGGCGGCGGAGTGTGTGTCCAGACCGCGCGGAGAGGCGCCCAACCGCCAG 540
Db 481 CGGGGCGGCGGCGGAGTGTGTGTCCAGACCGCGCGGAGAGGCGCCCAACCGCCAG 540
Qy 541 CAGGAGTCAAGAGCCCGGCGGAGCTTCTTGAAGGCAAGTCACTGTGACATCCGCGTC 600
Db 541 CAGGAGTCAAGAGCCCGGCGGAGCTTCTTGAAGGCAAGTCACTGTGACATCCGCGTC 600
Qy 601 CGGGTTCGAGCAGAGTACTGCGAGCATGCGGCGCTTGAGAGCAGGCGGTGACATCCGCG 660
Db 601 CGGGTTCGAGCAGAGTACTGCGAGCATGCGGCGCTTGAGAGCAGGCGGTGACATCCGCG 660
Qy 661 CGGGCCCGGCGGCGGCGGAGCTGAGACGTGTTTGAGGCGAGCCAGCGAGTGTGCGC 720
Db 661 CGGGCCCGGCGGCGGCGGAGCTGAGACGTGTTTGAGGCGAGCCAGCGAGTGTGCGC 720
Qy 721 TCAAGGAGCCTGGGCTGTGTGTGTGTGACATCAAGTTCTCAGAGCTCTCTATCTGAGC 780
Db 721 TCAAGGAGCCTGGGCTGTGTGTGTGTGACATCAAGTTCTCAGAGCTCTCTATCTGAGC 780
Qy 781 GCTTCTGCGGCGGAGCTACTGAGTGTGCGGCGCTGTCGAGGCGCTGCGGCGGTGTCG 840
Db 781 GCTTCTGCGGCGGAGCTACTGAGTGTGCGGCGCTGTCGAGGCGCTGCGGCGGTGTCG 840
Qy 841 ACTGAGGCGCTGCGAGAGGCTGTGAGCGCGGAGGAGCTGTGCGCTGCTGTCAGTGTGAT 900
Db 841 ACTGAGGCGCTGCGAGAGGCTGTGAGCGCGGAGGAGCTGTGCGCTGCTGTCAGTGTGAT 900
Qy 901 GAGGCTGAC 909
Db 901 GAGGCTGAC 909

RESULT 4
ABA94362
ID ABA94362 standard; DNA; 1230 BP.
AC ABA94362;
XX
XX 26-MAR-2002 (first entry)
DT
XX
XX Human APRG polypeptide (Incyte ID. 3102521CD1) encoding cDNA.
DE
XX
KW APRG; apoptosis regulator; cytosolic; antiatherosclerotic; osteopathic;
KW antiarteriosclerotic; hepatotropic; antipsoriatic; antihelminthic; human;
KW antiallergic; antianemic; antiasphatic; antihypertoid; anti-HIV; cancer;
KW antiinflammatory; antidiabetic; antispout; nephrotropic; ophthalmological;
KW immunosuppressive; dermatological; antitumor; antirheumatic; fungicide;
KW antidiarrhetic; antibacterial; virucide; antiparasitic; protozoacide;
KW tranquilizer; vulnery; gynecological; vasotropic; gene therapy; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX CDS 127..1107
XX /tag=a
XX /product="APRG polypeptide"
XX
XX W020192527-A2.
XX
XX 06-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-US017581.
XX
XX 01-JUN-2000; 2000US-0209407P.
XX
XX 30-NOV-2000; 2000US-0250326P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Tang YT, Azimzal Y, Yue H, Burford N, Ding L, Elliott VS;
PI

```

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PI Paterson C, Baughn MR;
XX
XX WPI; 2002-114350/15.
DR
DR P-PSDB; ABB07263.
XX
XX Novel human apoptosis regulator polypeptides and polynucleotides for
PT diagnosing, preventing, treating cell proliferative, immunological and
PT reproductive disorders and for identifying modulators of therapeutic use.
PS Claim 5; Page 101; 103pp; English.
XX
XX The invention provides human apoptosis regulator (APRG) polypeptides and
XX polynucleotides. The APRG polypeptides, polynucleotides and modulators
XX are useful for diagnosis, treatment and prevention of cell proliferative,
XX immunological and reproductive disorders. The cell proliferative
XX disorders include cancers, actinic keratosis, arteriosclerosis,
XX atherosclerosis, burns, cirrhosis, hepatitis, psoriasis, and
XX immunological disorders include acquired immunodeficiency syndrome
XX (AIDS), adult respiratory distress syndrome, Addison's disease,
XX ankylosing spondylitis, amyloidosis, allergies, anemia, osteoporosis,
XX autoimmune hemolytic anemia, asthma, autoimmune thyroiditis, Crohn's
XX disease, contact dermatitis, diabetes mellitus, gout, Graves' disease,
XX glomerulonephritis, rheumatoid arthritis, scleroderma, systemic lupus
XX erythematosus, systemic sclerosis, ulcerative colitis, hemodialysis,
XX uveitis; viral, bacterial, fungal, parasitic, protozoal, helminthic
XX infections and trauma. Reproductive disorders include disorders of
XX prolactin production, infertility, endometriosis, polycystic ovary
XX syndrome, ectopic pregnancies, galactorrhea, abnormal sperm physiology,
XX disruptions of spermatogenesis, cancer of testis and prostate, impotence,
XX carcinoma of male breast and gynecomastia. The APRG polynucleotides are
XX useful for creating knockin humanized animals or transgenic animals to
XX model human disease and to detect and quantify gene expression in
XX biopsied tissues in which expression of APRG is correlated with disease.
XX APRG, fragments of it and antibodies specific for APRG are useful as
XX elements on a microarray which is useful to monitor or measure protein-
XX protein interactions, drug-target interactions and gene expression
XX profiles. The present sequence represents a human APRG polypeptide
XX encoding cDNA
XX
XX Sequence 1230 BP; 205 A; 382 C; 433 G; 210 T; 0 U; 0 Other;
XX
XX
XX Query Match 99.8%; Score 907.4; DB 6; Length 1230;
XX Best Local Similarity 99.9%; Pred. No. 4,4e-171;
XX Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGGCGCTATCCGGGTGAGACCCCGCGCTGAGAGAGAGTGAAGTCTGAGTAC 60
Db 127 ATGGCGCTATCCGGGTGAGACCCCGCGCTGAGAGAGAGTGAAGTCTGAGTAC 186
Qy 61 TACGGAGTCTGTGCTTACCGTATGTTGAGGTGAGTGGCGGCAACTGACCGAGTGC 120
Db 187 TACGGAGTCTGTGCTTACCGTATGTTGAGGTGAGTGGCGGCAACTGACCGAGTGC 246
Qy 121 GAGCTGAGAGCTCCCGGCTTCTGCTGAGTGAAGCTCTTGCGCGCGCGAGAGCTTGGC 180
Db 247 GAGCTGAGAGCTCCCGGCTTCTGCTGAGTGAAGCTCTTGCGCGCGCGAGAGCTTGGC 306
Qy 247 GAGCTGAGAGCTCCCGGCTTCTGCTGAGTGAAGCTCTTGCGCGCGCGAGAGCTTGGC 306
Db 181 CGGGCCCGGAGCGGCTGAGAGCTCTGCTGAGAGCGCGCGGAGAGTGTGCGAG 240
Qy 307 CGGGCCCGGAGCGGCTGAGAGCTCTGCTGAGAGCGCGCGGAGAGTGTGCGAG 366
Db 241 AGCAACTGCGGCTGTGCGGCAACTCTGTGCGGTGAGCGCGCGCAAGACTGTGCGG 300
Qy 367 AGCAACTGCGGCTGTGCGGCAACTCTGTGCGGTGAGCGCGCGCAAGACTGTGCGG 426
Db 301 CACCTGGCGGCGGAGCGGCGCGCGCGAGTCTTCCAAAGCTATAGCACTGCC 360
Qy 427 CACCTGGCGGCGGAGCGGCGCGCGCGAGTCTTCCAAAGCTATAGCACTGCC 486
Db 361 AGCTCTTCAAGAGAGAGAGAGAGTGTGCGGTGCGGTGCGAGTCAAGAGATTGTGCA 420
Qy 487 AGCTCTTCAAGAGAGAGAGAGTGTGCGGTGCGGTGCGAGTCAAGAGATTGTGCA 546
Db

```


Qy	421	AATTCTCAGCAGGGGTCAGTGGGGAGCAGGCTCCCCCCCAACCAACGGCAGCGGGGAGT	480
Db	547	AATTCTCAGCAGGGTCAGTGGGGAGCAGGCTCCCCCAACCAACGGCAGCGGGGAGT	606
Qy	481	CGGGGCGGGCCAGTGTGTGTGCCAGACGGCGGGCGAGAGGGGGCCCAAGCGCACCCGAG	540
Db	607	CGGGGCGGGCCAGTGTGTGTGCCAGACGGCGGGCGAGAGGGGGCCCAAGCGCACCCGAG	666
Qy	541	CAGCAGTCAGAGCCCGCCAGACCTTCTCTGAAGGCAAAAGTACCTGTGACATCCGGCTC	600
Db	667	CAGCAGTCAGAGCCCGCCAGACCTTCTCTGAAGGCAAAAGTACCTGTGACATCCGGCTC	726
Qy	601	CGGGTTCAGAGCAGATCTGCGAGCATGGGCGACGCTTGAGACAGGGGCGTGACATCCGG	660
Db	727	CGGGTTCAGAGCAGATCTGCGAGCATGGGCGACGCTTGAGACAGGGGCGTGACATCCGG	786
Qy	661	CGGCCCCCAGGCGCTGGCGCGCAGCTGACAGTGTGGGCGAGGCCACCGCAATGCTCGGC	720
Db	787	CGGCCCCCAGGCGCTGGCGCGCAGCTGACAGTGTGGGCGAGGCCACCGCAATGCTCGGC	846
Qy	721	TCAAGGAGCCTGGGCTCTGTGGTTGTGACATCAAGTTCCTAGAGCTCTCCATCTGGAC	780
Db	847	TCAAGGAGCCTGGGCTCTGTGGTTGTGACATCAAGTTCCTAGAGCTCTCCATCTGGAC	906
Qy	781	GCTTCTTGGGGGACCTACCTGAGTGGCGGCTGTGCAAGCCCTTGCGGGGCGTGTTCCTG	840
Db	907	GCTTCTTGGGGGACCTACCTGAGTGGCGGCTGTGCAAGCCCTTGCGGGGCGTGTTCCTG	966
Qy	841	ACTGAGGCCCTGCGAGAGGCTGTGGGCGGGAGAGGCTGTCCGCTGCTGGTCAGTGGAGT	900
Db	967	ACTGAGGCCCTGCGAGAGGCTGTGGGCGGGAGAGGCTGTCCGCTGCTGGTCAGTGGAGT	1026
Qy	901	GAGGCTGAC 909	
Db	1027	GAGGCTGAC 1035	

RESULT 5	
AA040080	
ID	AA040080 standard; DNA; 1924 BP.
XX	
AC	AA040080;
XX	
DT	22-OCT-2002 (first entry)
XX	
DE	Human DED4 (death effector domain) gene.
XX	
KW	Human; death domain; DD; death effector domain; DED; Chlamydia infection;
KW	NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;
KW	inflammation; allergy; autoimmunity; allograft rejection; cell division;
KW	immune-based pathology; fibrosis; arthritis; graft versus host disease;
KW	immunosuppressive; gene therapy; antitense therapy; gene; ds.
XX	
OS	Homo sapiens.
XX	
PH	Key
FT	Location/Qualifiers
FT	CDS
FT	91..1044
FT	/*tag= a
FT	/product= "Human DED4"
FT	/note= "No stop codon"
FT	/partial
FT	misc_feature
FT	157..222
FT	/*tag= b
FT	/note= "Nuclear localisation sequence"
XX	
PN	W0200240680-A2.
XX	
PD	23-MAY-2002.
XX	
PE	15-NOV-2001; 2001MO-US044844.
XX	
XX	17-NOV-2000; 2000US-00715893.
PR	29-JUN-2001; 2001US-0301889P.
PR	

XX	(BORN-) BORNHAM INST.
PA	
XX	
Pi	Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
Pi	Stenner-Liewen F;
XX	
DR	WPI; 2002-500222/53.
XX	
PS	P-PsDB; AA624860.
PS	
Claim 19;	Page 184-186; 209pp; English.
CC	The invention relates to an isolated polypeptide comprising a death
CC	domain (DD), death effector domain (DED) or NB-ARC domain. The invention
CC	is useful for identifying a binding agent, preferably a protein or a drug
CC	that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC
CC	domain from DAP3, IRAK4, CTSD (Chlamydia trachomatis DD protein), DED4 or
CC	NIDD (NGFp-interacting Death Domain), with a candidate binding agent and
CC	detecting the association of the domain and the candidate binding agent,
CC	by yeast two hybrid assay, immunoprecipitation, SP, ultraviolet (UV) or
CC	chemical crosslinking, nuclear magnetic resonance (NMR), mass
CC	spectroscopy (MS) and FFA. The invention is useful for modulating the
CC	level of a cell process such as cell proliferation, cell adhesion, cell
CC	stress responses, responses to microbial infection and B cell
CC	immunoglobulin class switching, in particular apoptosis within a cell.
CC	Antibody specifically reactive with CTSD DD of C. trachomatis , C.
CC	muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the
CC	CTSD DD protein is useful for detecting a Chlamydia infection. The
CC	invention is useful for modulating the activity of oncogenic proteins,
CC	for treating a pathology caused by the oncogenic proteins and for
CC	treating bacterial infections by modulating the activity of bacterial
CC	proteins. The protein and antibody specific for it are useful for
CC	discovery of drugs that suppress infection, inflammation, allergy,
CC	sepsis, autoimmunity, allograft rejection and other diseases. The protein
CC	is useful for treating immune-based pathologies, pathologies associated
CC	with cell division, inflammatory diseases such as sepsis, fibrosis,
CC	arthritis, graft versus host disease. The invention is used in antisense
CC	therapy and gene therapy. The present sequence is human DED4 gene
XX	
SQ	Sequence 1924 BP; 360 A; 599 C; 594 G; 368 T; 0 U; 3 Other;
Query Match	99.8%; Score 907.4; DB 6; Length 1924;
Best Local Similarity	99.9%; Pred. No.4.6e-17;
Matches 908; Conservative	0; Mismatches 1; Indels 0; Gaps 0
QY	1 ATGGCGCATATCCGGGTGCAGCCCCGCGCCCGTCTGGAGAAGAGATGATGCTCTGAATAC 60
DB	91 ATGGCGCATATCCGGGTGCAGCCCCGCGCCCGTCTGGAGAAGAGATGATGATGCTCTGAATAC 150
QY	61 TACGGGAATGCTGTGCGTTCAACCGTAATGTTTCGAAGTGATGGGCGGCAACTGACCGAATGCC 120
DB	151 TACGGGAATGCTGTGCGTTCAACCGTAATGTTTCGAAGTGATGGGCGGCAACTGACCGAATGCC 210
QY	121 GAGCTGGAGATCCTCGGACCCTTTCTGTGTGATGAGAGTCTCGTGGCGCGCGCGAGGACTTAGCC 180
DB	211 GAGCTGGAGATCCTCGGACCCTTTCTGTGTGATGAGAGTCTCGTGGCGCGCGCGAGGACTTAGCC 270
QY	181 CGGGCCCGCAGACGGGCTTAGAGATCTCTGTGTGAGAGTGAAGCGCGCGGCGAGTGCGCGAG 240
DB	271 CGGGCCCGCAGACGGGCTTAGAGATCTCTGTGTGAGAGTGAAGCGCGCGGCGAGTGCGCGAG 330
QY	241 AGCAACTGTGGGCTGTGTTGGGGCAACTCTGTGGCGCTGTGGGCCCGCACAGACTTGGTGGCG 300
DB	331 AGCAACTGTGGGCTGTGTTGGGGCAACTCTGTGGCGCTGTGGGCCCGCACAGACTTGGTGGCG 390
QY	301 CACCTGGGGCGCAAGCGGCGCGCGCAATGTCTCCAGAAAGCTAATAGCATATGGACAATGCC 360
DB	391 CACCTGGGGCGCAAGCGGCGCGCGCAATGTCTCCAGAAAGCTAATAGCATATGGACAATGCC 450
QY	361 AGCTTTCAAAGAGACAGAGGGTATGATGCTGCGTCCGTCGCGCATCAAGCATTTCTGCA 420


```

Db      451  |||
      421  |||
      511  |||
      481  |||
      571  |||
      541  |||
      631  |||
      601  |||
      691  |||
      661  |||
      751  |||
      721  |||
      811  |||
      781  |||
      871  |||
      930  |||
      900  |||
      991  |||
      991  |||

RESULT 6
AADS9062
ID      AADS9062 standard; cDNA, 1924 BP.
XX      AADS9062;
XX      18-DEC-2003 (first entry)
XX      Human DED4 full length gene.
XX      Human, death Domain; DD, death effector domain; DED, cell proliferation;
XX      Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;
XX      neural growth factor receptor-interacting protein; cell adhesion;
XX      vasotrophic; microbial infection; inflammation; allograft rejection; CMTD;
XX      cell stress response; benign prostatic hypertrophy; antibacterial; NIDP;
XX      apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;
XX      neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;
XX      keloid; gene; ss.
XX      Homo sapiens.
XX      OS
XX      FH
XX      Key
XX      CDS
XX      91..1044
XX      Location/Qualifiers
XX      /tag= a
XX      /product= "Human DED4 protein"
XX      /note= "No stop codon"
XX      /partial
XX      157..222
XX      misc_signal
XX      /tag= b
XX      /note= "Nuclear localisation sequence"
XX      US2003049702-A1.

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PD      13-MAR-2003.
XX      15-NOV-2001; 2001US-00001254.
PF      17-NOV-2000; 2000US-00715893.
PR      17-NOV-2000; 2000US-0367360P.
PR      29-JUN-2001; 2001US-0301889P.
XX      (REED) REED J C.
XX      (GODZ) GODZIK A.
XX      (PAWL) PAWLOWSKI K.
XX      (FIOR) FIORENTINO L.
XX      (LEES) LEES S H.
XX      (ROTH) ROTH W.
XX      (STEN) STENNER-LIEWEN F.
PI      Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
PI      Stenner-Liewen F;
XX      WPI, 2002-500222/53.
XX      P-PsDB; AAB38903.
DR      New polypeptide comprising a death domain or death effector domain,
DR      useful for discovery of drugs that suppress infection, inflammation,
PT      allergy, sepsis, autoimmunity, allograft rejection and other diseases.
PT      Claim 19; Page 42-44; 99pp; English.
XX      The present invention provides novel death Domain (DD) and death effector
XX      domain (DED) proteins and nucleic acids encoding them. The invention also
XX      provides death domain containing protein such as Chlamydia trachomatis
XX      death domain containing protein (CTDP) DD and neural growth factor
XX      receptor-interacting death domain (NIDP) DD. The invention is useful for
XX      identifying a binding agent (e.g. protein or drug) that binds a DD, DED
XX      or NB-ARC domain from DAP3, IRAK4, CMTD, DED4 or NIDP with a candidate
XX      binding agent and identifying an effective agent (e.g. protein or drug)
XX      that modulates the association of a DD, DED or NB-ARC domain with protein
XX      that binds the DD, DED or NB-ARC domain. The invention is also useful for
XX      modulating the level of cell process such as apoptosis, cell adhesion,
XX      cell proliferation, cell stress responses, responses to microbial
XX      infection and B cell immunoglobulin class switching. DDs, DEDs and NB-ARC
XX      domains and/or anti-DD, anti-DED or anti-NB-ARC domain antibodies are
XX      useful for discovery of drugs that suppress infection, autoimmunity,
XX      inflammation, allergy, allograft rejection, sepsis and other diseases.
XX      DD, DED or NB-ARC domain proteins are used to treat infection, allergy,
XX      autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte
XX      hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis,
XX      inflammatory hyperplasia and smooth muscle cell proliferation in arteries
XX      following balloon angioplasty (restenosis). The invention is also used in
XX      antibody therapy and gene therapy. The present sequence is human DED4
XX      full length gene. The DED4 gene is located on chromosome 19
XX      Sequence 1924 BP; 360 A; 599 C; 594 G; 368 T; 0 U; 3 Other;
SQ      Query Match
SQ      Best Local Similarity 99.8%; Score 907.4; DB 6; Length 1924;
SQ      Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY	241	AGCAACCTGGCGGCTGTGGGAGCAACTCGGCGGTCTGGCCCGGACAGACCTGCTGGC	300
Db	331	AGCAACCTGGCGGCTGTGGGAGCAACTCTCTGGCGGTCTGGCCCGGACAGACCTGCTGGC	390
QY	301	CACCTGGCGCGCAAGCGGCGCCGGCCAGTGTCTCCAGAAAGCTATAGCTATGGCACCTCC	360
Db	391	CACCTGGCGCGCAAGCGGCGCCGGCCAGTGTCTCCAGAAAGCTATAGCTATGGCACCTCC	450
QY	361	AGCTCTTCAAAAGAGACAGAGGGTATGCTCCCGTGGCGGTGGGAGTCAAGCAATTCGTGA	420
Db	451	AGCTCTTCAAAAGAGACAGAGGGTATGCTCCCGTGGCGGTGGGAGTCAAGCAATTCGTGA	510
QY	421	AATTTCTCAGCAGGAGTCAGTGGGAGACAGGCTCCCGCCCAACCAAGGCGGACGCGGAGT	480
Db	511	AATTTCTCAGCAGGAGTCAGTGGGAGACAGGCTCCCGCCCAACCAAGGCGGACGCGGAGT	570
QY	481	CGGGGCGCGGCCCAAGTGTGTGTGCACAGCGCGCGGAGAGGGGCCCCAGTCCGACCCGAG	540
Db	571	CGGGGCGCGGCCCAAGTGTGTGTGCACAGCGCGCGGAGAGGGGCCCCAGTCCGACCCGAG	630
QY	541	CAGCAGTCAAGACCCCGCCAGACCTTCTCTGAAGGCAAAAGTGCATGTGCATCCGAGCTC	600
Db	631	CAGCAGTCAAGACCCCGCCAGACCTTCTCTGAAGGCAAAAGTGCATGTGCATCCGAGCTC	690
QY	601	CGGGTTTCGAGCAGAGTACTTGCAGAGCATYGGGCCAGCCTTGGAGCAGGAGCGGTGGCATCCGG	660
Db	691	CGGGTTTCGAGCAGAGTACTTGCAGAGCATYGGGCCAGCCTTGGAGCAGGAGCGGTGGCATCCGG	750
QY	661	CGGGCCCGCAGGGCCTGGCGCGGCGAGCGTGAACGTGTGGCCAGGCGCACCGCAGTGGCTGGCG	720
Db	751	CGGGCCCGCAGGGCCTGGCGCGGCGAGCGTGAACGTGTGGCCAGGCGCACCGCAGTGGCTGGCG	810
QY	721	TCAAGGAGACTTGGGCTGTGTGGTTTGTGAATCAAGATTCTCAGAGCTCTCTTAATTGGAC	780
Db	811	TCAAGGAGACTTGGGCTGTGTGGTTTGTGAATCAAGATTCTCAGAGCTCTCTTAATTGGAC	870
QY	781	GCCTTCTGGGGGGAATCACTGAAGTGGCGGCTTGTGACAGGCCCCCTGGGGGCGTGTCTCTG	840
Db	871	GCCTTCTGGGGGGAATCACTGAAGTGGCGGCTTGTGACAGGCCCCCTGGGGGCGTGTCTCTG	930
QY	841	ACTGAGGCGCCTCGAGAGGCTGTGGGCGGGGAGGCTGTTTCGCTGCTGATCAATGTGGAT	900
Db	931	ACTGAGGCGCCTCGAGAGGCTGTGGGCGGGGAGGCTGTTTCGCTGCTGATCAATGTGGAT	990
QY	901	GAGGCTTGAC 909	
Db	991	GAGGCTTGAC 999	

RESULT 7
ADQ86891
ID ADQ86891 standard; cDNA; 1979 BP.

DT	07-OCT-2004	(first entry)
XX		
DE	Human tumour-associated antigenic target (TAT) cDNA sequence #3766.	
XX		
KW	human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;	
KW	cancer; cell proliferative disorder; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2004060270-A2.	
XX		
PD	22-JUL-2004.	
XX		
PF	15-OCT-2003; 2003WO-US029126.	
XX		
PR	18-OCT-2002; 2002US-0418988P.	
XX		

PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
XX
XX
P1 Wu TD, Zhou Y;
XX
XX WPI; 2004-534300/51.
XX
XX
PT New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT preventing or treating cell proliferative disorders such as cancer.
XX
XX Claim 1; SEQ ID NO 3766; 5504dp; English.

The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridizes to (a)-(c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identical to (a) or (b); (5) a chimeric polypeptide comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytotoxic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.

Sequence 1979 BP; 365 A; 617 C; 627 G; 370 T; 0 U; 0 Other;

Query Match 99.8%; Score 907.4; DB 12; Length 1979;

```
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Oy	ATGAGCGTATCCGAGGTCGACCCCGAGCCCCGGCTCGGAGAGAGATGATGCTGTGATAC	60
Db	ATGAGCGTATCCGAGGTCGACCCCGAGCCCCGGCTCGGAGAGAGATGATGCTGTGATAC	220
Oy	TACGGGATGCTGTCGCTTACCCGTAATGTTTCGAGGTGTGTGGGCAACTGACCGAGTGC	120
Db	TACGGGATGCTGTCGCTTACCCGTAATGTTTCGAGGTGTGTGGGCAACTGACCGAGTGC	280
Oy	GACCTGAGCTCCTTGAGCTTTCTGCTGTGATGAGGCTCCTTGAGCGCGCCGAGGCTTAGCC	180
Db	GACCTGAGGCTCCTTGAGCTTTCTGCTGTGATGAGGCTCCTTGAGCGCGCCGAGGCTTAGCC	340
Oy	CGAGCCCGGAGCGGCTTAGAGCTCTTGCTGAGAGCTGAGCGCGCGGGCAGTGTGCGCGAG	240
Db	CGAGCCCGGAGCGGCTTAGAGCTCTTGCTGAGAGCTGAGCGCGCGGGCAGTGTGCGCGAG	400

Db 661 CAGAGTCAGAGCCCGCAGACCTTCTCTGAAAGCAAGTGAAGCTGTGACATCCGGCTC 720
Qy 601 CGGTTTCAGACAGATCTGCGAGCATATGGCCAGCTTTGAGACAGGGCTGCATCCCGG 660
Db 721 CGGGTTTCAGACAGATCTGCGAGCATATGGCCAGCTTTGAGACAGGGCTGCATCCCGG 780
Qy 661 CGGGCCCGAGGCGCTGGCGCGAGCTGAGACGTGTTTGGGACAGGCCACCGCAGTGTGGGC 720
Db 781 CGGGCCCGAGGCGCTGGCGCGAGCTGAGACGTGTTTGGGACAGGCCACCGCAGTGTGGGC 840
Qy 721 TCAAGGAGCTGGGCTGTGTGTTTGTGACATCAAGTTCTCAGAGCTCTCTATCTGAGC 780
Db 841 TCAAGGAGCTGGGCTGTGTGTTTGTGACATCAAGTTCTCAGAGCTCTCTATCTGAGC 900
Qy 781 GCTTTCTGGGGGAGATCTAGTGGCCGCTGTGACAGGCCCTTGGCGGGGCTGTTCCTG 840
Db 901 GCTTTCTGGGGGAGATCTAGTGGCCGCTGTGACAGGCCCTTGGCGGGGCTGTTCCTG 960
Qy 841 ACTGAGGCGCTGGAGAGGCTGTGGGCGGGAGGCGTTCGCTGTGGTCAGTGTGAT 900
Db 961 ACTGAGGCGCTGGAGAGGCTGTGGGCGGGAGGCGTTCGCTGTGGTCAGTGTGAT 1020
Qy 901 GAGGCTGAC 909
Db 1021 GAGGCTGAC 1029

RESULT 9
AAH33283
ID AAH33283 standard; cDNA; 2045 BP.
XX
AC AAH33283;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen encoding cDNA SEQ ID NO:339.
XX
KM Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX colorectal carcinoma; ss.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US026524.
XX
PR 29-SEP-1999; 99US-0157137P.
XX 03-NOV-1999; 99US-0163280P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI: 2001-233537/24.
XX P-PSDB; AAG73852.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers.
XX
PS Claim 1; Page 2451; 9803bp; English.
XX
XX
XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
XX cancer-associated nucleic acid molecules (N) and proteins (P), where the
XX proteins are collectively known as colon cancer antigens. The colon
XX cancer antigens have cytostatic activity and can be used in gene therapy
XX and vaccine production. N and P may be used in the prevention, diagnosis
XX and treatment of diseases associated with inappropriate P expression. For
XX example, N and P may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of P by expressing inactive proteins or to

CC supplement the patients own production of P. Additionally, N may be used
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P
CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027
CC to 1052, 7921 and 7922
XX
SQ Sequence 2045 BP; 457 A; 620 C; 604 G; 364 T; 0 U; 0 Other;

Query Match 99.8%; Score 907.4; DB 4; Length 2045;
Best Local Similarity 99.9%; Pred. No. 4.6e-171;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGCGCTATCCGGGTGCAACCCCGGCGCTGCTGGAGAGAGATGATGCTTGGACATAC 60
Db 121 ATGGCGCTATCCGGGTGCAACCCCGGCGCTGCTGGAGAGAGATGATGCTTGGACATAC 180
Qy 61 TACGGGATGCTGTGCTTCAACGTAATGTTGAGGTGTGGGCGGCACTGACCGAGTGC 120
Db 181 TACGGGATGCTGTGCTTCAACGTAATGTTGAGGTGTGGGCGGCACTGACCGAGTGC 240
Qy 121 GAGCTGAGACTCTTGCCCTTCTGTGTGATGAGGCTCTTGAGCGCCGCGAGGCTTAAGC 180
Db 241 GAGCTGAGACTCTTGCCCTTCTGTGTGATGAGGCTCTTGAGCGCCGCGAGGCTTAAGC 300
Qy 181 CGGGCCCGAGCGGCTTGAAGCTCTGTGTGAGTGAAGCTCGCGCGGCGAGGCTTGGCCG 240
Db 301 CGGGCCCGAGCGGCTTGAAGCTCTGTGTGAGTGAAGCTCGCGCGGCGAGGCTTGGCCG 360
Qy 241 AGCAACCTGGGCTGCTGGGCAACTCTGGGCGGCTGTGGCCCGCAGACCTGTGCGG 300
Db 361 AGCAACCTGGGCTGCTGGGCAACTCTGGGCGGCTGTGGCCCGCAGACCTGTGCGG 420
Qy 361 CACTGTGGCGGCAAGCGGCGCGGCGAGTGTCTCCAGAAAGCTATAGTATGACCTTCC 360
Db 421 CACTGTGGCGGCAAGCGGCGCGGCGAGTGTCTCCAGAAAGCTATAGTATGACCTTCC 480
Qy 421 AGCTTTTCAAGAGGACAGAGGATGCTGCGCTGCGCTCGGCACTCAAGCAGTTCTGCA 420
Db 481 AGCTTTTCAAGAGGACAGAGGATGCTGCGCTGCGCTCGGCACTCAAGCAGTTCTGCA 540
Qy 481 AATTCTCAGACAGGCTCACTGGGAGACAGGCTTCCGCGGCAAGCGGAGGCGGAGT 480
Db 541 AATTCTCAGACAGGCTCACTGGGAGACAGGCTTCCGCGGCAAGCGGAGGCGGAGT 600
Qy 541 CGGGGCGGCGGCAAGTGTGTGTCAGACGCGCGGCGGAGAGGCGGCGGCGGCGGAG 540
Db 601 CGGGGCGGCGGCAAGTGTGTGTCAGACGCGCGGCGGAGAGGCGGCGGCGGCGGAG 660
Qy 601 CAGAGTCAGAGCCCGCAGACCTTCTCTGAAAGCAAGTGAAGCTGTGACATCCGGCTC 720
Db 721 CAGAGTCAGAGCCCGCAGACCTTCTCTGAAAGCAAGTGAAGCTGTGACATCCGGCTC 780
Qy 601 CGGGTTTCAGACAGATCTGCGAGCATATGGCCAGCTTTGAGACAGGGCTGCATCCCGG 660
Db 781 CGGGTTTCAGACAGATCTGCGAGCATATGGCCAGCTTTGAGACAGGGCTGCATCCCGG 780
Qy 661 CGGGCCCGAGGCGCTGGCGCGAGCTGAGACGTGTTTGGGACAGGCCACCGCAGTGTGGGC 720
Db 781 CGGGCCCGAGGCGCTGGCGCGAGCTGAGACGTGTTTGGGACAGGCCACCGCAGTGTGGGC 840
Qy 721 TCAAGGAGCTGGGCTGTGTGTTTGTGACATCAAGTTCTCAGAGCTCTCTATCTGAGC 780
Db 841 TCAAGGAGCTGGGCTGTGTGTTTGTGACATCAAGTTCTCAGAGCTCTCTATCTGAGC 900
Qy 781 GCTTTCTGGGGGAGATCTAGTGGCCGCTGTGACAGGCCCTTGGCGGGGCTGTTCCTG 840
Db 901 GCTTTCTGGGGGAGATCTAGTGGCCGCTGTGACAGGCCCTTGGCGGGGCTGTTCCTG 960
Qy 841 ACTGAGGCGCTGGAGAGGCTGTGGGCGGGAGGCGTTCGCTGTGGTCAGTGTGAT 900

Db 961 ACTGAGGCGCCCTCGAGAGGCTGTGGGCGCGAGGCGTTTCGCTCTGTGTGAT 1022
QY 901 GAGGCTGAC 909
Db 1021 GAGGCTGAC 1029

RESULT 10
AAFI8296
ID AAFI8296 standard; DNA; 2044 BP.
XX AAFI8296;
XX AC
XX DT 14-MAR-2001 (first entry)
XX DE Lung cancer associated polynucleotide sequence SEQ ID 315.
XX
XX Human; lung cancer associated protein; neuroprotective; cytosolic;
XX cardiocactive; immunomodulatory; muscular active; vulnerary;
XX gastrointestinal; nephrotoxic; antinfective; gynecological;
XX antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
XX proliferative disorder; wound healing; infectious disease; ds.
XX
XX Homo sapiens.
XX OS
XX WO200055180-A2.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US005918.
XX PF
XX 12-MAR-1999; 99US-0124270P.
XX PR
XX (HDMA-) HUMAN GENOME SCI INC.
XX PA (ROSE/) ROSEN C A.
XX
XX Ruben SM;
XX
XX WPI: 2000-587514/55.
XX DR P-PSDB; AAB58420.
XX
XX Lung cancer associated gene sequences, referred to as lung cancer
XX PT antigens, useful for treatment, prevention, and diagnosis of disorders
XX PT such as lung cancer.
XX
XX Claim 1; Page 772-773; 1425bp; English.

Polynucleotide sequences AAFI7982 - AAFI8424 encode human lung cancer associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytosolic; cardiocactive; immunomodulatory; muscular active general; vulnerary; gastrointestinal general; nephrotoxic; antinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences may be used for detection of lung cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The proteins may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences AAFI8425 - AAFI8433 and peptide AAB58549 are used in the course of the invention for the identification and characterisation of the polynucleotide and protein sequences

Sequence 2044 BP; 457 A; 620 C; 603 G; 364 T; 0 U; 0 Other;

Query Match 98.5%; Score 895.4; DB 3; Length 2044;
Best Local Similarity 99.8%; Pred. No. 1,18-168;
Matches 907; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

1 ATGGCGCTATTCGGGCTGACCCCGGCGCCCTGCTGTGAGAGATGATGCTGGACTAC 60

Db	121	ATGGCGCTATCCGGGTCGACCCCGCCCGCTGTGTGGAGAGAGATATAGTCTTGACTAC	180
Qy	61	TACGGGATGCTGTGCTTACCGTATGTTGAGGTGTGGCGGGCACTGACCGAGTGC	120
Db	181	TACGGGATGCTGTGCTTACCGTATGTTGAGGTGTGTGGCGGGCACTGACCGAGTGC	240
Qy	121	GAGCTGTGAGACTCTGTGGCTTTTCTGTGTGATGAGAGCTCTGTGGCGCGCCGGAGGCTTAGCC	180
Db	241	GAGCTGTGAGACTCTGTGGCTTTTCTGTGTGATGAGAGCTCTGTGGCGCGCCGGAGGCTTAGCC	300
Qy	181	CGGGCCCGGAGCGGCTTAGAGCTCCGCTGTGAGACTGTGAGAGCGCGCGGGAGATGTGGCGAG	240
Db	301	CGGGCCCGGAGCGGCTTAGAGCTCTGTGTGAGACTGTGAGAGCGCGCGGGAGATGTGGCGAG	360
Qy	241	AGCAACTGTGGCTGTGGGCAACTCTGTGGCACTGTGGCGCGCCGACAGCACTGTGGCG	300
Db	361	AGCAACTGTGGCTGTGGGCAACTCTGTGGCACTGTGGCGCGCCGACAGCACTGTGGCG	420
Qy	301	CACCTGTGGCGGCAAGCGGCGCGGCCGCAAGTGTCTCCAGAACGCTTAGTAGGACCTCC	360
Db	421	CACCTGTGGCGGCAAGCGGCGCGGCCGCAAGTGTCTCCAGAACGCTTAGTAGGACCTCC	480
Qy	361	AGCTTTTCAAAAGAGACAGAGGATGTGGCGCTCCCGCGGCAAGTGTGTGCA	420
Db	481	AGCTTTTCAAAAGAGACAGAGGATGTGGCGCTCCCGCGGCAAGTGTGTGCA	540
Qy	421	AATTCTCAGCAGGGTCACTGTGGAGACAGGGCTCCCCCAACAAGCGGCAAGCGGCGAGT	480
Db	541	AATTCTCAGCAGGGTCACTGTGGAGACAGGGCTCCCCCAACAAGCGGCAAGCGGCGAGT	600
Qy	481	CGGGCGCGCCCACTGTGTGTGTCCAGACGGCGCGGAGAGAGGGGCCCAAGCGCACCCAG	540
Db	601	CGGGCGCGCCCACTGTGTGTGTCCAGACGGCGCGGAGAGAGGGGCCCAAGCGCACCCAG	660
Qy	541	CAGCAGTACAGGCCCGGCAAGCTTCTCTGAAGGCAAAAGTACCTGTGACATCCGGCTTC	600
Db	661	CAGCAGTACAGGCCCGGCAAGCTTCTCTGAAGGCAAAAGTACCTGTGACATCCGGCTTC	720
Qy	601	CGGGTTCAGAGAGATCTGTGAGATGGGCGAGGCTTGTGAGACAGGCGGTGACATCCCGG	660
Db	721	CGGGTTCAGAGAGATCTGTGAGATGGGCGAGGCTTGTGAGACAGGCGGTGACATCCCGG	780
Qy	661	CGGGCCCAAGCGGTGTGGCGCGGCAAGCTGATGTTTGGCGAGGCCACCGCAAGTGTGCGC	720
Db	781	CGGGCCCAAGCGGTGTGGCGCGGCAAGCTGATGTTTGGCGAGGCCACCGCAAGTGTGCGC	840
Qy	721	TCAAGGAGACTGTGGCTCTGTGTGTGTGTGACATCAAGTTCTCAGAGCTCTCTATCTGGAC	780
Db	841	TCAAGGAGACTGTGGCTCTGTGTGTGTGTGACATCAAGTTCTCAGAGCTCTCTATCTGGAC	900
Qy	781	GCTTCTGTGGGAGACTACCTGAGTGTGGCGCCCTGTGAGAGCGCTGTGGGGCGTGTTCG	840
Db	901	GCTTCTGTGGGAGACTACCTGAGTGTGGCGCCCTGTGAGAGCGCTGTGGGGCGTGTTCG	959
Qy	841	ACTGAGGCGCTGTGAGAGGCTGTGTGGCGCGGAGAGGCTGTTCGCTGTGTCACTGTGAT	900
Db	960	ACTGAGGCGCTGTGAGAGGCTGTGTGGCGCGGAGAGGCTGTTCGCTGTGTCACTGTGAT	1011
Qy	901	GAGGCTGAC	909
Db	1020	GAGGCTGAC	1028

RESULT 11

ABL39692

ID ABL39692 standard; cDNA; 1084 BP.

XX ABL39692;

XX AC

XX 10-MAY-2002 (first entry)

DE Human NS cDNA sequence SEQ ID NO.2

XX Human; cytostatic; osteopathic; gynaecological; neuroprotective;
 KW antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;
 KW vasotropic; antiarteriosclerotic; antiinflammatory; dermatological;
 KW anorectic; muscular; antidiabetic; cardiovascular; anticoagulant;
 KW antifibrinolytic; hypotension; antiaslathmic; immunomodulator; cardiant;
 KW anticonvulsant; antidiabetic; tranquilizer; antidepressant; neuroleptic;
 KW gastrointestinal; virucide; antitumor; cerebroprotective; nootropic;
 KW contraceptive; vaccine; gene therapy; cancer; osteoporosis; dyscrasia;
 KW endometriosis; degenerative disease; multiple sclerosis; psoriasis;
 KW rheumatoid arthritis; cataract; reestenosis; atherosclerosis; glaucoma;
 KW inflammation; skin disorder; obesity; muscular dystrophy; AIDS;
 KW infertility; cardiovascular disease; coagulation disease; hypertension;
 KW ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration;
 KW diabetes; anxiety; depression; schizophrenia; viral disease; stroke;
 KW gastric ulcer; Alzheimer's disease; gene; ss.
 XX Homo sapiens.
 OS WO200206315-A2.
 PN 24-JAN-2002.
 XX 17-JUL-2001; 2001WO-IL000653.
 XX 18-JUL-2000; 2000IL-00137345.
 PR 15-DEC-2000; 2000IL-00140354.
 XX (COMP-) COMPUEN LTD.
 PA Mintz U, Freilich S, Bernstein J;
 PI MPI: 2002-155037/20.
 DR P-PSDB; ABB06038.
 XX One hundred and twenty eight novel nucleic acid sequences, useful for
 PT treating and diagnosing e.g. cancer, asthma and Alzheimer's.
 XX Claim 1; Page 76-77; 290pp; English.
 PS ABL39691 to ABL39818 represent novel human nucleic acid sequences
 CC encoding the proteins given in ABB06037 to ABB06164. The novel sequences
 CC (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective,
 CC antirheumatic, antiarthritic, antipsoriatic, ophthalmological, virucide,
 CC vasotropic, antiarteriosclerotic, antiinflammatory, dermatological,
 CC anorectic, muscular, anti-HIV, antidiabetic, cardiovascular, cardiant,
 CC anticonvulsant, antidiabetic, antiaslathmic, immunomodulator, cardiant,
 CC immunomodulator, anticonvulsant, antidiabetic, tranquilizer, antitumor,
 CC antidepressant, gastrointestinal, neuroleptic, cerebroprotective,
 CC nootropic and contraceptive activities. The NS can be used in vaccines,
 CC gene therapy and antisense therapy. Nucleic acids, expression vectors and
 CC antibodies from the present invention can be used for treating and
 CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
 CC diseases, dyscrasia, multiple sclerosis, rheumatoid arthritis, psoriasis,
 CC cataracts, reestenosis, atherosclerosis, inflammation, skin disorders,
 CC glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular
 CC disease, coagulation disease, ischaemia, hypertension, asthma, immune
 CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,
 CC depression, schizophrenia, viral disease, gastric ulcers, stroke,
 CC Alzheimer's disease and as a contraceptive
 CC
 SQ Sequence 1084 BP; 174 A; 332 C; 378 G; 190 T; 0 U; 10 Other;

Query Match 90.8%; Score 825.8; DB 6; Length 1084;
 Best Local Similarity 98.0%; Pred. No. 7.3e-155;
 Matches 891; Conservative 7; Mismatches 4; Indels 7; Gaps 6;

QY 1 ATGGGCTATCCGCGTGAAGCCCGGCGCGTGTGGAGAGAGATGATGCTGAGCTAC 60
 DB 84 ATGGGCTATCCGCGTGAAGCCCGGCGCGTGTGGAGAGAGATGATGCTGAGCTAC 143
 QY 61 TACGGGATCTGTGCTTACCGGTATGAGGTGTGGCGGGGCACTGACCGAGTGC 120

Db 144 TACGGGATCTGTGCTTACCGGTATGAGGTGTGGCGGGGCACTGACCGAGTGC 203
 QY 121 GAGCTGAGAGCTCTGAGCTTCTGTGATGAGGTCTCTGAGCGCGCGAGAGCTTAC 180
 Db 204 RAGCTGAGAGCTCTGAGCTTCTGTGATGAGGTCTCTGAGCGCGCGAGAG-TTAGCC 262
 QY 181 CGGGCCCGAGCGGCTTGAAGTCTCTGTGAGGTGAGCGCGCGGCGAGTGCAGAG 240
 Db 263 CGGGCCCGAGCGGCTTGAAGTCTCTGTGAGGTGAGCGCGCGGCGAGTGCAGAG 322
 QY 241 AGCAACTCTGCGCTCTGAGGAGTCTCTGTGAGGTGAGCGCGCGGCGAGTGCAGAG 300
 Db 323 AGCAACTCTGCGCTCTGAGGAGTCTCTGTGAGGTGAGCGCGCGGCGAGTGCAGAG 382
 QY 301 GAGCTGAGAGCGGAGCGGCGGCGGAGTCTCTGAGGAGTCTCTGAGGAGTCTCTGAG 360
 Db 383 GAGCTGAGAGCGGAGCGGCGGAGTCTCTGAGGAGTCTCTGAGGAGTCTCTGAG 440
 QY 361 AGCTCTTCAAGAGAGAGAGAGGTAGTCCGCTGCGGCTGCGAGTCAAGAGTCTGCA 420
 Db 441 AGCTCTTCAAGAGAGAGAGAGGTAGTCCGCTGCGGCTGCGAGTCAAGAGTCTGCA 500
 QY 421 AATTCTCAGAGAGTCAAGTGAAGAGAGAGTCTCTGAGGAGTCTCTGAGGAGTCTCTGAG 480
 Db 501 AATTCTCAGAGAGTCAAGTGAAGAGAGAGTCTCTGAGGAGTCTCTGAGGAGTCTCTGAG 559
 QY 481 CGGGGCGGCGGCGGAGTGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 Db 560 CGGGGCGGCGGCGGAGTGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 618
 QY 541 CAGCAGTCAAG 600
 Db 619 CAGCAGTCAAG 678
 QY 601 CGGGTTCAGAGAGAGTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 Db 679 CGGGTTCAGAGAGAGTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 738
 QY 661 CGGGCCCGAGCGGCGGAGTGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 Db 739 CGG-CCGAGCGCTGAGCGGAG 797
 QY 721 TCAAGGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 780
 Db 798 TCAAGGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 857
 QY 781 GCTTCTGAGGAGAGTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 Db 858 GCTTCTGAGGAGAGTCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 917
 QY 841 ACTGAGGCGCTGAGAGAGTGTGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
 Db 918 ACTGAGGCGCTGAGAGAGTGTGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 976
 QY 901 GAGGCTGAC 909
 Db 977 GAGGCTGAC 985

RESULT 12
 ABL39693
 ID ABL39693 standard; cDNA; 1106 BP.
 AC ABL39693;
 XX
 DT 10-MAY-2002 (first entry)
 XX
 DE Human NS cDNA sequence SEQ ID NO:3.
 XX
 KW Human; cytostatic; osteopathic; gynaecological; neuroprotective;
 KW antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;
 KW vasotropic; antiarteriosclerotic; antiinflammatory; dermatological;
 KW anorectic; muscular; antidiabetic; cardiovascular; anticonvulsant;

KW	antifibronolytic; hypotension; antiaspheric; immunomodulator; cardiant;
KW	anticonvulsant; antidiabetic; tranquilliser; antidepressant; neuroleptic;
KM	gastrointestinal; viricide; antileuc; cerebroprotective; nootropic;
KM	contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia;
KW	endometriosis; degenerative disease; multiple sclerosis; psoriasis;
KM	rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma;
KW	inflammation; skin disorder; obesity; muscular dystrophy; AIDS;
KW	infertility; cardiovascular disease; coagulation disease; hypertension;
KW	ischemia; asthma; immune disease; epilepsy; angina; neurodegeneration;
KW	diabetes; anxiety; depression; schizophrenia; viral disease; stroke;
KW	gastric ulcer; Alzheimer's disease; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200206315-A2.
XX	
PD	24-JAN-2002.
XX	
PF	17-JUL-2001; 2001WO-IL000653.
XX	
XX	18-JUL-2000; 2000IL-00137345.
PR	15-DEC-2000; 2000IL-00140354.
XX	
PA	(COMP-) COMPUGEN LTD.
XX	
PI	Mintz L, Freilich S, Bernstein J;
DR	WPI; 2002-155037/20.
XX	
XX	P-PSDB; ABB06039.
PT	One hundred and twenty eight novel nucleic acid sequences, useful for
XX	treating and diagnosing e.g. cancer, asthma and Alzheimer's.
PS	Claim 1; Page 77; 290pp; English.
XX	
CC	AB139691 to AB139818 represent novel human nucleic acid sequences
CC	encoding the proteins given in ABB06037 to ABB06164. The novel sequences
CC	(NS) can have cyrostatic, osteopathic, gynaecological, neuroprotective,
CC	antirheumatic, antiallergic, antipsoriatic, ophthalmological, viricide,
CC	vasorelaxant, antiarteriosclerotic, antiinflammatory, dermatological,
CC	anorectic, muscular, anti-HIV, antifertility, cardiovascular,
CC	anticonvulsant, antifibronolytic, hypotension, antiaspheric, cardiant,
CC	immunomodulator, anticonvulsant, antidiabetic, tranquilliser, antileuc,
CC	antidepressant, gastrointestinal, neuroleptic, cerebroprotective,
CC	nootropic and contraceptive activities. The NS can be used in vaccines,
CC	gene therapy and antisense therapy. Nucleic acids, expression vectors and
CC	antibodies from the present invention can be used for treating and
CC	diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
CC	diseases, dysnomia, multiple sclerosis, rheumatoid arthritis, psoriasis,
CC	cataracts, restenosis, atherosclerosis, inflammation, skin disorders,
CC	glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular
CC	disease, coagulation disease, ischaemia, hypertension, asthma, immune
CC	disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,
CC	depression, schizophrenia, viral disease, gastric ulcers, stroke,
CC	Alzheimer's disease and as a contraceptive
XX	
XX	
SO	Sequence 1106 BP; 162 A; 340 C; 365 G; 189 T; 0 U; 10 Other;
	Query Match 90.8%; Score 825.8; DB 6; Length 1106;
	Best Local Similarity 98.0%; Pied. No. 7.3e-155;
	Matches 891; Conservative 7; Mismatches 4; Indels 7; Gaps 6
QY	1 ATGGCGCTATCCGGGTGCAGCCCGGCCCGCTGCTGGAGAGAGATGAGTCTTGACATAC 60
DB	106 ATGGGCGCTATCCGGGTGCAGCCCGGCCCGCTGCTGGAGAGAGATGAGTCTTGACATAC 165
QY	61 TACGGGAATGCTGTGCTTACCCGATATGTTCCAGATGAGTGAGCGGAGCACTGACCGAGTGC 120
DB	166 TACGGGAATGCTGTGCTTACCCGATATGTTCCAGATGAGTGAGCGGAGCACTGACCGAGTGC 225
QY	121 GAGCTGAGAGCTCCGAGCCCTTTCTGTGTGATGAGAGTCTCTGGCGCCCGGAGGCTTACGC 180
DB	226 GAGCTGAGAGCTCCGAGCCCTTTCTGTGTGATGAGAGTCTCTGGCGCCCGGAGG-TTACCC 284

QY	181	CGGGCCCCGAGCGCGCTTAGAGGCTCCGTGAGAGCTGAGAGCGCCGCGGGAGAGTGCGGGAG	24
Db	285	CGGGCCCCGAGCGCGCTTAGAGGCTCCGTGAGAGCTGAGAGCGCCGCGGGAGAGTGCGGGAG	344
QY	241	AGCAACCTGCGGCTGCTGAGGCACTCTGCGCGTCTGGCCCGCCAGCACTTGCTCCG	300
Db	345	AGCAACCTGCGGCTGCTGAGGCACTCTGCGCGTCTGGCCCGCCAGCACTTGCTCCG	404
QY	301	CACCTGGCGCGCAAGCGCGCGCCGCGCAAGTGTCCAGAACGCTATATGCTATGGCACCTCC	366
Db	405	CACCTGGCGCGCAAGCGCGCGCCGCGCAAGTGTCCAGAACGCTATATGCTATGGCACCTCC	462
QY	361	AGCTCTTCAAAGAGGACAGAGGGTATGCTCCGTCGCGCGTCCGCGAGTCAAGCACTTCGCA	420
Db	463	AGCTCTTCAAAGAGGACAGAGGGTATGCTCCGTCGCGCGTCCGCGAGTCAAGCACTTCGCA	522
QY	421	AATTCACAGCAGGCTCAGTGGAGACAGGCTCCCGCCCAACCAAGCGGACGGCGGAGT	480
Db	523	AATTCACAGCAGGCTCAGTGGAGACAGGCTCCCGCCCAACCAAGCGGACGGCGGAGT	581
QY	481	CGGGGCGCGGCCCAAGTGTGTGTGTCACAGCGCGCGCGGAGAGGGGCCCGCCAGCCGACCCAG	540
Db	582	CGGGGCGCGGCCCAAGTGTGTGTGTCACAGCGCGCGCGGAGAGGGGCCCGCCAGCCGACCCAG	640
QY	541	CAGCAGTCAGAGCCCGCGCCAGACCTTCCTGAAAGCAAGTGACCTGTGACATCCGGCTC	600
Db	641	CAGCAGTCAGAGCCCGCGCCAGACCTTCCTGAAAGCAAGTGACCTGTGACATCCGGCTC	700
QY	601	CGGATTCCAGCAGAGTACTCTGAGCATGAGCCAGCCTTGAGCAGGGCGTGGCATCCCG	660
Db	701	CGGATTCCAGCAGAGTACTCTGAGCATGAGCCAGCCTTGAGCAGGGCGTGGCATCCCG	760
QY	661	CGGGCCCCGAGCGCTGGCGCGGACGCTGACGTTGTTGGGCAAGCCACCGCAGTGTCTCCG	720
Db	761	CGGCCCCCGAGCGCTGGCGCGGACGCTGACGTTGTTGGGCAAGCCACCGCAGTGTCTCCG	819
QY	721	TCAAAGGACCTGGGCTCTGTGTGTGTGATCATCAAGTTCTCAGAGCTCTCCTATCGAGAC	780
Db	820	TCAAAGGACCTGGGCTCTGTGTGTGTGATCATCAAGTTCTCAGAGCTCTCCTATCGAGAC	879
QY	781	GCTTCTGAGGCGGACTTACCTGAGTGGCGCGCTGCTGACAGGCCCTGGGGGCGGTTCCTG	840
Db	880	GCTTCTGAGGCGGACTTACCTGAGTGGCGCGCTGCTGACAGGCCCTGGGGGCGGTTCCTG	939
QY	841	ACTGAGGCGCTGCCAGAGGCTGTGGGCGCGGAGGCTGTTCCGCTGTGATGATGGAT	900
Db	940	ACTGAGGCGCTGCCAGAGGCTGTGGGCGCGGAGGCTGTTCCGCTGTGATGATGGAT	998
QY	901	GAGGCTGAC	909
Db	999	GAGGCTGAC	1007
RESULT 13			
AAS62603			
ID	AAS62603 standard; cDNA, 1966 BP.		
XX	AAS62603;		
AC	14-FEB-2002 (first entry)		
DT	CDNA sequence #390 encoding novel human secreted protein.		
XX	Human secreted protein; hyperproliferative disorder; autoimmune disorder;		
KW	immune deficiency disorder; blood disorder; inflammatory disorder;		
KW	infectious disorder; gene therapy; antimicrobial; hepatotropic;		
KW	immunosuppressive; antineumatic; ss.		
OS	Homo sapiens.		
XX	WO200177291-A2.		
XX			

PD 18-OCT-2001.
 XX 29-WAR-2001; 2001WO-US010485.
 PF 06-APR-2000; 2000US-0195604P.
 PR (GENY) GENETICS INST INC.
 XX
 PA
 PI Wong GG, Clark HP, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;
 PI Gulukota K, Graham JR;
 DR WPI; 2002-010900/01.
 XX
 PT New polynucleotides encoding secreted proteins useful for treating e.g.
 PT asthma, HIV and Crohn's disease.
 XX
 XX
 XX Claim 1; Page 280; 391p; English.
 XX
 CC The present invention relates to the isolation of novel cDNA sequences
 CC which encode human secreted proteins. The cDNA sequences have been
 CC derived from a variety of human tissues. The invention also provides a
 CC method for producing proteins from these polynucleotide sequences. The
 CC proteins are useful for identifying compounds that modulate their
 CC activity and production, and the cell is also useful for identifying
 CC compounds that modulate expression of the polynucleotide sequences
 CC encoding the secreted proteins. The sequences of the invention are useful
 CC for treating diseases such as hyperproliferative disorders (e.g. cancer),
 CC immune deficiency disorders (e.g. severe combined immunodeficiency
 CC (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders
 CC (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis) and
 CC infectious disorders (e.g. hepatitis). The polynucleotide sequences of
 CC the invention are also useful in gene therapy. AAS62214-AAS62838
 CC represent the cDNA sequences of the invention that encode for novel human
 CC secreted proteins
 XX
 SQ Sequence 1966 BP; 356 A; 618 C; 614 G; 378 T; 0 U; 0 Other;

Query Match 87.9%; Score 799.4; DB 6; Length 1966;
 Best Local Similarity 90.2%; Pred. No. 1.3e-149;
 Matches 908; Conservative 0; Mismatches 1; Indels 99; Gaps 1;

QY 1 ATGGCGCTATCCGGGTGACCCCGGCCGCTCTGGGAGAGATGAGCTGACTAC 60
 DB 50 ATGGCGCTATCCGGGTGACCCCGGCCGCTCTGGGAGAGATGAGCTGACTAC 109
 DB 61 TACGGGATCTCTGCTTACCGTATGTTGAGGTGGGCGGCAATGACCGAGTGC 120
 DB 110 TACGGGATCTCTGCTTACCGTATGTTGAGGTGGGCGGCAATGACCGAGTGC 169
 QY 121 GAGCTGAGACTCTGGCCCTTTGCGCGATGAGGCTCTGGGCGCGGAGGCTTACGC 180
 DB 170 GAGCTGAGACTCTGGCCCTTTGCGCGATGAGGCTCTGGGCGCGGAGGCTTACGC 229
 QY 181 CGGGCCCGGAGCGGCTTAGAGCTCTGCTGAGCTGAGCGCGCGGAGTGGCGGAG 240
 DB 230 CGGGCCCGGAGCGGCTTAGAGCTCTGCTGAGCTGAGCGCGCGGAGTGGCGGAG 289
 QY 241 AGCAACTCTGGGCTGTGGGGCACTCTGCGCGTGTGGCCCGGCAAGCTGCTGCCG 300
 DB 290 AGCAACTCTGGGCTGTGGGGCACTCTGCGCGTGTGGCCCGGCAAGCTGCTGCCG 349
 QY 301 CACCTGGGCGGAGGCGGCGGCGGCGGAGTCTCCAGAAAGCTATAGTGGACCTCC 360
 DB 350 CACCTGGGCGGAGGCGGCGGCGGCGGAGTCTCCAGAAAGCTATAGTGGACCTCC 409
 QY 361 AGCTCTTCAAGAGAGCAGAGGGATAGCTGCGTGGCGCTGGCAGTCAAGACTTCTGCA 420
 DB 410 AGCTCTTCAAGAGAGCAGAGGGATAGCTGCGTGGCGCTGGCAGTCAAGACTTCTGCA 469
 QY 421 AATTCTCAGCAGGCTAGTGGAGAGAGGCTCCCCCAACCAAGGGGCGAGGAGT 480
 DB 470 AATTCTCAGCAGGCTAGTGGAGAGAGGCTCCCCCAACCAAGGGGCGAGGAGT 529

QY 481 CGGGCCCGGCGGAGTGTGTGTGTCAGACGCGCGGAGAGGGGCCCGGACCGCAG 540
 DB 530 CGGGCCCGGCGGAGTGTGTGTGTCAGACGCGCGGAGAGGGGCCCGGACCGCAG 589
 QY 541 CAGCAGTCAAGAGCCCGGCAACCTTCTCTGAAGCAAGTGAAGCTGCTGCTGCTG 587
 DB 590 CAGCAGTCAAGAGCCCGGCAACCTTCTCTGAAGCAAGTGAAGCTGCTGCTGCTG 649
 QY 588 ----- 587
 DB 650 AGCAGGGTCCAGCATCTCTTCTGTTGAGGACCTCCGGAAGCTTCAATGATGTGAA 709
 QY 588 -----TGACATCCGGCTCCGGGTTTCAGACAGATAGTGC 622
 DB 710 GGGCAAGGGAGAGAGGCTTTCATGATGATCCGGCTCCGGGTTTCAGACAGATAGTGC 769
 QY 623 AGCATGGGCGAGCTTGGAGAGAGGCGTGGGATCCCGGCGGCCCGGCTGCGCGGC 682
 DB 770 AGCATGGGCGAGCTTGGAGAGAGGCGTGGGATCCCGGCGGCCCGGCTGCGCGGC 829
 QY 683 AGCTGGAGAGTGTGGGAGGCGACCGGAGTGGCGCTCAAGAGGACCTGGGCTGTGG 742
 DB 830 AGCTGGAGAGTGTGGGAGGCGACCGGAGTGGCGCTCAAGAGGACCTGGGCTGTGG 889
 QY 743 TTTGTGATCATGAAGTCTCAGAGCTCTCTATCTGAGAGCTTCTGGGGCGCATCTGA 802
 DB 880 TTTGTGATCATGAAGTCTCAGAGCTCTCTATCTGAGAGCTTCTGGGGCGCATCTGA 949
 QY 803 GTGGCGCCCTGCTGAGGAGCCCTGCGGGCGTGTCTGACTGAGGCTCTGCGAGAGCTG 862
 DB 950 GTGGCGCCCTGCTGAGGAGCCCTGCGGGCGTGTCTGACTGAGGAGCTCTGCGAGAGCTG 1009
 QY 863 TGGGCGGGGAGGCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 909
 DB 1010 TGGGCGGGGAGGCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1056

RESULT 14
 AAH99646
 ID AAH99646 standard; cDNA, 1570 BP.
 XX
 XX AAH99646;
 DT 16-OCT-2001 (first entry)
 XX
 DE Human protein encoding cDNA sequence SEQ ID NO:481.
 XX
 KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
 KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
 KW antibacterial; endocrine; cardiant; central nervous system; virucide;
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antianemic; anaemia;
 KW antiagregant; haemostatic; antiallergic; antidiabetic; cytostatic;
 KW dermatological; antidepressant; nootropic; antiparkinsonian; infection;
 KW neuroprotective; gene therapy; antisense therapy; vaccine; inflammation;
 KW immunostimulant; rheumatoid arthritis; septic shock; pancreatitis;
 KW antianaphylactic; neuropathology; cardiac anaphylaxis; autoimmunity;
 KW cardiac dysfunction; haemopoietic disorder; platelet disorder; asthma;
 KW genetic disease; haemopoietic disorder; severe combined immunodeficiency;
 KW thrombocytopaenia; osteoporosis; multiple sclerosis; depression;
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
 KW neurological disorder; ss.
 KW
 OS Homo sapiens.
 XX
 PN WO200153455-A2.
 XX
 PD 26-JUL-2001.
 XX
 PF 22-DEC-2000; 2000WO-US035017.
 XX
 XX 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.

CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

XX
SQ Sequence 1067 BP; 191 A; 349 C; 328 G; 199 T; 0 U; 0 Other;

Query Match 59.5%; Score 541; DB 4; Length 1067;

Best Local Similarity 95.8%; Pred. No. 3e-98;

Matches 572; Conservative 0; Mismatches 10; Indels 15; Gaps 1;

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QY      1  ATGGCGCTATCCGGGTCGACCCCGGCCGCTGCTGGAGAGATGATGCTTGACTAC 60
      |||
DB      151 ATGGCGCTATCCGGGTCGACCCCGGCCGCTGCTGGAGAGATGATGCTTGACTAC 210
      |||

QY      61  TACGGGATGCTGCTGCTTCACTGATGTTGAGAGTGTGGCGGGCACTGACCGAGTGC 120
      |||
DB      211 TACGGGATGCTGCTGCTTCACTGATGTTGAGAGTGTGGCGGGCACTGACCGAGTGC 270
      |||

QY      121 GAGCTGAGAGCTCTGGGCTTTTGTGCTGATGAGGGCTCTGGGCGCGCGGAGGCTTAGCC 180
      |||
DB      271 GAGCTGAGAGCTCTGGGCTTTTGTGCTGATGAGGGCTCTGGGCGCGCGGAGGCTTAGCC 330
      |||

QY      181 CGGGCCCGCAGCGGCTAGAGCTCTGCTGAGCTGAGCGCGCGCGGCGAGTGCAG 240
      |||
DB      331 CGGGCCCGCAGCGGCTTAAGCTCTGCTGAGCTGAGCGCGCGCGGCGAGTGCAG 390
      |||

QY      241 AGCAACTGCGGCTGTGGGGCAACTCTGCGCGTGTGCGCCCGCACTGCTGCCG 300
      |||
DB      391 AGCAACTGCGGCTGTGGGGCAACTCTGCGCGTGTGCGCCCGCACTGCTGCCG 450
      |||

QY      301 CACCTGGGCGGCAAGGGCGCGCGCGCAGTGTCCAGAAAGCTATAGCTATAGCACTCC 360
      |||
DB      451 CACCTGGGCGGCAAGGGCGCGCGCGCAGTGTCCAGAAAGCTATAGCTATAGCACTCC 510
      |||

QY      361 AGCTTTCAAGAGGACAGAGGGTAGCTCCGTCGCGCGTCCGAGTCAAGCAGTTCTGCA 420
      |||
DB      511 AGCTTTCAAGAGGACAGAGGGTAGCTCCGTCGCGCGTCCGAGTCAAGCAGTTCTGCA 570
      |||

QY      421 AATTCTCAGCAGGCTCAGTGGAGAGGCTCCCCCAACCAAGGGGCAAGCGGGAGT 480
      |||
DB      571 AATTCTCAGCAG-----GGCTCCCCCAACCAAGGGGCAAGCGGGAGT 615
      |||

QY      481 CGGGGCGGGCCAGTGTGTGTGTCAGACGGCGGGCGGAGAGGGGCCCAAGCCGACCCGAG 540
      |||
DB      616 CGGGGCGGGCCAGTGTGTGTGTCAGACGGCGGGCGGAGAGGGGCCCAAGCCGACCCGAG 675
      |||

QY      541 CAGCAGTCAGAGCCCGCAGACCTTCTCTGAAGGCAAGTGAACCTGTGACATCCGG 597
      |||
DB      676 CAGCAGTCAGAGCCCGCAGACCTTCTCTGAAGGCAAGTGAACCAACCAACTCG 732
      |||
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Search completed: February 12, 2005, 11:11.16
Job time : 430 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 12:44:53 / Search time 2935 Seconds
(without alignments)
15007.084 Million cell updates/sec

Title: US-10-030-271-1
Perfect score: 909
Sequence: 1 atgctcctatccggctgac.....tcagtgtgagtgcgctgac 909

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pal:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_pro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	909	100.0	909	6	BD093311 Apoptosis
2	909	100.0	1883	6	BD093312 Apoptosis
3	909	100.0	1883	6	BD093312 Apoptosis
4	858	94.4	981	6	CQ119642 Sequence
5	858	94.4	981	6	CQ119642 Sequence
6	858	94.4	1230	6	AX322754 Sequence
7	858	94.4	1230	6	AX322754 Sequence
8	756	83.2	1951	9	BC027930 Homo sapi
9	603	66.3	981	9	AF457575 Homo sapi
10	411	45.2	2012	9	AY125488 Homo sapi
11	383	42.1	2005	9	BC013372 Homo sapi
12	334	36.7	626	6	BD149917 Primer fo
13	334	36.7	626	6	BD149917 Primer fo
14	322	35.4	1659	9	AX130203 Homo sapi
15	321	35.3	95663	9	AC010247 Homo sapi
16	321	30.9	1067	6	AR339362 Sequence
17	277	30.5	111084	9	AC006486 Homo sapi
18	252	27.7	303	6	AX431298 Sequence
19	187	20.6	1084	6	AX364851 Sequence

20	187	20.6	1106	6	AX364852 Sequence
21	177	19.5	603	6	AX136449 Sequence
22	177	19.5	603	6	BD123689 Secretory
23	144	15.8	167108	2	AC068283 Homo sapi
24	56	6.2	993	10	AF457576 Mus muscu
25	56	6.2	993	10	AF457576 Mus muscu
26	56	6.2	1540	2	BC037043 Mus muscu
27	56	6.2	1540	2	BC037043 Mus muscu
28	56	6.2	1540	2	BC037043 Mus muscu
29	56	6.2	1540	2	BC037043 Mus muscu
30	56	6.2	1540	2	BC037043 Mus muscu
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87	56	6.2	1540	2	BC037043 Mus muscu
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90	56	6.2	1540	2	BC037043 Mus muscu
91	56	6.2	1540	2	BC037043 Mus muscu
92	56	6.2	1540	2	BC037043 Mus muscu

C 93	20	2.2	277000	1	SC0939109	AL939109 Streptomy	C 166	19	2.1	102151	9	HS979N1	AL035659 Human DNA
C 94	20	2.2	300029	1	AE016787	AE016787 Pseudomon	C 167	19	2.1	103522	9	AC021080	AC021080 Homo sapi
C 95	20	2.2	301925	1	AP005046	AP005046 Streptomy	C 168	19	2.1	104388	2	AC007905	AC007905 Homo sapi
C 96	20	2.2	346289	1	BX640435	BX640435 Bordetell	C 169	19	2.1	110000	1	AP006618	AP006618_32
C 97	20	2.2	346287	1	BX640450	BX640450 Bordetell	C 170	19	2.1	110000	1	AY305578	AY305578_0
C 98	19	2.1	360	6	AX794353	AX794353 Sequence	C 171	19	2.1	110000	2	AC091343	AC091343_6
C 99	19	2.1	360	6	AX803613	AX803613 Sequence	C 172	19	2.1	110000	2	LMFLCHR25_02	LMFLCHR25_02
C 100	19	2.1	377	11	G48211	G48211 SHGC-60419	C 173	19	2.1	110000	2	LMFLCHR31_19	LMFLCHR31_19
C 101	19	2.1	553	10	AF299351	AF299351 Cavia por	C 174	19	2.1	110000	2	LMFLCHR36_32	LMFLCHR36_32
C 102	19	2.1	606	6	AX119213	AX119213 Sequence	C 175	19	2.1	110931	9	AC0098512	AC0098512
C 103	19	2.1	759	6	CO730798	CO730798 Sequence	C 176	19	2.1	111714	2	AL359432	AL359432
C 104	19	2.1	878	6	ARS22606	ARS22606 Sequence	C 177	19	2.1	112065	8	AC109596	AC109596
C 105	19	2.1	906	6	CQ769320	CQ769320 Sequence	C 178	19	2.1	114285	8	AP001870	AP001870 Homo sapi
C 106	19	2.1	943	6	AX574584	AX574584 Sequence	C 179	19	2.1	122322	2	AC008580	AC008580 Homo sapi
C 107	19	2.1	943	6	AY358178	AY358178 Homo sapi	C 180	19	2.1	132636	9	AC108369	AC108369 Pan trogl
C 108	19	2.1	988	6	ARS06943	ARS06943 Sequence	C 181	19	2.1	135983	2	AC134767	AC134767
C 109	19	2.1	1536	5	BC067160	BC067160 Dario rer	C 182	19	2.1	138009	2	CR759952	CR759952
C 110	19	2.1	1641	8	BC004932	BC004932 Homo sapi	C 183	19	2.1	138740	2	AC009113	AC009113
C 111	19	2.1	1660	8	AK069852	AK069852 Oryza sat	C 184	19	2.1	141320	2	AC017833	AC017833
C 112	19	2.1	1680	3	AY070936	AY070936 Drosophi1	C 185	19	2.1	146578	9	AC012468	AC012468 Homo sapi
C 113	19	2.1	1870	6	AK024551	AK024551 Homo sapi	C 186	19	2.1	147651	8	AC099774	AC099774
C 114	19	2.1	1871	6	CQ798278	CQ798278 Sequence	C 187	19	2.1	148667	9	HS1018E9	HS1018E9
C 115	19	2.1	1871	9	AY676494	AY676494 Homo sapi	C 188	19	2.1	150184	2	AC134554	AC134554
C 116	19	2.1	2021	10	AB057765	AB057765 Mus muscu	C 189	19	2.1	151796	2	AC096595	AC096595
C 117	19	2.1	2089	9	HS0802333	HS0802333	C 190	19	2.1	152050	1	ML0672113	ML0672113
C 118	19	2.1	2225	5	AF014368	AF014368 Dario rer	C 191	19	2.1	154333	5	EX005316	EX005316 Zebrafish
C 119	19	2.1	2247	6	AF128112	AF128112 Drosophi1	C 192	19	2.1	154818	9	AL157711	AL157711 Human DNA
C 120	19	2.1	2247	6	CO614409	CO614409 Sequence	C 193	19	2.1	156652	2	EX927374	EX927374
C 121	19	2.1	2317	5	AF014369	AF014369 Dario rer	C 194	19	2.1	156814	2	AP005004	AP005004
C 122	19	2.1	2320	5	AF014367	AF014367 Dario rer	C 195	19	2.1	159082	2	AC110724	AC110724 Mus muscu
C 123	19	2.1	2403	5	AF014370	AF014370 Dario rer	C 196	19	2.1	159420	2	AC009017	AC009017 Homo sapi
C 124	19	2.1	2528	6	BD373750	BD373750 Novel BAG	C 197	19	2.1	163377	9	AC087714	AC087714 Homo sapi
C 125	19	2.1	2533	6	AR477557	AR477557 Sequence	C 198	19	2.1	163384	9	AC026409	AC026409 Homo sapi
C 126	19	2.1	2538	6	AX794344	AX794344 Sequence	C 199	19	2.1	164737	2	AC118967	AC118967 Rattus no
C 127	19	2.1	2533	6	AX803611	AX803611 Sequence	C 200	19	2.1	165902	2	AC023721	AC023721 Drosophi1
C 128	19	2.1	2534	6	BD373757	BD373757 Novel BAG	C 201	19	2.1	167213	2	AC146379	AC146379 Pan trogl
C 129	19	2.1	2534	6	AR477564	AR477564 Sequence	C 202	19	2.1	167508	10	CR354750	CR354750 Mus muscu
C 130	19	2.1	2534	9	AF071218	AF071218 Homo sapi	C 203	19	2.1	167962	2	AC073484	AC073484 Homo sapi
C 131	19	2.1	2534	9	AF095193	AF095193 Homo sapi	C 204	19	2.1	168799	9	AC009531	AC009531 Homo sapi
C 132	19	2.1	2536	6	CQ729403	CQ729403 Sequence	C 205	19	2.1	169091	2	AC025852	AC025852
C 133	19	2.1	2550	6	AF127139	AF127139 Homo sapi	C 206	19	2.1	170606	2	EX957335	EX957335 Dario rer
C 134	19	2.1	2586	9	BC006418	BC006418 Homo sapi	C 207	19	2.1	174227	5	AL923392	AL923392
C 135	19	2.1	2700	10	BC030913	BC030913 Mus muscu	C 208	19	2.1	174234	8	AC090486	AC090486 Genomic B
C 136	19	2.1	2739	6	AX654352	AX654352 Sequence	C 209	19	2.1	174215	2	AL159984	AL159984 Homo sapi
C 137	19	2.1	2739	6	AF105060	AF105060 Rificia pa	C 210	19	2.1	175039	2	AC118633	AC118633 Mus muscu
C 138	19	2.1	4688	1	RCAMUP	M932348 Rhodobacter	C 211	19	2.1	176547	9	AC092447	AC092447 Homo sapi
C 139	19	2.1	4697	3	CELTRA1A	M932356 Caenorhabdi	C 212	19	2.1	177585	9	AC005826	AC005826 Homo sapi
C 140	19	2.1	4756	6	CO574955	CO574955 Sequence	C 213	19	2.1	177750	9	AC005874	AC005874
C 141	19	2.1	4850	10	BC051383	BC051383 Mus muscu	C 214	19	2.1	177864	9	AF134471	AF134471
C 142	19	2.1	4856	10	BC052326	BC052326 Mus muscu	C 215	19	2.1	177883	2	AC046159	AC046159 Homo sapi
C 143	19	2.1	5082	10	BC082331	BC082331 Mus muscu	C 216	19	2.1	178073	1	SC0590464	SC0590464
C 144	19	2.1	5268	6	CO614408	CO614408 Sequence	C 217	19	2.1	178239	3	AC009367	AC009367
C 145	19	2.1	5670	6	AX616761	AX616761 Sequence	C 218	19	2.1	180270	9	AC007923	AC007923
C 146	19	2.1	7781	1	AF298190	AF298190 Sinorhizo	C 219	19	2.1	180387	3	AC009378	AC009378
C 147	19	2.1	9937	1	AE004563	AE004563 Pseudomon	C 220	19	2.1	182312	2	AC087709	AC087709 Homo sapi
C 148	19	2.1	11103	1	AE001944	AE001944 Pseudomon	C 221	19	2.1	182445	2	AC132717	AC132717 Rattus no
C 149	19	2.1	11974	1	AE007247	AE007247 Sinorhizo	C 222	19	2.1	184062	9	AC149232	AC149232 Pan trogl
C 150	19	2.1	12753	1	AE007233	AE007233 Sinorhizo	C 223	19	2.1	184661	4	AC124156	AC124156 Equus cab
C 151	19	2.1	32492	10	MUSPACOL	M65161 Mouse pro-a	C 224	19	2.1	185398	10	AC121926	AC121926
C 152	19	2.1	38516	1	AF540992	AF540992 Pseudomon	C 225	19	2.1	186495	2	AC147081	AC147081 Pan trogl
C 153	19	2.1	44653	9	HS38085	HS38085 Human DNA	C 226	19	2.1	186633	10	AC140047	AC140047 Mus muscu
C 154	19	2.1	51729	9	AC118276	AC118276 Homo sapi	C 227	19	2.1	187006	2	AC120295	AC120295 Rattus no
C 155	19	2.1	66696	9	AL359743	AL359743 Human DNA	C 228	19	2.1	188095	4	AC091505	AC091505 Sus scrofa
C 156	19	2.1	69348	2	AC020525	AC020525 Drosophi1	C 229	19	2.1	188389	2	AC024199	AC024199 Homo sapi
C 157	19	2.1	72895	2	AC116400	AC116400 Mus muscu	C 230	19	2.1	189537	2	AC113444	AC113444 Mus muscu
C 158	19	2.1	77740	9	AF540993	AF540993 Pseudomon	C 231	19	2.1	190287	2	AC134249	AC134249 Mus muscu
C 159	19	2.1	79884	9	AC109440	AC109440 Homo sapi	C 232	19	2.1	191783	2	AC139604	AC139604
C 160	19	2.1	81931	10	AL611987	AL611987 Mouse DNA	C 233	19	2.1	191966	9	AC150280	AC150280 Pan trogl
C 161	19	2.1	88588	9	AC010453	AC010453 Homo sapi	C 234	19	2.1	192203	3	AC034102	AC034102 Homo sapi
C 162	19	2.1	90348	1	AF497482	AF497482 Micromono	C 235	19	2.1	194308	3	AC009377	AC009377 Drosophi1
C 163	19	2.1	91468	2	AP002334	AP002334 Homo sapi	C 236	19	2.1	195964	2	AC018879	AC018879 Homo sapi
C 164	19	2.1	95477	9	AC007076	AC007076 Homo sapi	C 237	19	2.1	196903	2	AC068424	AC068424
C 165	19	2.1	100976	9	HS1005F21	AL078633 Human DNA	C 238	19	2.1	199814	3	CEY47D3A	CEY47D3A

239	19	2.1	200109	9	CNS07EBZ	AL451071 Human chr	312	18	2.0	918	6	C0817218	C0817218 Sequence
C 240	19	2.1	201060	10	AL929382	AL929382 Mouse DNA	313	18	2.0	918	6	C0817221	C0817221 Sequence
241	19	2.1	202157	4	AC124907	AC124907 Equus cab	314	18	2.0	918	6	C0817223	C0817223 Sequence
C 242	19	2.1	204684	10	AC127581	AC127581 Mus muscu	315	18	2.0	1023	11	G10653	G10653 human STS C
243	19	2.1	207974	10	ALB31771	ALB31771 Mouse DNA	316	18	2.0	1023	8	AB107992	AB107992 Trilicium
C 244	19	2.1	210886	2	AC017051	AC017051 Homo sapi	317	18	2.0	1032	4	AF497260	AF497260 Vombatius
C 245	19	2.1	212030	2	AC019148	AC019148 Homo sapi	318	18	2.0	1056	6	AR156614	AR156614 Sequence
C 246	19	2.1	223040	2	AC128102	AC128102 Rattus no	319	18	2.0	1056	6	BS1749	BS1749 Xylitol deH
C 247	19	2.1	226416	10	AC092752	AC092752 Genomic B	320	18	2.0	1105	9	CR533526	CR533526 Homo sapi
C 248	19	2.1	227682	2	AC122603	AC122603 Rattus no	321	18	2.0	1179	6	C0801209	C0801209 Sequence
C 249	19	2.1	230263	2	AC111787	AC111787 Rattus no	322	18	2.0	1287	6	CQ736225	CQ736225 Sequence
C 250	19	2.1	230930	2	AC130854	AC130854 Rattus no	323	18	2.0	1314	6	BD269207	BD269207 Vaccine.
C 251	19	2.1	232415	2	AC095640	AC095640 Rattus no	324	18	2.0	1314	6	AX028478	AX028478 Sequence
C 252	19	2.1	232945	2	AC103156	AC103156 Rattus no	325	18	2.0	1317	6	CQ717442	CQ717442 Sequence
C 253	19	2.1	234065	2	AC140765	AC140765 Rattus no	326	18	2.0	1328	9	AK057774	AK057774 Homo sapi
C 254	19	2.1	234950	2	AC094003	AC094003 Rattus no	327	18	2.0	1355	6	BS3699	BS3699 Human prote
C 255	19	2.1	236774	10	AC124516	AC124516 Mus muscu	328	18	2.0	1355	6	BD095394	BD095394 Human pro
C 256	19	2.1	237974	2	AC094771	AC094771 Rattus no	329	18	2.0	1360	9	BC000788	BC000788 Homo sapi
C 257	19	2.1	238367	2	AC094187	AC094187 Rattus no	330	18	2.0	1366	9	AK000578	AK000578 Homo sapi
C 258	19	2.1	238937	2	AC094926	AC094926 Rattus no	331	18	2.0	1400	9	BC006244	BC006244 Homo sapi
C 259	19	2.1	243661	5	CR392340	CR392340 Zebrafish	332	18	2.0	1409	6	AK025970	AK025970 Homo sapi
C 260	19	2.1	247887	2	AC110342	AC110342 Rattus no	333	18	2.0	1409	6	BD76508	BD76508 FULL-LENG
C 261	19	2.1	251533	2	AC125364	AC125364 Rattus no	334	18	2.0	1409	6	AX048072	AX048072 Sequence
C 262	19	2.1	251710	2	AC117065	AC117065 Rattus no	335	18	2.0	1422	6	CQ726719	CQ726719 Sequence
C 263	19	2.1	253184	2	AC137219	AC137219 Rattus no	336	18	2.0	1447	6	AX086256	AX086256 Sequence
C 264	19	2.1	253746	2	AC135747	AC135747 Rattus no	337	18	2.0	1473	3	AJ831833	AJ831833 Drosophil
C 265	19	2.1	256354	2	AC150070	AC150070 Gallus ga	338	18	2.0	1630	8	AK072181	AK072181 Oryza sat
C 266	19	2.1	257692	3	AB003517	AB003517 Drosophil	339	18	2.0	1767	9	AP007191	AP007191 Homo sapi
C 267	19	2.1	258193	10	AC101221	AC101221 Mus muscu	340	18	2.0	1815	8	AK105585	AK105585 Oryza sat
C 268	19	2.1	258786	2	AC125773	AC125773 Rattus no	341	18	2.0	1861	10	AY033912	AY033912 Mus muscu
C 269	19	2.1	260468	2	AC073771	AC073771 Mus muscu	342	18	2.0	1922	6	AX330178	AX330178 Sequence
C 270	19	2.1	260829	2	AC109419	AC109419 Rattus no	343	18	2.0	1922	6	AX336103	AX336103 Sequence
C 271	19	2.1	263399	2	AC111251	AC111251 Rattus no	344	18	2.0	1922	6	AX336456	AX336456 Sequence
C 272	19	2.1	269739	10	AC139108	AC139108 Mus muscu	345	18	2.0	1922	6	AX336717	AX336717 Sequence
C 273	19	2.1	274560	2	AC099350	AC099350 Rattus no	346	18	2.0	1922	6	AX337848	AX337848 Sequence
C 274	19	2.1	279011	9	AB006467	AB006467 Homo sapi	347	18	2.0	1922	6	AX337848	AX337848 Sequence
C 275	19	2.1	284913	2	AC129698	AC129698 Rattus no	348	18	2.0	1922	6	AX049454	AX049454 Sequence
C 276	19	2.1	291799	3	AB003489	AB003489 Drosophil	349	18	2.0	1944	9	HSM801815	HSM801815 Human (clon
C 277	19	2.1	292145	2	AC091459	AC091459 Mus muscu	350	18	2.0	1953	10	AF013145	AF013145 Rattus no
C 278	19	2.1	292900	2	AC097163	AC097163 Rattus no	351	18	2.0	2005	10	AF116896	AF116896 Rattus no
C 279	19	2.1	300029	8	AB017076	AB017076 Oryza sat	352	18	2.0	2015	10	BC078788	BC078788 Rattus no
C 280	19	2.1	302300	1	AP005034	AP005034 Streptomy	353	18	2.0	2098	5	BC076738	BC076738 Xenopus 1
C 281	19	2.1	303774	2	AC105878	AC105878 Rattus no	354	18	2.0	2192	10	AF233646	AF233646 Mus muscu
C 282	19	2.1	308050	1	SC0939124	SC0939124 Streptomy	355	18	2.0	2199	9	BC001522	BC001522 Homo sapi
C 283	19	2.1	314746	2	AC106421	AC106421 Rattus no	356	18	2.0	2283	10	BC026539	BC026539 Mus muscu
C 284	19	2.1	322635	2	AC095310	AC095310 Rattus no	357	18	2.0	2283	6	C0843341	C0843341 Sequence
C 285	19	2.1	323222	2	AC112459	AC112459 Rattus no	358	18	2.0	2283	9	AK124305	AK124305 Homo sapi
C 286	19	2.1	344805	1	BX640434	BX640434 Bordetell	359	18	2.0	2334	9	BC062549	BC062549 Homo sapi
C 287	19	2.1	348074	1	BX640449	BX640449 Bordetell	360	18	2.0	2395	1	AF123492	AF123492 Pseudomon
C 288	19	2.1	348134	1	BX640420	BX640420 Bordetell	361	18	2.0	2412	6	AX835205	AX835205 Sequence
C 289	19	2.1	348866	1	BX640426	BX640426 Bordetell	362	18	2.0	2412	9	AK098120	AK098120 Homo sapi
C 290	19	2.1	349008	1	BX640444	BX640444 Bordetell	363	18	2.0	2487	9	BC035906	BC035906 Homo sapi
C 291	18	2.0	142	6	AX927406	AX927406 Sequence	364	18	2.0	2569	9	HUMSCNA421	HUMSCNA421
C 292	18	2.0	142	8	AJ718774	AJ718774 Nicotiana	365	18	2.0	2745	9	AF301906	AF301906 Homo sapi
C 293	18	2.0	142	8	AJ718775	AJ718775 Nicotiana	366	18	2.0	2753	6	AX554768	AX554768 Sequence
C 294	18	2.0	204	4	CATPES03	M16667 Feline c-Fe	367	18	2.0	2823	6	BD180452	BD180452 Highly ch
C 295	18	2.0	251	11	BV168193	BV168193 scdm7640	368	18	2.0	2906	9	AB188491	AB188491 Homo sapi
C 296	18	2.0	303	11	BV034559	BV034559 S212P6009	369	18	2.0	2946	14	PCGGAONC	PCGGAONC
C 297	18	2.0	324	6	CQ727703	CQ727703 Sequence	370	18	2.0	2977	9	AB032993	AB032993 Homo sapi
C 298	18	2.0	339	6	CQ734705	CQ734705 Sequence	371	18	2.0	2996	8	AK101081	AK101081 Oryza sat
C 299	18	2.0	397	6	AX918678	AX918678 Sequence	372	18	2.0	2997	6	AX960776	AX960776 Sequence
C 300	18	2.0	397	6	BD054211	BD054211 Sequence	373	18	2.0	3063	4	S80649	S80649 SP-B-pulmon
C 301	18	2.0	475	6	CQ739992	CQ739992 Sequence	374	18	2.0	3069	3	AF219383	AF219383 Drosophil
C 302	18	2.0	497	11	BV180580	BV180580 sqm10157	375	18	2.0	3120	9	AB089939	AB089939 Homo sapi
C 303	18	2.0	500	4	AF201724	AF201724 Sus scrof	376	18	2.0	3175	10	MM062907	MM062907 Mus muscu
C 304	18	2.0	513	6	AX437028	AX437028 Sequence	377	18	2.0	3181	9	HSM806774	HSM806774 Homo sapi
C 305	18	2.0	612	11	GS5269	GS5269 SHGC-81470	378	18	2.0	3181	10	AF251347	AF251347 Mus muscu
C 306	18	2.0	618	6	AX432088	AX432088 Sequence	379	18	2.0	3257	9	HSM807947	HSM807947 Homo sapi
C 307	18	2.0	698	5	HS4336514	AJ336514 Homo sapi	380	18	2.0	3257	8	HSM807950	HSM807950 Homo sapi
C 308	18	2.0	706	5	AB098253	Echis mul	381	18	2.0	3307	8	AF340030	AF340030 Aspergill
C 309	18	2.0	788	5	CR407323	CR407323 Gallus ga	382	18	2.0	3399	6	BD183250	BD183250 Walker fo
C 310	18	2.0	885	5	CR390901	CR390901 Gallus ga	383	18	2.0	3403	6	C0609945	C0609945 Sequence
C 311	18	2.0	894	5	AF071874	AF071874 Gallus ga	384	18	2.0	3468	9	HUMSCNA22	HUMSCNA22 Human type

385	18	2.0	3505	10	EC060248	BC060248 Mus muscu	458	18	2.0	102148	2	AP000597	AP000597 Homo sapi
386	18	2.0	3515	9	AK123604	AK123604 Homo sapi	459	18	2.0	103216	2	HSB09318	AL080251 Human DNA
387	18	2.0	3539	9	LC0579911	AJ579911 Lotus cor	460	18	2.0	103636	8	AP004940	AP004940 Lotus cor
388	18	2.0	3777	10	AK173086	AK173086 Mus muscu	461	18	2.0	105940	9	AC010606	AC010606 Homo sapi
389	18	2.0	3994	10	AL626766	AL626766 Mouse DNA	462	18	2.0	107655	2	AC084840	AC084840 Homo sapi
390	18	2.0	4210	8	AK103401	AK103401 Oryza sat	463	18	2.0	108523	9	AC000159	AC000159 Homo sapi
391	18	2.0	4507	5	BC078008	BC078008 Xenopus l	464	18	2.0	108727	8	AP004020	AP004020 Oryza sat
392	18	2.0	4856	9	AK024480	AK024480 Homo sapi	465	18	2.0	110000	1	AE016822	AE016822_01
393	18	2.0	5164	9	AB058719	AB058719 Homo sapi	466	18	2.0	110000	1	AE017333	AE017333_03
394	18	2.0	5197	9	RLFI1XKL	Z70305 R. leguminos	467	18	2.0	110000	1	AE017333	AE017333_33
395	18	2.0	5768	6	AX329625	AX329625 Sequence	468	18	2.0	110000	1	CP000002	CP000002_03
396	18	2.0	5768	6	HUMAN1	J04982 Human heart	469	18	2.0	110000	1	CP000002	CP000002_33
397	18	2.0	6032	6	AB074880	AB074880 Chlamydom	470	18	2.0	110000	2	AC091352	AC091352_2
398	18	2.0	6222	6	CQ609944	CQ609944 Sequence	471	18	2.0	110000	2	AC106675	AC106675_0
399	18	2.0	7819	6	CQ730498	CQ730498 Sequence	472	18	2.0	110000	2	AC114021	AC114021_0
400	18	2.0	7823	8	AY289797	M81758 Homo sapien	473	18	2.0	110000	2	AC141330	AC141330_1
401	18	2.0	8177	8	AY289797	AY289797 Chlamydom	474	18	2.0	110000	2	AP006501	AP006501_02
402	18	2.0	10029	1	AE012267	AE012267 Xanthomon	475	18	2.0	110000	2	LMF1CHR3	LMF1CHR3_15
403	18	2.0	10081	1	AE004512	AE004512 Pseudomon	476	18	2.0	110000	2	LMF1CHR3	LMF1CHR3_31
404	18	2.0	10094	1	AE012871	AE012871 Chlorobiu	477	18	2.0	110000	3	AC125735	AC125735_1
405	18	2.0	10147	1	AE004900	AE004900 Pseudomon	478	18	2.0	110000	3	AC125735	AC125735_2
406	18	2.0	10412	1	AE012064	AE012064 Xanthomon	479	18	2.0	110794	9	AL133268	AL133268 Human DNA
407	18	2.0	10789	1	AE009051	AE009051 Agrobacte	480	18	2.0	111568	2	AC083908	AC083908 Homo sapi
408	18	2.0	10866	1	AE008017	AE008017 Agrobacte	481	18	2.0	111865	2	AL355883	AL355883 Homo sapi
409	18	2.0	11064	1	AE012296	AE012296 Xanthomon	482	18	2.0	112961	9	HS322112	AL591675
410	18	2.0	11653	1	AE012442	AE012442 Xanthomon	483	18	2.0	113049	10	AL591675	AL591675 Mouse DNA
411	18	2.0	15658	4	MVRYR3	Y07749 M. vison mRN	484	18	2.0	113733	9	AP003159	AP003159 Homo sapi
412	18	2.0	22810	6	AB009668	AB009668 Homo sapi	485	18	2.0	115407	2	HS1000N6	AL034378 Homo sapi
413	18	2.0	30943	6	CQ801140	CQ801140 Sequence	486	18	2.0	115431	2	AC010880	AC010880 Homo sapi
414	18	2.0	33847	1	CO868646	CO868646 Sequence	487	18	2.0	117612	8	AC104427	AC104427 Oryza sat
415	18	2.0	35026	1	AY233211	AY233211 Streptomy	488	18	2.0	117927	8	AC013416	AC013416 Homo sapi
416	18	2.0	36888	1	AY046057	Y13383 Bordetella	489	18	2.0	118828	9	AP006333	AP006333 Homo sapi
417	18	2.0	37115	2	AC139098	AY046057 Escherich	490	18	2.0	119304	8	AP004255	AP004255 Oryza sat
418	18	2.0	37909	1	AP005232	AC139098 Homo sapi	491	18	2.0	120000	10	AC132084	AC132084 Mus muscu
419	18	2.0	38957	9	AY120852	AY120852 Synchoco	492	18	2.0	120992	2	AC127673	AC127673 Leishmani
420	18	2.0	39188	1	AC144899	AC144899 Homo sapi	493	18	2.0	126982	2	AC133008	AC133008 Oryza sat
421	18	2.0	39576	3	AC008054	AC008054 Leishmani	494	18	2.0	127149	2	AC008655	AC008655 Homo sapi
422	18	2.0	40327	3	AP005379	AP005379 Homo sapi	495	18	2.0	123430	9	AP001824	AP001824 Homo sapi
423	18	2.0	40592	9	HS1191F1	Z68756 Human DNA s	496	18	2.0	123658	2	AC104742	AC104742 Mus muscu
424	18	2.0	41303	9	AC005175	AC005175 Homo sapi	497	18	2.0	125992	5	BX649211	BX649211 Zebrafilsh
425	18	2.0	41831	7	BP0550940	AJ550940 Bacteriop	498	18	2.0	126766	9	HS154733	HS154733 Human DNA
426	18	2.0	42271	9	AC020952	AC020952 Homo sapi	499	18	2.0	126803	9	AC007032	AC007032 Homo sapi
427	18	2.0	44566	2	AC139088	AC139088 Homo sapi	500	18	2.0	126982	9	AC117515	AC117515 Homo sapi
428	18	2.0	46024	2	AC100659	AC100659 Mus muscu	501	18	2.0	127098	8	AC144426	AC144426 Oryza sat
429	18	2.0	46077	2	AC137289	AC137289 Rattus no	502	18	2.0	128501	9	AC012614	AC012614 Homo sapi
430	18	2.0	46391	9	HS8554C12	AL080242 Human DNA	503	18	2.0	128600	9	AC005192	AC005192 Homo sapi
431	18	2.0	47077	9	AL161648	AL161648 Human DNA	504	18	2.0	132803	2	AC011051	AC011051 Homo sapi
432	18	2.0	48177	7	AY369265	AY369265 Burtholide	505	18	2.0	134163	2	AY331134	AY331134 Homo sapi
433	18	2.0	49764	2	AC101107	AC101107 Mus muscu	506	18	2.0	135237	2	AP000814	AP000814 Homo sapi
434	18	2.0	53352	2	AC083969	AC083969 Homo sapi	507	18	2.0	135569	2	AC073997	AC073997 Homo sapi
435	18	2.0	52687	2	AC068390	AC068390 Homo sapi	508	18	2.0	136773	5	CR392330	CR392330 Zebrafilsh
436	18	2.0	5307	2	AC014684	AC014684 Drosophill	509	18	2.0	137367	2	AC150200	AC150200 Papio anu
437	18	2.0	55307	2	AC137177	AC137177 Rattus no	510	18	2.0	138033	2	AP002339	AP002339 Homo sapi
438	18	2.0	58143	2	AC099864	AC099864 Mus muscu	511	18	2.0	138376	8	AP003578	AP003578 Oryza sat
439	18	2.0	59314	2	AC135246	AC135246 Rattus no	512	18	2.0	138390	14	AY261359	AY261359 Bovine he
440	18	2.0	60914	2	AC091112	AC091112 Homo sapi	513	18	2.0	138824	8	AC051633	AC051633 Oryza sat
441	18	2.0	66615	2	AL831709	AL831709 Homo sapi	514	18	2.0	138966	2	AC008803	AC008803 Homo sapi
442	18	2.0	72207	9	AL592947	AL592947 Homo sapi	515	18	2.0	139544	8	AP004878	AP004878 Oryza sat
443	18	2.0	72279	9	AL592444	AL592444 Human DNA	516	18	2.0	139953	8	HSB45043	HSB45043 Homo sapi
444	18	2.0	75015	5	AP0091626	AP0091626 Datto rer	517	18	2.0	140513	8	AP007253	AP007253 Oryza sat
445	18	2.0	77204	2	AC010449	AC010449 Homo sapi	518	18	2.0	142272	2	AL513474	AL513474 Homo sapi
446	18	2.0	80772	2	AC138269	AC138269 Mus muscu	519	18	2.0	142402	2	CR847574	CR847574 Datto rer
447	18	2.0	83715	2	AL023578	AL023578 Human DNA	520	18	2.0	143223	9	AL162725	AL162725 Human DNA
448	18	2.0	84107	2	HS24881	HS24881 Sequence	521	18	2.0	143701	8	HS29C18	HS29C18 Human DNA
449	18	2.0	86000	2	AC136951	AC136951 Leishmani	522	18	2.0	145491	8	AP002883	AP002883 Oryza sat
450	18	2.0	86000	2	CO870090	CO870090 Sequence	523	18	2.0	147640	5	EX323035	EX323035 Zebrafilsh
451	18	2.0	89873	6	AC084449	AC084449 Caenorhab	524	18	2.0	147788	9	AP005360	AP005360 Homo sapi
452	18	2.0	90243	3	AP006074	AP006074 Lotus cor	525	18	2.0	148750	9	AL596225	AL596225 Human DNA
453	18	2.0	92724	8	BX908807	BX908807 Neutrospor	526	18	2.0	148803	2	EX510998	EX510998 Homo sapi
454	18	2.0	93134	8	AC090214	AC090214 Homo sapi	527	18	2.0	148891	9	AL162274	AL162274 Human DNA
455	18	2.0	95648	9	AC131182	AC131182 Homo sapi	528	18	2.0	149095	9	AC022683	AC022683 Homo sapi
456	18	2.0	101396	9	AC127029	AC127029 Homo sapi	529	18	2.0	149200	9	AL355645	AL355645 Human DNA
457	18	2.0	101990	9	AC127029	AC127029 Mus muscu	530	18	2.0	149316	10	AC123791	AC123791 Mus muscu

C 677	18	2.0	201543	2	AC1233914	AC1233914 Mus muscu	C 750	18	2.0	237992	2	AC102617	AC102617 Mus muscu
C 678	18	2.0	202239	2	CR759882	Danio rer	C 751	18	2.0	238297	2	AC126703	AC126703 Rattus no
C 679	18	2.0	202509	2	AC132505	Rattus no	C 752	18	2.0	238543	2	AC133701	AC133701 Rattus no
C 680	18	2.0	203042	2	AC116261	Rattus no	C 753	18	2.0	240059	2	AC108769	AC108769 Mus muscu
C 681	18	2.0	203132	8	AP004071	Oryza sat	C 754	18	2.0	240059	2	AC124154	AC124154 Rattus no
C 682	18	2.0	203492	2	AC107826	Mus muscu	C 755	18	2.0	240809	2	AC098059	AC098059 Rattus no
C 683	18	2.0	203566	2	AC092179	Homo sapi	C 756	18	2.0	241681	2	AC094546	AC094546 Rattus no
C 684	18	2.0	203710	2	AC107762	Mus muscu	C 757	18	2.0	242984	2	AC130775	AC130775 Rattus no
C 685	18	2.0	203710	2	AC107762	Mus muscu	C 758	18	2.0	244105	2	AC098897	AC098897 Rattus no
C 686	18	2.0	203905	2	AC073720	Mus muscu	C 759	18	2.0	244220	10	AC122941	AC122941 Mus muscu
C 687	18	2.0	204782	2	AC011168	Homo sapi	C 760	18	2.0	244856	2	AC094026	AC094026 Rattus no
C 688	18	2.0	205222	10	AC123534	Mus muscu	C 761	18	2.0	245499	2	AC107173	AC107173 Rattus no
C 689	18	2.0	205350	2	AC078946	Mus muscu	C 762	18	2.0	245828	2	AC098403	AC098403 Rattus no
C 690	18	2.0	206123	2	AC017106	Homo sapi	C 763	18	2.0	246173	2	AC110096	AC110096 Rattus no
C 691	18	2.0	206310	9	AY371697	Homo sapi	C 764	18	2.0	246542	2	AC125601	AC125601 Rattus no
C 692	18	2.0	206373	5	AL954133	Zebrafish	C 765	18	2.0	246913	2	AC113620	AC113620 Rattus no
C 693	18	2.0	206500	2	AC150823	Callithr	C 766	18	2.0	246970	2	AC121035	AC121035 Rattus no
C 694	18	2.0	206512	2	AC135435	Rattus no	C 767	18	2.0	247084	2	AC125534	AC125534 Rattus no
C 695	18	2.0	206509	9	AC016397	Homo sapi	C 768	18	2.0	247200	2	AC123570	AC123570 Rattus no
C 696	18	2.0	207304	4	AC125499	Equus cab	C 769	18	2.0	247910	2	AB017307	AB017307 Thermus t
C 697	18	2.0	207304	4	AC125499	Equus cab	C 770	18	2.0	247936	2	AC112533	AC112533 Rattus no
C 698	18	2.0	207743	4	AC121066	Oryctolag	C 771	18	2.0	249456	2	AC093475	AC093475 Mus muscu
C 699	18	2.0	207791	2	AC116771	Mus muscu	C 772	18	2.0	250277	2	AC122757	AC122757 Mus muscu
C 700	18	2.0	210784	2	AC119293	Rattus no	C 773	18	2.0	251021	2	AC129763	AC129763 Rattus no
C 701	18	2.0	210842	2	AC140748	Rattus no	C 774	18	2.0	251533	2	AC125364	AC125364 Rattus no
C 702	18	2.0	211583	9	AC069025	Homo sapi	C 775	18	2.0	251710	2	AC117065	AC117065 Rattus no
C 703	18	2.0	211585	10	AL626784	Mouse DNA	C 776	18	2.0	251872	2	AC125598	AC125598 Rattus no
C 704	18	2.0	212178	2	AC125925	Rattus no	C 777	18	2.0	253184	2	AC137219	AC137219 Rattus no
C 705	18	2.0	213033	2	AC131482	Rattus no	C 778	18	2.0	253358	2	AC138303	AC138303 Rattus no
C 706	18	2.0	213745	2	BX469890	Homo sapi	C 779	18	2.0	260639	2	AC134258	AC134258 Rattus no
C 707	18	2.0	213853	2	AC150608	Callithr	C 780	18	2.0	260963	2	AC105828	AC105828 Rattus no
C 708	18	2.0	213967	2	AC121395	Rattus no	C 781	18	2.0	263706	2	AC120895	AC120895 Rattus no
C 709	18	2.0	214911	2	AC010537	Homo sapi	C 782	18	2.0	263901	2	AC115371	AC115371 Rattus no
C 710	18	2.0	215087	2	AC113594	Mus muscu	C 783	18	2.0	264464	2	AC107410	AC107410 Rattus no
C 711	18	2.0	215628	2	CR847847	Danio rer	C 784	18	2.0	264501	2	AC136579	AC136579 Rattus no
C 712	18	2.0	216069	2	AC122086	Rattus no	C 785	18	2.0	271975	2	AC111856	AC111856 Rattus no
C 713	18	2.0	216340	2	AC073754	Mus muscu	C 786	18	2.0	272400	2	AC110146	AC110146 Rattus no
C 714	18	2.0	216345	4	AC122153	Oryctolag	C 787	18	2.0	273684	2	AC113630	AC113630 Rattus no
C 715	18	2.0	216410	2	AC148046	AP004168	C 788	18	2.0	274560	2	AC099390	AC099390 Rattus no
C 716	18	2.0	217205	8	AP004168	Oryza sat	C 789	18	2.0	275200	10	AC116392	AC116392 Mus muscu
C 717	18	2.0	217514	2	AC145779	Sus scrofa	C 790	18	2.0	276079	2	AC117102	AC117102 Rattus no
C 718	18	2.0	217584	2	AC113329	Mus muscu	C 791	18	2.0	277993	2	AC055705	AC055705 Mus muscu
C 719	18	2.0	217636	10	AC127411	Mus muscu	C 792	18	2.0	279449	2	AC126636	AC126636 Rattus no
C 720	18	2.0	217722	5	BX284621	Zebrafish	C 793	18	2.0	282148	2	AC097022	AC097022 Rattus no
C 721	18	2.0	217794	2	AC111124	Mus muscu	C 794	18	2.0	283299	2	AC112576	AC112576 Rattus no
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C 723	18	2.0	221545	10	AL844855	Mouse DNA	C 796	18	2.0	295117	2	AC118895	AC118895 Rattus no
C 724	18	2.0	222175	2	AC094189	Rattus no	C 797	18	2.0	295117	2	AL499603	AL499603 Rattus no
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C 727	18	2.0	223061	2	AC098658	Rattus no	C 800	18	2.0	299800	1	AP005028	AP005028 Streptomy
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C 731	18	2.0	226256	10	AC125082	Mus muscu	C 804	18	2.0	300242	1	AE016790	AE016790 Pseudomon
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C 735	18	2.0	227452	2	AC105558	Rattus no	C 808	18	2.0	300957	8	AE017233	AE017233 Oryza sat
C 736	18	2.0	227570	2	AC117132	Rattus no	C 809	18	2.0	301399	1	AE017233	AE017233 Oryza sat
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C 744	18	2.0	234560	2	AC097419	Rattus no	C 817	18	2.0	323450	2	SME591790	SME591790 Sinorhizo
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ACCESSION	BD093312				
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ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Ota,T., Ieogai,T., Nishikawa,T., Kawai,Y., Miyoshi,S. and Sato,S.				
TITLE	Apoptosis Relating Factor				
JOURNAL	Patient: MO 0104300-A 2 18-JAN-2001; HEIIX RESEARCH INSTITUTE, TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI KAWAI, SOUSUKE MIYOSHI, SUSUMU SATO				
COMMENT	OS Homo sapiens (human) PN MO 0104300-A/2 PD 18-JAN-2001 PF 06-JUL-2000 MO 2000JP004516 PR 08-JUL-1999 JP 99P 194179, 18-OCT-1999 US 60/159586 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI KAWAI, SOUSUKE MIYOSHI, PI SUSUMU SATO				
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RESULT 3
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to Homo sapiens death effector domain-containing testicular
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1
AUTHORS Ota, T., Nishikawa, T., Suzuki, Y., Kawai-Hio, Y., Hayaishi, K.,
Ishii, S., Saito, K., Yamamoto, J., Wakamatsu, A., Nagai, T.,
Nakamura, Y., Nagahari, K., Sugano, S. and Isogai, T.
TITLE HRI human cDNA sequencing project
REFERENCE Unpublished
JOURNAL 2 (bases 1 to 1883)
AUTHORS Isogai, T. and Yamamoto, J.
TITLE Direct Submission
JOURNAL Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@ri.co.jp, Tel:81-438-52-1975, Fax:81-438-52-1986)
COMMENT HRI human cDNA sequencing project: cDNA 5'- & 3'-end one pass
sequencing, clone selection and full insert sequencing: Helix
Research Institute (supported by Japan Key Technology Center etc.)
cDNA library construction: Institute of Medical Science, University
of Tokyo, Laboratory of Genome Structure, Human Genome Center.

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ORIGIN

Query Match 100.0%; Score 909; DB 9; Length 1883;
Best Local Similarity 100.0%; Pred. No. 0;
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Db 964 ACTGAGGCGCTTCCGAGAGGCTGTGGGCGGAGAGGCTGTTCGCTGCTGAGTGTGAT 1023
Qy 901 GAGGCTGAC 909
Db 1024 GAGGCTGAC 1032

RESULT 4
LOCUS CQ719642 981 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 5576 from Patent WO02068579.
ACCESSION CQ719642
VERSION CQ719642.1 GI:42280499
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 5576 06-SEP-2002;
PE Corporation (NY) (US)

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/db_xref="taxon:9606"

ORIGIN

Query Match 94.4%; Score 858; DB 6; Length 981;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 901 GAGGCTGAC 909
Db 901 GAGGCTGAC 909

RESULT 5
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LOCUS Homo sapiens death effector domain-containing DNA-binding protein 2
DEFINITION (DEBD2) mRNA, complete cds.
ACCESSION AF443591
VERSION AF443591.1 GI:17933266
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 981)
AUTHORS Roth,W., Stemmer-Liwen,F., Pawlowski,K., Godzik,A. and Reed,J.C.
TITLE Identification and characterization of DEBD2, a death effector
domain-containing protein
JOURNAL J. Biol. Chem. 277 (9), 7501-7508 (2002)
MEDLINE 21850646
PUBMED 11741985
REFERENCE 2 (bases 1 to 981)
AUTHORS Roth,W. and Reed,J.C.
TITLE Direct Submission
JOURNAL Submitted (05-NOV-2001) Burnham Institute, 10901 N. Torrey Pines
Rd, La Jolla, CA 92037, USA
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ORIGIN

Query Match 94.4%; Score 858; DB 9; Length 981;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 901 GAGGCTGAC 909

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DEFINITION	Sequence 4 from Patent WO0192527.						
ACCESSION	AX322754						
VERSION	AX322754.1						
KEYWORDS	GI:18093742						
SOURCE							
ORGANISM	Homo sapiens (human)						
REFERENCE	Homo sapiens						
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
TITLE	1 Tang, Y.T., Azimzai, Y., Yue, H., Burford, N., Ding, L., Elliott, V.S., Patterson, C. and Baughn, M.R.						
JOURNAL	Regulators of apoptosis Patent: WO 0192527-A 4 06-DEC-2001;						
FEATURES	Incyte Genomics, Inc. (US) Location/Qualifiers						
source	1. 1230						
ORIGIN	1. 1230						
Query Match	94.4%; Score 858; DB 6; Length 1230;						
Best Local Similarity	99.9%; Pred. No. 0;						
Matches	908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;						
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DB	187 TACGGGAATGCTGTGCTTCAACCGTATGTTTCAAGTGCTGTGGCGGCACTGACGAGTGC	246					
QY	121 GAGCTGAGAGCTTCCTGAGCCCTTCTGTGTGTGATGAGGCTCTGTGGCGCGCGAGGCTTATCC	180					
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DB	307 CGGGCGCGCAGCGGCTTGAAGCTCTGTGTGAGCTGAGCGCGCGGCGAGTGGCGGCGAG	366					
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QY	301 CACCTGGCGCGCAAGCGCGCGCGCAAGTGTCTCCAGAACGCTATAGCTATGGCACTTCC	360					
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QY	361 AGCTTTTCAAAAGAGACAGAGGGTACTGCTGCGCGGTGGCGAGTCAAGAGTTTTCGA	420					
DB	487 AGCTTTTCAAAAGAGACAGAGGGTACTGCTGCGCGGTGGCGAGTCAAGAGTTTTCGA	546					
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DB	547 AATTCTCAGCAGGGGTCAAGTGGGAGACAGGCTTCCCCCAACCAAGCGGCAAGCGGAGT	606					
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QY	541 CAGCAGTCAAGAGCCCGCCAGACTTCTCTTGAAGGCAAAAGTACCTGTGACATCCGCTC	600					
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QY	661	CGGCCCCAGGCGCTGGCCGCGAGCTGACGTTTGGGACAGGCCACCGCAGTGTGCGC	720
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DEFINITION	Sequence 17 from Patent WO0240680.			
ACCESSION	AX431308			
VERSION	AX431308.1	GI:21656177		
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
AUTHORS	1			
TITLE	Pawlowski, K., Fiorentino, L., Goddik, A., Lee, S. H., Reed, J. C.,			
JOURNAL	Novel death domain proteins			
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Query Match	94.4%; Score 858; DB 6; Length 1924;			
Best Local Similarity	99.9%; Pred. No. 0;			
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Oy 930 GAGGCTGAC 909
Db 991 GAGGCTGAC 999

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RESULT 8
LOCUS BC027930
DEFINITION Homo sapiens death effector domain containing 2, mRNA (cDNA clone
ACCESSION BC027930
VERSION BC027930.1
KEYWORDS GC
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schaeetz, T.E., Brownstein, M.J., Udell, T.B., Toshitaki, S.,

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REMARK

COMMENT

JOURNAL
PUBMED
TITLE
AUTHORS
JOURNAL

TITLE

JOURNAL

PUBMED

TITLE

AUTHORS

JOURNAL

FEATURES

source

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNLT at: <http://image.llnl.gov>
Series: IRAX Plate: 49 Row: b Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19923049.
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ORIGIN

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Best Local Similarity 99.7%; Pred. No. 0;

Matches 906; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 781 GCTTTCGAGGAGATGCTGAGGAGGCGGCTGAGGAGGCGGCGGAGGCTTCTTCTG 840
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DB 909 ACTGAGGCGCTGAGGAGGCTGAGGCGGAGGCTGTTGCGCTGCTGCTGAGTGGAT 968
QY 901 GAGGCTGAGC 909
DB 969 GAGGCTGAGC 977
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RESULT 9

AF457575

981 bp mRNA linear PRI 10-APR-2002

LOCUS

AF457575

DEFINITION

(FLAME-3) mRNA, complete cds.

ACCESSION

AF457575

GI:20126793

VERSION

AF457575.1

KEYWORDS

Homo sapiens

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

Zhan, Y., Hegde, R., Srinivasula, S.M., Fernandes-Alnemri, T. and Alnemri, E.S.

AUTHORS

Zhan, Y., Hegde, R., Srinivasula, S.M., Fernandes-Alnemri, T. and Alnemri, E.S.

TITLE

Death effector domain-containing proteins DEDD and FLAME-3 form nuclear complexes with the TRILC102 subunit of human transcription factor TIFC

JOURNAL

Cell Death Differ. 9 (4), 439-447 (2002)

MEDLINE

21961615

PUBMED

11965497

REFERENCE

2 (bases 1 to 981)

AUTHORS

Alnemri, E.S.

TITLE

Direct Submission

JOURNAL

Submitted (11-DEC-2001) Microbiology and Immunology, Thomas Jefferson University, 233 S. 10th Street, Philadelphia, PA 19107, USA

FEATURES

source

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location/Qualifiers

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ORIGIN

Query Match 66.3%; Score 603; DB 9; Length 981;
Best Local Similarity 99.3%; Pred. No. 66-275;
Matches 903; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 181 CGGGCCCGGAGCGGCTTAGAGCTCTGCTGAGAGGCGCGCGGAGGCTGCGCGAG 240
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QY 241 AGCAACTGCGGCTGCTGGGCAACTCTGCGCGCGCTGCGCGCGGAGGCTGCGCGAG 300
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Db	301	CACCTGGCGCGCAAGCGGCGCCGGCCAGTGTCTCCAGAACCTATAGTTATGGCACTCC	360
Qy	361	AGCTCTTCAAAAGAGGACAGAGGGTATGCTGACCGGTGGCGAGTCAAGAGATTCTGCA	420
Db	361	AGCTCTTCAAAAGAGGACAGAGGGTATGCTGACCGGTGGCGAGTCAAGAGATTCTGCA	420
Qy	421	AATTCTCAGCAGGGGTCACTGGGAGACAGAGTCTCCGCCCAACAAGCGGCAGCGGAGT	480
Db	421	AATTCTCAGCAGGGGTCACTGGGAGACAGAGTCTCCGCCCAACAAGCGGCAGCGGAGT	480
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Qy	541	CAGCAGTCAAGAGCCCGGCCAGACCTTCTCTGAAGCAAAATGACCTGTGACATCCGGCTC	600
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Qy	601	CGGGTTCAGACAGAGTATGCGGAGCATGAGGCGAGGCTTGAGACAGGGGCGTGGACCCCG	660
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DEFINITION			Homo sapiens death effector domain-containing DNA-binding 2
ACCESSION	AY125488		
VERSION	AY125488.1	GI:22475163	
KEYWORDS			
SOURCE			
ORGANISM			Homo sapiens (human)
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS			Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE			Lee,J.C., Schickling,O., Stegh,A.H., Oshima,R.G., Dinsdale,D., Cohen,G.M. and Peter,M.E.
JOURNAL			DEDD regulates degradation of intermediate filaments during apoptosis
MEDLINE			J. Cell Biol. 158 (6), 1051-1066 (2002)
PUBMED			22220288
REFERENCE			12335123
AUTHORS			2 (bases 1 to 2012)
TITLE			Peter, M.E.
JOURNAL			Direct Submission
FEATURES			Submitted (21-JUN-2002) Ben May Cancer Institute, University of Chicago, 924 E. 57th Street, R112, Chicago, IL 60637, USA
			Location/Qualifiers

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		GGARRRGAAPAPQOQSEBPASSEKVTCDRLRVRAEYCEHGPALGQVSRPQ
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Qy	448 GGCTCCCCCAACCAAGCGGACGGCGAGTGGGAGCCCGCCAGTGTGTGCCAGA	507
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Qy	628 GGGCCAGCCTTGGAGAGAGGGGGTGGCATCCCGGCGGCCCGACGGCTGGCGGACGTG	687
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Qy	748 GACATCAAGTCTGAGAGCTCTCTATCTGGAGGCTTCTGGGGGCGACTACCTAGTGGC	807
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Qy	808 GCCCTGCTGACAGGCCCTCGCGGGGCGTGTCTCTGACTAGAGCCCTGCGAGAGGCTGTGGGC	867
Db	876 GCCCTGCTGACAGGCCCTCGCGGGGCGTGTCTCTGACTAGAGCCCTGCGAGAGGCTGTGGGC	935
Qy	868 CGGAGGCGTGTTCGCTGCTGTGCTAGTGTGATGAGGCTGAC	909
Db	936 CGGAGGCGTGTTCGCTGCTGTGCTAGTGTGATGAGGCTGAC	977
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DEFINITION	2005 bp mRNA linear PRI 24-FEB-2004	
ACCESSION	BC013372	
VERSION	BC013372.2	
KEYWORDS	GI:33872465	
SOURCE	MGC.	
ORGANISM	Homo sapiens (human)	
REFERENCE	Homo sapiens	
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. (bases 1 to 2005)	
	Strauberg,R.L., Feingold,E.A., Grouse,L.H., Derge,U.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenman,C.M., Schuller,G.D.,	

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhac, N.K., Hopfins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hasleh, F., Diatchenko, L., Martusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stappleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheer, T.E., Brownstein, M.J., Uedlin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Iguellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hally, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shenchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skaleka, U., Smalins, D.E., Schermer, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932
2 (bases 1 to 2005)
Strausberg, R.
Direct Submission
Submitted (31-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
On Aug 19, 2003 this sequence version replaced gi:15426522.
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbiology.org>
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: <http://image.llnl.gov>
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ORIGIN
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Best Local Similarity 99.8%; Pred. No. 1,6e-170;
Matches 433; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 435 AGCTCTTCAAG 494
QY 421 AATTCTAGCAGCGG 434
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RESULT 12
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LOCUS 626 bp DNA linear PAT 17-JAN-2003
DEFINITION BD149917
ACCESSION BD149917
VERSION BD149917.1 GI:27855675
KEYWORDS JP 2002191363-A 4760
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 626)
Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Iehii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002191363-A 4760 09-JUL-2002;
HEILIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002191363-A/4760
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
PI SAITO,
PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
PI KEIICHI NAGAI,TETSUJI OHSUKI
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Location/Qualifiers
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ORIGIN

Query Match 36.7%; Score 334; DB 6; Length 626;
Best Local Similarity 99.7%; Pred. No. 3.3e-147;
Matches 384; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 208 GAGCTGAGAGCTCTGGCGCTTTCTGCTGATGATGAGCTCTGAGCGCGCGGAGGCTTAAAGCC 267
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RESULT 13
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DEFINITION Sequence 4760 from Patent EP1074617.
ACCESSION AX869855
VERSION AX869855.1 GI:40024718

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Ota,T., Iwogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primers for synthesizing full-length cDNA and their use
JOURNAL Patent: EP 1074617-A 4760 07-FEB-2001;
Research Association for Biotechnology (JP)
FEATURES
source 1..626
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ORIGIN

Query Match 36.7%; Score 334; DB 6; Length 626;
Best Local Similarity 99.7%; Pred. No. 3.3e-147;
Matches 384; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 ATGGCGCTATCCGGGTCGACCCCGGCGCTCTGGAGAGAGATGAGTCTGACTAC 60
DB 88 ATGGCGCTATCCGGGTCGACCCCGGCGCTCTGGAGAGAGATGAGTCTGACTAC 147
OY 61 TACGGGAGTCTGCTTCCCTTCAACGATATGTCGAGTGTGGGGGCAACTGACCGAGTGC 120
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DB 208 GAGCTGAGAGCTCTGGCGCTTTCTGCTGATGATGAGCTCTGAGCGCGCGGAGGCTTAAAGCC 267
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OY 181 CGGAGCCCGCAGCGGCTTAGAGCTCTGCTGAGAGTGCAGCGCGCGGCACTGCGCGAG 240
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DB 448 AGCTCTTCAAGAGACAGAGGGTA 472
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RESULT 14
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DEFINITION Homo sapiens cDNA FLJ26693 f18, clone MFG07953.
ACCESSION AK130203
VERSION AK130203.1 GI:34526957
KEYWORDS oligo capping; f18 (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Tashiro,H., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S.,
Fukuzumi,Y., Fujimori,Y., Komiyama,M., Suzuki,Y., Hata,H.,
Nakagawa,K., Mizuno,S., Morinaga,M., Kawamura,M., Sugiyama,T.,
Irie,R., Otsuki,T., Sato,H., Nishikawa,T., Sugiyama,A.,
Kawakami,B., Nagai,K., Iwogai,T. and Sugano,S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1659)
AUTHORS Sugano,S. and Suzuki,Y.
TITLE Direct Submission

COMMENT
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction and 5'-end one pass sequencing; Institute of Medical
Science, University of Tokyo, Laboratory of Genome Structure, Human
Genome Center; 3'-end one pass sequencing: RAB; clone selection for
full insert sequencing: RAB and Helix Research Institute.

FEATURES
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ORIGIN

Query Match 35.4%; Score 322; DB 9; Length 1659;
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Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 648 CGTGGCATCCGGGCGGCCCGGCGCTGGCGCGGACGCTGACGTGTTGGGACAGGCGAC 707
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QY 828 GGGCGGTTCCTGACTGAGAGCCCTGAGAGAGCTGTGGGCGCGGAGGCTGTCGCTGT 887
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AC010247
AC010247.9 GI:21743752
VERSION HTG.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butaleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
JOURNAL DOE Joint Genome Institute and Stanford Human Genome Center.
REFERENCE
AUTHORS Unpublished
TITLE 2 (bases 1 to 95663)
JOURNAL DOE Joint Genome Institute.
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
JOURNAL Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE
AUTHORS 3 (bases 1 to 95663)
JOURNAL DOE Joint Genome Institute and Stanford Human Genome Center.
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (01-JUL-2002) DOE Joint Genome Institute, 2800 Mitchell
JOURNAL Drive, Walnut Creek, CA 94598, USA
REFERENCE
AUTHORS 4 (bases 1 to 95663)
JOURNAL DOE Joint Genome Institute and Stanford Human Genome Center.
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (13-JUL-2002) DOE Joint Genome Institute, 2800 Mitchell
JOURNAL Drive, Walnut Creek, CA 94598, USA
REFERENCE
AUTHORS On Jul 13, 2002 this sequence version replaced gi:21637454.
JOURNAL Draft Sequence Produced by DOE Joint Genome Institute
COMMENT www.jgi.doe.gov

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ORIGIN
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Db 90684 GTCAGTGTGATGAGGCTGAC 90664

Search completed: February 12, 2005, 14:43:14
Job time : 3018 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OW nucleic - nucleic search, using sw model

Run on: February 12, 2005, 10:59:32 ; Search time 2934 Seconds
(without alignments)
15012.199 Million cell updates/sec

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Perfect score: 909
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_hcg:*
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6: gb_pal:*
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11: gb_scs:*
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13: gb_un:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	909	100.0	1883	BD093312	BD093312 Apoptosis
3	909	100.0	1883	AK075328	AK075328 Homo sapi
4	907.4	99.8	981	CQ719642	CQ719642 Sequence
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6	907.4	99.8	1230	AX322754	AX322754 Sequence
7	907.4	99.8	1924	AX431308	AX431308 Sequence
8	904.2	99.5	1951	BC027930	BC027930 Homo sapi
9	899.4	98.9	981	AF457575	AF457575 Homo sapi
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VERSION	BD093311.1	GI:22638899			
KEYWORDS	WO 0104300-A/1.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Miyoshi,S. and Sato,S.				
AUTHORS	1 (bases 1 to 909)				
TITLE	Apoptosis Relating Factor				
JOURNAL	Patent: WO 0104300-A 1 18-JAN-2001;				
COMMENT	HELIX RESEARCH INSTITUTE,TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA, YURI KAWAI,SOUSUKE MIYOSHI,SUSUMU SATO				
OS	Homo sapiens (human)				
PN	WO 0104300-A/1				
PD	18-JAN-2001				
PF	06-JUL-2000 WO 2000JP004516				
PR	08-JUL-1999 JP 99P 194179,18-OCT-1999 US 60/155586				
PT	TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,SOUSUKE MIYOSHI,				
PI	SUSUMU SATO				
PC	C12N15/12,C07K14/47,C12N5/10,C12N1/21,C12N1/19,C12N1/15,C12P21/				
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ACCESSION BD093312
VERSION BD093312.1 GI:22638900
KEYWORDS MO 0104300-A/2.
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ORGANISM Homo sapiens
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AUTHORS Apoptosis Relating Factor
TITLE Helix Research Institute, TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA,
JOURNAL YURI KAWAI, SOTSUKE MIYOSHI, SUSUMU SATO
COMMENT OS Homo sapiens (human)
PN WO 0104300-A/2
PD 18-JUN-2001
PF 06-JUL-2000 WO 2000JP004516
PR 08-JUL-1999 JP 99P 194179, 18-OCT-1999 US 60/159586 PI
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PI SUSUMU SATO
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LOCUS
DEFINITION
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molecule mRNA.

ACCESSION
AK075328
VERSION
AK075328.1 GI:22761346
KEYWORDS
oligo capping; f1s (full insert sequence).
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
AUTHORS
Ota, T., Nishikawa, T., Suzuki, Y., Kawai-Hio, Y., Hayashi, K.,
Ishii, S., Saito, K., Yamamoto, J., Nakamatsu, A., Nagai, T.,
Nakanura, Y., Nagahari, K., Sugano, S. and Isogai, T.
HRI human cDNA sequencing project
1 (bases 1 to 1883)
2 (bases 1 to 1883)
TITLE
JOURNAL
AUTHORS
Isogai, T. and Yamamoto, J.
REFERENCE
JOURNAL
TITLE
Direct Submission
SUBMITTED (2004MAR-2002) Nakao Isogai, Helix Research Institute,
Genomic Laboratory, 1532-3 Yana, Kiseazuru, Chiba 282-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass
sequencing, clone selection and full insert sequencing; Helix
Research Institute (supported by Japan Key Technology Center etc.);
cDNA library construction; Institute of Medical Science, University
of Tokyo, Laboratory of Genome Structure, Human Genome Center.

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REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
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AUTHORS				
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FEATURES				
SOURCE				
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CDS				
ORIGIN				

Best Local Similarity 99.9%; Pred. No. 2.1e-134;
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DB 241 AGCAACTGCGGCTGCTGAGGAGCACTCTGCGGCTGCTGAGCGCGCGGAGAGCTGAGTCC 300
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RESULT 6
AX322754 1230 bp DNA linear PAT 07-JAN-2002
LOCUS AX322754
DEFINITION Sequence 4 from Patent WO192527.
ACCESSION AX322754

VERSION AX322754.1 GI:18093742
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens

REFERENCE
AUTHORS Tang, Y.T., Azimzal, Y., Yue, H., Burford, N., Ding, L., Elliott, V.S.,
Patterson, C. and Baughn, M.R.
TITLE Regulation of apoptosis
JOURNAL Patent NO 0192527-A ~~906-DEC-2001~~
Incyte Genomics, Inc. (US)
FEATURES
source location/Qualifiers
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ORIGIN

Query Match 99.8%; Score 907.4; DB 6; Length 1230;
Best Local Similarity 99.9%; Pred. No. 2e-134;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 187 TACGGGATGCTGCTGCTTCAACCGTATGTTGAGAGTGTGGGGGCAACTGACCGAGTTC 246
OY 121 GAGCTGAGAGCTCTGAGCTCTTCTGCTGAGTGAAGGCTCTGAGCGCGCGGAGAGCTTAC 180
DB 247 GAGCTGAGAGCTCTGAGCTCTTCTGCTGAGTGAAGGCTCTGAGCGCGCGGAGAGCTTAC 306
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DB 727 CGGGTTCAGAGAGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 786
OY 661 CGGGCCCGGAGCGGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
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Qy 841 ACTGAGGCCCTTCGAGAGAGGCTGTGGCGCGGAGGCTGTTGCGCTGTCTGTGATGTGANT 900
Db 967 ACTGAGGCCCTTCGAGAGAGGCTGTGGCGCGGAGGCTGTTGCGCTGTCTGTGATGTGANT 1026
Qy 901 GAGGCTGAC 909
Db 1027 GAGGCTGAC 1035

RESULT 7
LOCUS AX431308 1924 bp DNA linear PAT 28-JUN-2002
DEFINITION Sequence 17 from Patent WO0240880.
ACCESSION AX431308
VERSION AX431308.1 GI:21656177
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1
AUTHORS Pawlowski, K., Fiorentino, L., Godzik, A., Lee, S.H., Reed, J.C.,
Roth, W. and Stenner-Liewen, F.
TITLE Novel death domain proteins
JOURNAL Patent: WO 0240880-A 17 23-MAY-2002;
BURNHAM INST (US)
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ORIGIN
Query Match 99.8%; Score 907.4; DB 6; Length 1924;
Best Local Similarity 99.9%; Pred. No. 1.7e-134;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 331 AGCAACCTGCGGCTGCTGGGGCACTCCTGCGCGTGTGAGCCCGCACAGCCTGTGCGG 390
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Qy 361 AGCTCTCAAAAGAGACAGAGGTAGTCCGTGCGCTGTGCACTGACATGCTGCA 420
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Qy 421 AATTCCTCAGAGGCTCACTGGGAGACAGGCTCCCCCAACCAAGCGGACAGGGAGT 480
Db 511 AATTCCTCAGAGGCTCACTGGGAGACAGGCTCCCCCAACCAAGCGGAGGAGT 570
Qy 481 CCGGGCCCGCCAGTGTGTGTGCGAGACGGCGCGAGAGGGGCCCGACCGCACCCAG 540
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Qy 661 CCGGCCCGAGCGCTGGCGCGCGCAGCTGAGCGTGTGTTGGGCGAGCCACCGCATGCTGCGC 720
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Db 991 GAGGCTGAC 999

RESULT 8
LOCUS BC027930 1951 bp mRNA linear PRI 29-JUN-2004
DEFINITION Homo sapiens death effector domain containing 2, mRNA (cDNA clone
MGC:35529 IMAGE:519972), complete cds.
ACCESSION BC027930
VERSION BC027930.1 GI:20379818
KEYWORDS MGC.
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1951)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buote, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hale, F.,
Datchenko, L., Marsina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schaefer, T.E., Brownstein, M.J., Ushed, T.B., Toshiyuki, S.,
Cernicni, P., Prange, C., Raha, S.S., Loggiano, N.A., Peters, G.J.,
Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hult, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,

TITLE
JOURNAL
PUBMED
AUTHORS
REFERENCE
JOURNAL
TITLE
JOURNAL

REMARK
COMMENT

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmitt, J., Myers, R.M., Butlerfield, S., Krzyzanski, M.I., Skalska, U., Smalins, D.E., Scherich, A., Schein, J.E., Jones, S.J. and Matra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12479932
2 (bases 1 to 1951)
Strausberg, R.
Direct Submission
Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Akhter, N., Ayala, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Larc, P., Legaspi, R., Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stancitop, S., Thomas, P.J., Touchman, J.W., Tsougen, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAX Plate: 49 Row: b Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19923049.

Location/Qualifiers

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CDS

gene

ORIGIN

Query Match 99.5%; Score 904.2; DB 9; Length 1951;
Best Local Similarity 99.7%; Pred. No. 5.6e-134;

Matches 906; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB	129	TACGGAGTCTGCTTCAACCGTATGTTGAGTGTGGGCGGCACTGAC	188
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DB	189	GAGCTGAGCTCTGCTTCTGCTGATGAGCTCTGCGGCGGCGGAGGCT	248
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RESULT 9
AF457575
LOCUS
DEFINITION
ACCESSION

AF457575 981 bp mRNA linear pri 10-APR-2002
Homo sapiens death effector domain-containing protein FLAME-3
(FLAME-3) mRNA, complete cds.
AF457575

VERSION AF457575.1 GI:20126793
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 981)
AUTHORS Zhan, Y., Hegde, R., Srinivasula, S.M., Fernandes-Alnemri, T. and Alnemri, E.S.
TITLE Death effector domain-containing proteins DEDD and FLAME-3 form nuclear complexes with the TFIIC102 subunit of human transcription factor TFIIC
JOURNAL Cell Death Differ. 9 (4), 439-447 (2002)
MEDLINE 21961615
PUBMED 11965497
REFERENCE 2 (bases 1 to 981)
AUTHORS Alnemri, E.S.
TITLE Direct Submission
JOURNAL Submitted (11-DEC-2001) Microbiology and Immunology, Thomas Jefferson University, 233 S. 10th Street, Philadelphia, PA 19107, USA

FEATURES
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gene
CDS
ORIGIN
Query Match 98.9%; Score 899.4; DB 9; Length 981;
Best Local Similarity 99.3%; Pred. No. 3.9e-133;
Matches 903; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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901 GAGGCTGAC 909

RESULT 10
LOCUS AY125488 2012 bp mRNA linear PRI 18-SEP-2002
DEFINITION Homo sapiens death effector domain-containing DNA-binding 2
ACCESSION AY125488
VERSION AY125488.1 GI:22475163
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2012)
AUTHORS Lee, J.C., Schickling, O., Stegh, A.H., Ohnima, R.G., Dinsdale, D., Cohen, G.M., and Peter, M.E.
TITLE DEDD regulates degradation of intermediate filaments during apoptosis
JOURNAL J. Cell Biol. 158 (6), 1051-1066 (2002)
MEDLINE 22220288
PUBMED 12235123
REFERENCE 2 (bases 1 to 2012)
AUTHORS Peter, M.E.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-2002) Ben May Cancer Institute, University of Chicago, 924 E. 57th Street, R112, Chicago, IL 60637, USA
FEATURES
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VERSION	BC013372.2 GI:33872465	
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SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
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AUTHORS	1 (bases 1 to 2005)	
	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Scheffer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loguailano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gumarane,P.H., Richard,S., Morley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butlerfield,Y.S., Krzywinski,M.I., Skalska,U., Smalton,D.B., Schnerch,A., Schein,J.E., Jones,S.J., and Marra,M.A.	
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
PUBMED	12477932	
REFERENCE	2 (bases 1 to 2005)	
AUTHORS	Strausberg,R.	
TITLE	Direct Submission	
JOURNAL	Submitted (31-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
REMARK		
COMMENT	NIH-MGC Project URL: http://mgc.nci.nih.gov On Aug 19, 2003 this sequence version replaced gi:15426522. Contact: MGC help desk Email: cgaps-remail.nih.gov Tissue Procurement: DCTD/DRP CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact: amadansystemsbiology.org Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting	
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ORIGIN

Query Match 93.0%; Score 845.4; DB 9; Length 2005;

Best Local Similarity 98.0%; Pred. No. 1.2e-124;

Matches 893; Conservative 0; Mismatches 1; Indels 17; Gaps 3;

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LOCUS

DEFINITION

SEQUENCE 2 from Patent WO0206315.

AX364851

VERSION

AX364851.1 GI:18696740

KEYWORDS

SOURCE

ORGANISM

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 Mintz, L., Freilich, S. and Bernstein, J.

Novel nucleic acid and amino acid sequences

Patent: WO 0206315-A 2 24-JAN-2002;

CompuGen Ltd. (IL)

FEATURES

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DEFINITION Sequence 3 from Patent WO0206315.
ACCESSION AX364852
VERSION AX364852.1 GI:18696741
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1
AUTHORS Mintz, L., Freilich, S. and Bernstein, J.
TITLE Novel nucleic acid and amino acid sequences
JOURNAL Patent: WO 0206315-A 3 24-JAN-2002;
CompuGen Ltd. (IL)
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RESULT 14
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ACCESSION AF457576
VERSION AF457576.1 GI:20126795
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 993)
AUTHORS Zhan, Y., Hegde, R., Srinivasula, S. M., Fernandes-Alnemri, T. and Alnemri, E. S.
TITLE Death effector domain-containing proteins DEDD and FLAME-3 form

ORIGIN

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Best Local Similarity 86.8%; Pred. No. 1,1e-101;

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DB      901 GTCAAGTGTGAGCAGAGGCTGAC 921
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Copyright (c) 1993 - 2005 CompuGen Ltd.

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4: /cgn2_6/ptodata/1/paa/US08_COMB.pep.*

5: /cgn2_6/ptodata/1/paa/US081_COMB.pep.*

6: /cgn2_6/ptodata/1/paa/US082_COMB.pep.*

7: /cgn2_6/ptodata/1/paa/US083_COMB.pep.*

8: /cgn2_6/ptodata/1/paa/US084_COMB.pep.*

9: /cgn2_6/ptodata/1/paa/US085_COMB.pep.*

10: /cgn2_6/ptodata/1/paa/US086_COMB.pep.*

11: /cgn2_6/ptodata/1/paa/US087_COMB.pep.*

12: /cgn2_6/ptodata/1/paa/US088_COMB.pep.*

13: /cgn2_6/ptodata/1/paa/US089_COMB.pep.*

14: /cgn2_6/ptodata/1/paa/US090_COMB.pep.*

15: /cgn2_6/ptodata/1/paa/US091_COMB.pep.*

16: /cgn2_6/ptodata/1/paa/US092_COMB.pep.*

17: /cgn2_6/ptodata/1/paa/US093_COMB.pep.*

18: /cgn2_6/ptodata/1/paa/US094_COMB.pep.*

19: /cgn2_6/ptodata/1/paa/US095_COMB.pep.*

20: /cgn2_6/ptodata/1/paa/US096_COMB.pep.*

21: /cgn2_6/ptodata/1/paa/US097A_COMB.pep.*

22: /cgn2_6/ptodata/1/paa/US097B_COMB.pep.*

23: /cgn2_6/ptodata/1/paa/US098_COMB.pep.*

24: /cgn2_6/ptodata/1/paa/US099A_COMB.pep.*

25: /cgn2_6/ptodata/1/paa/US099B_COMB.pep.*

26: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*

27: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*

28: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*

29: /cgn2_6/ptodata/1/paa/US103_COMB.pep.*

30: /cgn2_6/ptodata/1/paa/US104_COMB.pep.*

31: /cgn2_6/ptodata/1/paa/US105_COMB.pep.*

32: /cgn2_6/ptodata/1/paa/US106_COMB.pep.*

33: /cgn2_6/ptodata/1/paa/US107_COMB.pep.*

34: /cgn2_6/ptodata/1/paa/US108_COMB.pep.*

35: /cgn2_6/ptodata/1/paa/US109_COMB.pep.*

36: /cgn2_6/ptodata/1/paa/US110_COMB.pep.*

37: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1550	100.0	303	26	US-10-030-271-2
2	1550	100.0	326	26	US-10-030-271-4
3	1543	99.5	318	26	US-10-001-254-18
4	1543	99.5	318	37	US-60-301-889-18
5	1543	99.5	326	27	US-10-170-205E-10544
6	1543	99.5	326	27	US-10-170-205E-11301
7	1543	99.5	326	28	US-10-226-539-1
8	1543	99.5	326	37	US-60-452-680-19741
9	1543	99.5	326	37	US-60-452-680-19745
10	1543	99.5	366	1	PCT-US00-26524B-4616
11	1543	99.5	366	27	US-10-106-688-4626
12	1413	91.2	304	20	US-09-669-445-11
13	1413	91.2	304	26	US-10-013-477-11
14	1413	91.2	304	27	US-10-100-683-7694
15	1413	91.2	304	36	US-11-001-793-7694
16	1404	90.6	319	1	PCT-US00-05918-758
17	1404	90.6	319	24	US-09-925-302-758
18	1366	88.1	266	21	US-09-715-893-18
19	987	63.7	242	1	PCT-US00-35017A-1220
20	987	63.7	242	28	US-10-236-115-1220
21	985	63.5	234	37	US-60-452-680-19742
22	950.5	61.3	277	18	US-09-488-725A-2950
23	950.5	61.3	277	28	US-10-258-898A-2950
24	950.5	61.3	277	28	US-10-286-897-2950
25	854	55.1	217	18	US-09-488-725A-6522
26	854	55.1	217	28	US-10-258-898A-6522
27	854	55.1	217	28	US-09-786-446-1208
28	703	45.4	220	22	US-10-212-759-1208
29	703	45.4	220	28	US-10-629-669A-14195
30	622.5	40.2	318	35	US-10-917-503-4195
31	622.5	40.2	318	35	US-10-935-223-4
32	614.5	39.6	318	24	US-10-170-205E-12295
33	614.5	39.6	318	27	US-10-170-205E-12596
34	614.5	39.6	318	35	US-10-990-328-11652
35	614.5	39.6	318	35	US-10-990-328-11653
36	614.5	39.6	318	35	US-10-990-328-11654
37	614.5	39.6	318	37	US-60-443-566-3778
38	614.5	39.6	318	37	US-60-443-566-3778
39	614.5	39.6	318	37	US-60-452-680-19405
40	614.5	39.6	318	37	US-60-452-680-19405
41	614.5	39.6	318	37	US-60-452-680-19406
42	614.5	39.6	318	37	US-60-453-050-11584
43	614.5	39.6	318	37	US-60-453-050-11585
44	614.5	39.6	318	37	US-60-453-135-11584
45	614.5	39.6	318	37	US-60-453-135-11585

ALIGNMENTS

RESULT 1

US-10-030-271-2

Sequence 2, Application US/10030271

GENERAL INFORMATION:

APPLICANT: OTA, TOSHIO

APPLICANT: ISOGAI, TAKAO

APPLICANT: NISHIKAWA, TETSUO

APPLICANT: HIO, YURI

APPLICANT: MIYOSHI, SOUSUKE

APPLICANT: SATOH, SUSUMU

TITLE OF INVENTION: APOPTOSIS-ASSOCIATED FACTOR

FILE REFERENCE: 217860USOPT

CURRENT APPLICATION NUMBER: US/10/030, 271

CURRENT FILING DATE: 2002-06-28

PRIOR APPLICATION NUMBER: JP 11-194179

PRIOR FILING DATE: 1999-07-08

PRIOR APPLICATION NUMBER: US 60/159, 586

PRIOR FILING DATE: 1999-10-18

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 303
TYPE: PRT
ORGANISM: Homo sapiens
US-10-030-271-2

Query Match 100.0%; Score 1550; DB 26; Length 303;
Best Local Similarity 100.0%; Pred. No. 7e-128;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALSGSTPAPCWEDECDLYGMLSLHMFVVGQOLTECELELLAFLLDEAPGAGGIA 60
DB 1 MALSGSTPAPCWEDECDLYGMLSLHMFVVGQOLTECELELLAFLLDEAPGAGGIA 60
QY 61 RARSGLELLLELERRGQCGESNRLGQLRLVLAHDLPHLARRRPVSPEYSGTS 120
DB 61 RARSGLELLLELERRGQCGESNRLGQLRLVLAHDLPHLARRRPVSPEYSGTS 120
QY 121 SSSKRTGSCRRRRSSSSANSQCGWETGSPPTKRRRSGRPGGARRRRRGAAPAQ 180
DB 121 SSSKRTGSCRRRRSSSSANSQCGWETGSPPTKRRRSGRPGGARRRRRGAAPAQ 180
QY 181 QOSEPARPSSSEKVTCDIRLRVRAECYCEHPALGQVASSRPPQALARQLDVFGQATAVLR 240
DB 181 QOSEPARPSSSEKVTCDIRLRVRAECYCEHPALGQVASSRPPQALARQLDVFGQATAVLR 240
QY 241 SRDLGSVVCDIKFSELSYLDLAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVD 300
DB 241 SRDLGSVVCDIKFSELSYLDLAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVD 300
QY 301 EAD 303
DB 301 EAD 303

RESULT 2
US-10-030-271-4
Sequence 4, Application US/10030271

extended out C terminal

GENERAL INFORMATION:
APPLICANT: ISOGAI, TOSHIO
APPLICANT: NISHIKAWA, TETSUO
APPLICANT: HIO, YORI
APPLICANT: MIYOSHI, SOUSUKE
TITLE OF INVENTION: APOPTOSIS-ASSOCIATED FACTOR
FILE REFERENCE: 21780USOPT
CURRENT FILING DATE: US/10/030,271
PRIOR FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: JP 11-194179
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: US 60/159,586
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 326
TYPE: PRT
ORGANISM: Homo sapiens
US-10-030-271-4

Query Match 100.0%; Score 1550; DB 26; Length 326;
Best Local Similarity 100.0%; Pred. No. 7e-128;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALSGSTPAPCWEDECDLYGMLSLHMFVVGQOLTECELELLAFLLDEAPGAGGIA 60
DB 1 MALSGSTPAPCWEDECDLYGMLSLHMFVVGQOLTECELELLAFLLDEAPGAGGIA 60
QY 61 RARSGLELLLELERRGQCGESNRLGQLRLVLAHDLPHLARRRPVSPEYSGTS 120
DB 61 RARSGLELLLELERRGQCGESNRLGQLRLVLAHDLPHLARRRPVSPEYSGTS 120

QY 121 SSSKRTGSCRRRRSSSSANSQCGWETGSPPTKRRRSGRPGGARRRRRGAAPAQ 180
DB 121 SSSKRTGSCRRRRSSSSANSQCGWETGSPPTKRRRSGRPGGARRRRRGAAPAQ 180
QY 181 QOSEPARPSSSEKVTCDIRLRVRAECYCEHPALGQVASSRPPQALARQLDVFGQATAVLR 240
DB 181 QOSEPARPSSSEKVTCDIRLRVRAECYCEHPALGQVASSRPPQALARQLDVFGQATAVLR 240
QY 241 SRDLGSVVCDIKFSELSYLDLAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVD 300
DB 241 SRDLGSVVCDIKFSELSYLDLAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVD 300
QY 301 EAD 303
DB 301 EAD 303

RESULT 3

US-10-001-254-18
Sequence 18, Application US/10001254

GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Fiorentino, Loredana
APPLICANT: Lee, Sung Hyung
APPLICANT: Roth, Wilfred
TITLE OF INVENTION: Novel Death Domain Proteins
FILE REFERENCE: P-LJ 5037
CURRENT FILING DATE: US/10/001,254
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/301,889
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/715,893
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapien
US-10-001-254-18

Query Match 99.5%; Score 1543; DB 26; Length 318;
Best Local Similarity 99.7%; Pred. No. 3.1e-127;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALSGSTPAPCWEDECDLYGMLSLHMFVVGQOLTECELELLAFLLDEAPGAGGIA 60
DB 1 MALSGSTPAPCWEDECDLYGMLSLHMFVVGQOLTECELELLAFLLDEAPGAGGIA 60
QY 61 RARSGLELLLELERRGQCGESNRLGQLRLVLAHDLPHLARRRPVSPEYSGTS 120
DB 61 RARSGLELLLELERRGQCGESNRLGQLRLVLAHDLPHLARRRPVSPEYSGTS 120
QY 121 SSSKRTGSCRRRRSSSSANSQCGWETGSPPTKRRRSGRPGGARRRRRGAAPAQ 180
DB 121 SSSKRTGSCRRRRSSSSANSQCGWETGSPPTKRRRSGRPGGARRRRRGAAPAQ 180
QY 181 QOSEPARPSSSEKVTCDIRLRVRAECYCEHPALGQVASSRPPQALARQLDVFGQATAVLR 240
DB 181 QOSEPARPSSSEKVTCDIRLRVRAECYCEHPALGQVASSRPPQALARQLDVFGQATAVLR 240
QY 241 SRDLGSVVCDIKFSELSYLDLAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVD 300
DB 241 SRDLGSVVCDIKFSELSYLDLAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVD 300
QY 301 EAD 303
DB 301 EAD 303

RESULT 4
US-60-301-889-18
; Sequence 18, Application US/60301889
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sung Hyung
; APPLICANT: Roth, Wilfred
; APPLICANT: Stehmer-Lewen, Frank
; TITLE OF INVENTION: Novel Death Domain Proteins
; FILE REFERENCE: P-LJ 4718
; CURRENT APPLICATION NUMBER: US/60/301,889
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatsSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-301-889-18

Query Match 99.5%; Score 1543; DB 37; Length 318;
Best Local Similarity 99.7%; Pred. No. 3.1e-127;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALSGTAPPCWBEDECDYGMLSLHMFVVGQLTCELELAFLLDEAPGAAGIA 60
DB 1 MALSGTAPPCWBEDECDYGMLSLHMFVVGQLTCELELAFLLDEAPGAAGIA 60
QY 61 RARSGLELLLELERRGQCESNLRLLGQLRLVLAHDDLPHLARRRRVPSPERYSYGTS 120
DB 61 RARSGLELLLELERRGQCESNLRLLGQLRLVLAHDDLPHLARRRRVPSPERYSYGTS 120
QY 121 SSSKRTGSCRRRRSSSSANSOQOMETGSPPTKRQRRSRGPGGARRRRRGAAPAPQ 180
DB 121 SSSKRTGSCRRRRSSSSANSOQOMETGSPPTKRQRRSRGPGGARRRRRGAAPAPQ 180
QY 181 QOSEPARPSSSEKVTCDRLRLVRAVYCEHGPALBEGVARRPOALARQLDVFGQATAVLR 240
DB 181 QOSEPARPSSSEKVTCDRLRLVRAVYCEHGPALBEGVARRPOALARQLDVFGQATAVLR 240
QY 241 SRDLGSVVCIDIKFSELSYLDAPFMGDYLSGALLQALRGVFLTEALREAVGREAVRLVSV 300
DB 241 SRDLGSVVCIDIKFSELSYLDAPFMGDYLSGALLQALRGVFLTEALREAVGREAVRLVSV 300
QY 301 EAD 303
DB 301 EAD 303

RESULT 5
US-10-170-205B-10544
; Sequence 10544, Application US/10170205B
; GENERAL INFORMATION:
; APPLICANT: ADAMS, Mark
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
; FILE REFERENCE: CL001381
; CURRENT APPLICATION NUMBER: US/10/170,205B
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 40312
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10544
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-205B-10544

Query Match 99.5%; Score 1543; DB 27; Length 326;
Best Local Similarity 99.7%; Pred. No. 3.2e-127;

Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MALSGTAPPCWBEDECDYGMLSLHMFVVGQLTCELELAFLLDEAPGAAGIA 60
DB 1 MALSGTAPPCWBEDECDYGMLSLHMFVVGQLTCELELAFLLDEAPGAAGIA 60
QY 61 RARSGLELLLELERRGQCESNLRLLGQLRLVLAHDDLPHLARRRRVPSPERYSYGTS 120
DB 61 RARSGLELLLELERRGQCESNLRLLGQLRLVLAHDDLPHLARRRRVPSPERYSYGTS 120
QY 121 SSSKRTGSCRRRRSSSSANSOQOMETGSPPTKRQRRSRGPGGARRRRRGAAPAPQ 180
DB 121 SSSKRTGSCRRRRSSSSANSOQOMETGSPPTKRQRRSRGPGGARRRRRGAAPAPQ 180
QY 181 QOSEPARPSSSEKVTCDRLRLVRAVYCEHGPALBEGVARRPOALARQLDVFGQATAVLR 240
DB 181 QOSEPARPSSSEKVTCDRLRLVRAVYCEHGPALBEGVARRPOALARQLDVFGQATAVLR 240
QY 241 SRDLGSVVCIDIKFSELSYLDAPFMGDYLSGALLQALRGVFLTEALREAVGREAVRLVSV 300
DB 241 SRDLGSVVCIDIKFSELSYLDAPFMGDYLSGALLQALRGVFLTEALREAVGREAVRLVSV 300
QY 301 EAD 303
DB 301 EAD 303

RESULT 6
US-10-170-205B-11301
; Sequence 11301, Application US/10170205B
; GENERAL INFORMATION:
; APPLICANT: ADAMS, Mark
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
; FILE REFERENCE: CL001381
; CURRENT APPLICATION NUMBER: US/10/170,205B
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 40312
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11301
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-205B-11301

Query Match 99.5%; Score 1543; DB 27; Length 326;
Best Local Similarity 99.7%; Pred. No. 3.2e-127;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALSGTAPPCWBEDECDYGMLSLHMFVVGQLTCELELAFLLDEAPGAAGIA 60
DB 1 MALSGTAPPCWBEDECDYGMLSLHMFVVGQLTCELELAFLLDEAPGAAGIA 60
QY 61 RARSGLELLLELERRGQCESNLRLLGQLRLVLAHDDLPHLARRRRVPSPERYSYGTS 120
DB 61 RARSGLELLLELERRGQCESNLRLLGQLRLVLAHDDLPHLARRRRVPSPERYSYGTS 120
QY 121 SSSKRTGSCRRRRSSSSANSOQOMETGSPPTKRQRRSRGPGGARRRRRGAAPAPQ 180
DB 121 SSSKRTGSCRRRRSSSSANSOQOMETGSPPTKRQRRSRGPGGARRRRRGAAPAPQ 180
QY 181 QOSEPARPSSSEKVTCDRLRLVRAVYCEHGPALBEGVARRPOALARQLDVFGQATAVLR 240
DB 181 QOSEPARPSSSEKVTCDRLRLVRAVYCEHGPALBEGVARRPOALARQLDVFGQATAVLR 240
QY 241 SRDLGSVVCIDIKFSELSYLDAPFMGDYLSGALLQALRGVFLTEALREAVGREAVRLVSV 300
DB 241 SRDLGSVVCIDIKFSELSYLDAPFMGDYLSGALLQALRGVFLTEALREAVGREAVRLVSV 300
QY 301 EAD 303
DB 301 EAD 303

RESULT 7
US-10-296-539-1
Sequence 1, Application US/10296539
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: TANG, Y. Tom
APPLICANT: AZIMZAI, Yalda
APPLICANT: YUE, Henry
APPLICANT: BURFORD, Neil
APPLICANT: DING, Li
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: PATTERSON, Chandra
APPLICANT: BAUGHN, Mariah R.
TITLE OF INVENTION: REGULATORS OF APOPTOSIS
FILE REFERENCE: PI-0307 PCT
CURRENT FILING DATE: 2002-11-21
CURRENT APPLICATION NUMBER: US/10/296,539
PRIOR APPLICATION NUMBER: 60/209,407; 60/250,326
PRIOR FILING DATE: 2000-06-01; 2000-11-30
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 326
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 3102521CD1
US-10-296-539-1

patch

Query Match 99.5%; Score 1543; DB 28; Length 326;
Best Local Similarity 99.7%; Pred. No. 3.2e-127;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALSGTAPCWEDECDIDYGMLSLHMFVVGQLTCECELELAFILDEAPGAAGLA 60
DB 1 MALSGTAPCWEDECDIDYGMLSLHMFVVGQLTCECELELAFILDEAPGAAGLA 60
QY 61 RARSGLELLELERRGQCESNLRLLGQLRLVLAHDLPLHARKRRPVSPERYSGTS 120
DB 61 RARSGLELLELERRGQCESNLRLLGQLRLVLAHDLPLHARKRRPVSPERYSGTS 120
QY 121 SSKRTGSCRRRRSSSSANSQOGWETGSPPTKQRRSRGRRPGGARRRRRGAAPAQ 180
DB 121 SSKRTGSCRRRRSSSSANSQOGWETGSPPTKQRRSRGRRPGGARRRRRGAAPAQ 180
QY 181 QOSEPARPSSSEKVTCDIRLRAVEYCEHGPALBOGVASRRPOALAROLDVFGQATAVLR 240
DB 181 QOSEPARPSSSEKVTCDIRLRAVEYCEHGPALBOGVASRRPOALAROLDVFGQATAVLR 240
QY 241 SRDLGSVVCIDIKFSELSYLDAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSD 300
DB 241 SRDLGSVVCIDIKFSELSYLDAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSD 300
QY 301 EAD 303
DB 301 EAD 303
RESULT 8
US-60-452-680-19741
Sequence 19741, Application US/60452680
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: GRUPE, Andrew
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001450
CURRENT APPLICATION NUMBER: US/60/452,680
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 116213
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 19741
LENGTH: 326
TYPE: PRT
ORGANISM: Homo sapiens
US-60-452-680-19741

Query Match 99.5%; Score 1543; DB 37; Length 326;
Best Local Similarity 99.7%; Pred. No. 3.2e-127;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALSGTAPCWEDECDIDYGMLSLHMFVVGQLTCECELELAFILDEAPGAAGLA 60
DB 1 MALSGTAPCWEDECDIDYGMLSLHMFVVGQLTCECELELAFILDEAPGAAGLA 60
QY 61 RARSGLELLELERRGQCESNLRLLGQLRLVLAHDLPLHARKRRPVSPERYSGTS 120
DB 61 RARSGLELLELERRGQCESNLRLLGQLRLVLAHDLPLHARKRRPVSPERYSGTS 120
QY 121 SSKRTGSCRRRRSSSSANSQOGWETGSPPTKQRRSRGRRPGGARRRRRGAAPAQ 180
DB 121 SSKRTGSCRRRRSSSSANSQOGWETGSPPTKQRRSRGRRPGGARRRRRGAAPAQ 180
QY 181 QOSEPARPSSSEKVTCDIRLRAVEYCEHGPALBOGVASRRPOALAROLDVFGQATAVLR 240
DB 181 QOSEPARPSSSEKVTCDIRLRAVEYCEHGPALBOGVASRRPOALAROLDVFGQATAVLR 240
QY 241 SRDLGSVVCIDIKFSELSYLDAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSD 300
DB 241 SRDLGSVVCIDIKFSELSYLDAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSD 300
QY 301 EAD 303
DB 301 EAD 303

RESULT 9
US-60-452-680-19745
Sequence 19745, Application US/60452680
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: GRUPE, Andrew
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001450
CURRENT APPLICATION NUMBER: US/60/452,680
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 116213
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19745
LENGTH: 326
TYPE: PRT
ORGANISM: Homo sapiens
US-60-452-680-19745

Query Match 99.5%; Score 1543; DB 37; Length 326;
Best Local Similarity 99.7%; Pred. No. 3.2e-127;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALSGTAPCWEDECDIDYGMLSLHMFVVGQLTCECELELAFILDEAPGAAGLA 60
DB 1 MALSGTAPCWEDECDIDYGMLSLHMFVVGQLTCECELELAFILDEAPGAAGLA 60
QY 61 RARSGLELLELERRGQCESNLRLLGQLRLVLAHDLPLHARKRRPVSPERYSGTS 120
DB 61 RARSGLELLELERRGQCESNLRLLGQLRLVLAHDLPLHARKRRPVSPERYSGTS 120
QY 121 SSKRTGSCRRRRSSSSANSQOGWETGSPPTKQRRSRGRRPGGARRRRRGAAPAQ 180
DB 121 SSKRTGSCRRRRSSSSANSQOGWETGSPPTKQRRSRGRRPGGARRRRRGAAPAQ 180
QY 181 QOSEPARPSSSEKVTCDIRLRAVEYCEHGPALBOGVASRRPOALAROLDVFGQATAVLR 240
DB 181 QOSEPARPSSSEKVTCDIRLRAVEYCEHGPALBOGVASRRPOALAROLDVFGQATAVLR 240

QY 241 SRDLGSVCDIKFSELSYLDATFWDYLSGALLQALRGVFLTEALREAVGREAVRLVSYD 300
DB 241 SRDLGSVCDIKFSELSYLDATFWDYLSGALLQALRGVFLTEALREAVGREAVRLVSYD 300
QY 301 EAD 303
DB 301 EAD 303
RESULT 10
PCT-US00-26524B-4616
Sequence 4616, Application PC/TUS0026524B
GENERAL INFORMATION:
APPLICANT: Birse et. al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005PCT
CURRENT APPLICATION NUMBER: PCT/US00/26524B
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4616
LENGTH: 366
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US00-26524B-4616

Query Match 99.5%; Score 1543; DB 1; Length 366;
Best Local Similarity 99.7%; Pred. No. 3.8e-127;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 161 SSSKRTGSCRRRRROSSSSANSQCGWETGSPPTKQRRSRGRRPGGARRRRGAPAPQ 220
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QY 241 SRDLGSVCDIKFSELSYLDATFWDYLSGALLQALRGVFLTEALREAVGREAVRLVSYD 300
DB 281 SRDLGSVCDIKFSELSYLDATFWDYLSGALLQALRGVFLTEALREAVGREAVRLVSYD 340
QY 301 EAD 303
DB 341 EAD 343
RESULT 11
US-10-106-698-4626
Sequence 4626, Application US/10106698
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 4626
LENGTH: 366
TYPE: PRT
ORGANISM: Homo sapiens
US-10-106-698-4626

Query Match 99.5%; Score 1543; DB 27; Length 366;
Best Local Similarity 99.7%; Pred. No. 3.8e-127;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 241 SRDLGSVCDIKFSELSYLDATFWDYLSGALLQALRGVFLTEALREAVGREAVRLVSYD 300
DB 281 SRDLGSVCDIKFSELSYLDATFWDYLSGALLQALRGVFLTEALREAVGREAVRLVSYD 340
QY 301 EAD 303
DB 341 EAD 343

RESULT 12
US-09-669-445-11
Sequence 11, Application US/09669445
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: Apoptosis Related Polynucleotides, Polypeptides, and Antibodies
FILE REFERENCE: P1002P1
CURRENT APPLICATION NUMBER: US/09/669,445
CURRENT FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: PCT/US00/06642
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: 60/126,018
PRIOR FILING DATE: 1999-03-24
PRIOR APPLICATION NUMBER: 60/139,638
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: 60/149,449
PRIOR FILING DATE: 1999-08-18
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 304
TYPE: PRT
ORGANISM: Homo sapiens
US-09-669-445-11

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Best Local Similarity 99.6%; Pred. No. 9.1e-116;
Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 83 LRLGQLRLVLAHDDLPHLARKRRRVPSPERYSGTSSSSKRTGSCRRRRROSSSANS 142


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Db      121 QOGWETGSPPTKQRRSRGRRPSSGARRRRRGAPAPPOQOSEPARPSSSEKVTCDIRLRV 180
Qy      203 RAEYCEHGPALAEQVASRRPQALARQLDVFGQATVILSRDLGSVCDIKFSELSYLDLF 262
Db      181 RAEYCEHGPALAEQVASRRPQALARQLDVFGQATVILSRDLGSVCDIKFSELSYLDLF 240
Qy      263 WGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 303
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RESULT 13
US-10-013-477-11
; Sequence 11, Application US/10013477
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Apoptosis Related Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: P1002P1
; CURRENT APPLICATION NUMBER: US/10/013,477
; PRIOR FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: 09/669,445
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US00/06642
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/126,018
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/139,638
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/149,449
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-477-11

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Query Match      91.2%; Score 1413; DB 26; Length 304;
Best Local Similarity 99.6%; Pred. No. 9,1e-116;
Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1 MLSHRMFEVVGQUTCELELILAFLLDEAPGAAGLARARSGLELLELERRGCGGSESN 60
Qy      83 LRLGQLRLVLRARDLPLHARKRRRPPVSPERYSTGTSSSKRTGSCRRRRQSSSSANS 142
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Qy      203 RAEYCEHGPALAEQVASRRPQALARQLDVFGQATVILSRDLGSVCDIKFSELSYLDLF 262
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RESULT 14
US-10-100-683-7694
; Sequence 7694, Application US/10100683
; GENERAL INFORMATION:
; APPLICANT: Rosen, et al.

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; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: P5900
; CURRENT APPLICATION NUMBER: US/10/100,683
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: US 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,845
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,539
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,632
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,892
; PRIOR FILING DATE: 1997-08-22
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13468
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7694
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-100-683-7694

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Query Match      91.2%; Score 1413; DB 27; Length 304;
Best Local Similarity 99.6%; Pred. No. 9,1e-116;
Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1 MLSHRMFEVVGQUTCELELILAFLLDEAPGAAGLARARSGLELLELERRGCGGSESN 60
Qy      83 LRLGQLRLVLRARDLPLHARKRRRPPVSPERYSTGTSSSKRTGSCRRRRQSSSSANS 142
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Qy      203 RAEYCEHGPALAEQVASRRPQALARQLDVFGQATVILSRDLGSVCDIKFSELSYLDLF 262
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Qy      263 WGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 303
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RESULT 15
US-11-001-793-7694
; Sequence 7694, Application US/11001793
; GENERAL INFORMATION:
; APPLICANT: Rosen, et al.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: P5900
; CURRENT APPLICATION NUMBER: US/11/001,793
; PRIOR FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/100,683
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: US 60/043,576
; PRIOR FILING DATE: 1997-04-11

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; PRIOR APPLICATION NUMBER: US 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,845
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,599
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,632
; PRIOR FILING DATE: 1997-05-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13468
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 7694
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-001-793-7694

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Query Match      91.2%; Score 1413; DB 36; Length 304;
Best Local Similarity 99.6%; Pred. No. 9.1e-116;
Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 181 RAYCEHGPALREGVSRRRPOLAROLDVFGQATAVLRSDIGSVYCDIKFSELSTYDAF 240
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QY 263 WGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 303
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DB 241 WGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 281
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Yao, L.
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GenCore version 5.1.6
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95: /cgn2_6/ptodata/1/pna/US6025_COMB.seq.*
96: /cgn2_6/ptodata/1/pna/US6026_COMB.seq.*
97: /cgn2_6/ptodata/1/pna/US6027_COMB.seq.*
98: /cgn2_6/ptodata/1/pna/US6028_COMB.seq.*
99: /cgn2_6/ptodata/1/pna/US6029_COMB.seq.*
100: /cgn2_6/ptodata/1/pna/US6030_COMB.seq.*
101: /cgn2_6/ptodata/1/pna/US6031_COMB.seq.*
102: /cgn2_6/ptodata/1/pna/US6032_COMB.seq.*
103: /cgn2_6/ptodata/1/pna/US6033_COMB.seq.*
104: /cgn2_6/ptodata/1/pna/US6034_COMB.seq.*
105: /cgn2_6/ptodata/1/pna/US6035_COMB.seq.*
106: /cgn2_6/ptodata/1/pna/US6036_COMB.seq.*
107: /cgn2_6/ptodata/1/pna/US6037_COMB.seq.*
108: /cgn2_6/ptodata/1/pna/US6038_COMB.seq.*
109: /cgn2_6/ptodata/1/pna/US6039_COMB.seq.*
110: /cgn2_6/ptodata/1/pna/US6040_COMB.seq.*
111: /cgn2_6/ptodata/1/pna/US6041_COMB.seq.*
112: /cgn2_6/ptodata/1/pna/US6042_COMB.seq.*
113: /cgn2_6/ptodata/1/pna/US6043_COMB.seq.*
114: /cgn2_6/ptodata/1/pna/US6044_COMB.seq.*
115: /cgn2_6/ptodata/1/pna/US6045_COMB.seq.*
116: /cgn2_6/ptodata/1/pna/US6046_COMB.seq.*

QY 601 CGGGTTCCAGCAGATTAAGTGGAGGCGAGCTTGGAGAGGCGGTGGCATCCCG 660
DB 601 CGGGTTCCAGCAGATTAAGTGGAGGCGAGCTTGGAGAGGCGGTGGCATCCCG 660
QY 661 CGGGCCCAAGGCGCTGGCGGCGAGCTGAGCGTGTGGGCGAGCGCAAGCGAGTCTGGCG 720
DB 661 CGGGCCCAAGGCGCTGGCGGCGAGCTGAGCGTGTGGGCGAGCGCAAGCGAGTCTGGCG 720
QY 721 TCAAGGAGCCTGGGCTGTGTGGTGTGATCAATCAAGTTCTGAGAGTCTCCATCTGAGC 780
DB 721 TCAAGGAGCCTGGGCTGTGTGGTGTGATCAATCAAGTTCTGAGAGTCTCCATCTGAGC 780
QY 781 GCGTTCTGGGCGAGCTAAGTGGAGGCGCGCTGTGGAGGCGCGGCGGCGGTGGTCTG 840
DB 781 GCGTTCTGGGCGAGCTAAGTGGAGGCGCGCTGTGGAGGCGCGGCGGCGGTGGTCTG 840
QY 841 ACTGAGGCGCTGGCGAGAGGCTGTGGGCGGAGGCGCTGTGGCTGTGAGTGTGAT 900
DB 841 ACTGAGGCGCTGGCGAGAGGCTGTGGGCGGAGGCGCTGTGGCTGTGAGTGTGAT 900
QY 901 GAGGCTGAC 909
DB 901 GAGGCTGAC 909

RESULT 2

US-10-030-271-3
; Sequence 3, Application US/10030271
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHIO
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: HIO, YURI
; APPLICANT: MIYOSHI, SOUSUKE
; APPLICANT: SATOH, SUSUMU
; TITLE OF INVENTION: APOPTOSIS-ASSOCIATED FACTOR
; FILE REFERENCE: 217860USOPT
; CURRENT APPLICATION NUMBER: US/10/030,271
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: JP 11-194179
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: US 60/159,586
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1883
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (124)..(1101)
; OTHER INFORMATION:
US-10-030-271-3

Don

Compared A/D 1 to 3

Query Match 100.0%; Score 909; DB 46; Length 1883;
Beet Local Similarity 100.0%; Pred. No. 4e-150;
Matches 909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGGCTATTCGGGTCGAGCCCGGCGCTGCTGGAGAGAGATGAGTGCCTGAGCTAC 60
DB 124 ATGGGCTATTCGGGTCGAGCCCGGCGCTGCTGGAGAGAGATGAGTGCCTGAGCTAC 183
QY 61 TAGGGAGTCTGCTGCTTCAACCGTATGTTGAGAGTGTGGGCGGCACTGACCGAGTGC 120
DB 184 TAGGGAGTCTGCTGCTTCAACCGTATGTTGAGAGTGTGGGCGGCACTGACCGAGTGC 243
QY 121 GAGGCTGAGACTCTGGCTTTCTGCTGAGAGAGGCTCTGGGCGGCGGAGGCTTAAGC 180
DB 244 GAGGCTGAGACTCTGGCTTTCTGCTGAGAGAGGCTCTGGGCGGCGGAGGCTTAAGC 303
QY 181 CGGGCCCGAGCGGCTTAGAGCTCTGTGAGAGCTGAGAGCGCGCGGAGTGCAGCGAG 240

DB 304 CGGGCCCCAGGCGCTAGAGCTCTGTGGAGCTGGAGCGCGCGGCGAGTGCAGCGAG 363
QY 241 AGCAACCTGGGCTGTGGGCAACTCTGTGGCGGCTGGAGCGCGGCGAGTGCAGCGAG 300
DB 364 AGCAACCTGGGCTGTGGGCAACTCTGTGGCGGCTGGAGCGCGGCGAGTGCAGCGAG 423
QY 301 CACTGGGCGGCAAGCGGCGCGGCGAGTGTCTCCAGAACTATAGTATGAGCACTTC 360
DB 424 CACTGGGCGGCAAGCGGCGCGGCGAGTGTCTCCAGAACTATAGTATGAGCACTTC 483
QY 361 AGCTTTCAAGAGAGACAGAGGTTAGTGTGCGTGTGGCTGTGGAGTCAAGCACTTCTGA 420
DB 484 AGCTTTCAAGAGAGACAGAGGTTAGTGTGCGTGTGGCTGTGGAGTCAAGCACTTCTGA 543
QY 421 AATTCTCAGAGGCTCAGTGGAGACAGGCTTCCCGCAACCAAGCGGAGGCGGAGT 480
DB 544 AATTCTCAGAGGCTCAGTGGAGACAGGCTTCCCGCAACCAAGCGGAGGCGGAGT 603
QY 481 CGGGGCGGCGGCGAGTGTGTGTCAGACGCGCGGCGAGAGGCGGCGGCGGCGGAGT 540
DB 604 CGGGGCGGCGGCGAGTGTGTGTCAGACGCGCGGCGAGAGGCGGCGGCGGCGGAGT 663
QY 541 CAGCAGTCAAGAGCGCGGCGAGACCTTCTGTGAAGCGAAAGTGAAGTGTGATTCGGCTC 600
DB 664 CAGCAGTCAAGAGCGCGGCGAGACCTTCTGTGAAGCGAAAGTGAAGTGTGATTCGGCTC 723
QY 601 CGGGTTCCAGCAGATTAAGTGGAGGCGCGCTTGGAGAGGCGGTGGCATCCCGG 660
DB 724 CGGGTTCCAGCAGATTAAGTGGAGGCGCGCTTGGAGAGGCGGTGGCATCCCGG 783
QY 661 CGGGCCCAAGGCGCTGGCGGCGAGCTGAGCGTGTGGGCGAGCGCAAGCGAGTCTGGCG 720
DB 784 CGGGCCCAAGGCGCTGGCGGCGAGCTGAGCGTGTGGGCGAGCGCAAGCGAGTCTGGCG 843
QY 721 TCAAGGAGCCTGGGCTGTGTGGTGTGATCAATCAAGTTCTGAGAGTCTCCATCTGAGC 780
DB 844 TCAAGGAGCCTGGGCTGTGTGGTGTGATCAATCAAGTTCTGAGAGTCTCCATCTGAGC 903
QY 781 GCGTTCTGGGCGAGCTAAGTGGAGGCGCGCTGTGGAGGCGCGGCGGCGGTGGTCTG 840
DB 904 GCGTTCTGGGCGAGCTAAGTGGAGGCGCGCTGTGGAGGCGCGGCGGCGGTGGTCTG 963
QY 841 ACTGAGGCGCTGGCGAGAGGCTGTGGGCGGAGGCTGTGGCTGTGAGTGTGAT 900
DB 964 ACTGAGGCGCTGGCGAGAGGCTGTGGGCGGAGGCTGTGGCTGTGAGTGTGAT 1023
QY 901 GAGGCTGAC 909
DB 1024 GAGGCTGAC 1032

RESULT 3

US-10-296-539-4
; Sequence 4, Application US/10296539
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: TANG, Y. TOM
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: YUE, Henry
; APPLICANT: BURFORD, Neil
; APPLICANT: DING, Li
; APPLICANT: ELIOTT, Vicki S.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: BAUGHN, Mariah R.
; TITLE OF INVENTION: REGULATORS OF APOPTOSIS
; FILE REFERENCE: PI-0307 PCT
; CURRENT APPLICATION NUMBER: US/10/296,539
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: 60/209,407; 60/250,326
; PRIOR FILING DATE: 2000-06-01; 2000-11-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program

SEQ ID NO 4
 LENGTH: 1230
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No: 3102521CB1
 US-10-236-539-4

Query Match 99.8%; Score 907.4; DB 51; Length 1230;
 Best Local Similarity 99.9%; Pred. No. 7.8e-150;
 Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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1 ATGGCGCTATCCGGGTGCAACCCCGGCTCTGGAGAGAGATGCTGACTAC 60
127 ATGGCGCTATCCGGGTGCAACCCCGGCTCTGGAGAGAGATGCTGACTAC 186
61 TACGGGATGCTGCTTCAACCGTATGTTCCAGGTGTGGGGGCACTGACGAGTGC 120
187 TACGGGATGCTGCTTCAACCGTATGTTCCAGGTGTGGGGGCACTGACGAGTGC 246
121 GAGCTGAGCTCTGCTTCTGCTGATGAGGCTCTGCGCGCGAGAGGCTTAGCC 180
247 GAGCTGAGCTCTGCTTCTGCTGATGAGGCTCTGCGCGCGAGAGGCTTAGCC 306
181 CGGGCCCGAGCGGCTTAGAGCTCTGCTGAGCTGAGCGCGCGGCACTGCGGCGAG 240
307 CGGGCCCGAGCGGCTTAGAGCTCTGCTGAGCTGAGCGCGCGGCACTGCGGCGAG 366
241 AGCAACCTGGCGGCTGCTGGGCACTCTGCGCGGCTGCTGGCGCGCAACCTGCTGCG 300
367 AGCAACCTGGCGGCTGCTGGGCACTCTGCGCGGCTGCTGGCGCGCAACCTGCTGCG 426
301 CACCTGGCGCGCAACCGCGCGCGAGTGTCTCAGAACGCTATAGCTATGSCACTCC 360
427 CACCTGGCGCGCAACCGCGCGCGAGTGTCTCAGAACGCTATAGCTATGSCACTCC 486
361 AGCTTTTAAAGAGAGACAGAGGTAAGTGTGCTGCTGCGCTGCGCACTGACAGTTCTGCA 420
487 AGCTTTTAAAGAGAGACAGAGGTAAGTGTGCTGCTGCGCTGCGCACTGACAGTTCTGCA 546
421 AATTCTGAGAGGGTCAAGTGGGAGACAGAGTCTCCCGCAACCAACCGGCAAGGGGAGT 480
547 AATTCTGAGAGGGTCAAGTGGGAGACAGAGTCTCCCGCAACCAACCGGCAAGGGGAGT 606
481 CGGGCCCGAGTGTGTGTCAGACGCGCGCGAGAGAGGGGCCCAAGCCGCAACCCAG 540
607 CGGGCCCGAGTGTGTGTCAGACGCGCGCGAGAGAGGGGCCCAAGCCGCAACCCAG 666
541 CAGCAGTCAAGAGCCCGGCAACCTTCTGTGAAGGCAAGTGAAGCTTGTGAATCCGAGTCC 600
667 CAGCAGTCAAGAGCCCGGCAACCTTCTGTGAAGGCAAGTGAAGCTTGTGAATCCGAGTCC 726
601 CGGGTTCAGAGAGTACTGAGAGATGAGGCAAGCTTGTGAAGAGGGGTGGCAATCCCGG 660
727 CGGGTTCAGAGAGTACTGAGAGATGAGGCAAGCTTGTGAAGAGGGGTGGCAATCCCGG 786
661 CGGGCCCGAGGCTGTGCGCGAGCTGAGCGTGTGTGGGCAAGCCAGCAAGTGTGCGG 720
787 CGGGCCCGAGGCTGTGCGCGAGCTGAGCGTGTGTGGGCAAGCCAGCAAGTGTGCGG 846
721 TCAAGGAGCTGGGCTTGTGTGTGTGAATCAAGTTCTCAAGCTTCTCTATTTGAGC 780
847 TCAAGGAGCTGGGCTTGTGTGTGTGAATCAAGTTCTCAAGCTTCTCTATTTGAGC 906
781 GCTTTCTGGGGGCACTACTAGTGGGCGCTGCTGAGGCGCTGCGGGGGGTGTTCTCG 840
907 GCTTTCTGGGGGCACTACTAGTGGGCGCTGCTGAGGCGCTGCGGGGGGTGTTCTCG 966
841 ACTGAGGCTGTGAGAGAGGCTGTGGGCGGAGAGGCTGTTCCTGCTGCTGATGATGAT 900
967 ACTGAGGCTGTGAGAGAGGCTGTGGGCGGAGAGGCTGTTCCTGCTGCTGATGATGAT 1026

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QY 901 GAGGCTGAC 909
 DB 1027 GAGGCTGAC 1035

RESULT 4

US-10-001-254-17

/ Sequence 17, Application US/10001254

/ GENERAL INFORMATION:

/ APPLICANT: Reed, John C.

/ APPLICANT: Godzik, Adam

/ APPLICANT: Pawlowski, Krzysztof

/ APPLICANT: Fiorentino, Loredana

/ APPLICANT: Lee, Sug Hyung

/ APPLICANT: Roth, Wilfred

/ APPLICANT: Stenmer-Liwenen, Frank

/ TITLE OF INVENTION: Novel Death Domain Proteins

/ FILE REFERENCE: P-1J 5037

/ CURRENT APPLICATION NUMBER: US/10/001,254

/ CURRENT FILING DATE: 2001-11-15

/ PRIOR APPLICATION NUMBER: 60/301,889

/ PRIOR FILING DATE: 2001-06-29

/ PRIOR APPLICATION NUMBER: 09/715,893

/ NUMBER OF SEQ ID NOS: 62

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 17

/ LENGTH: 1924

/ TYPE: DNA

/ ORGANISM: Homo sapien

/ FEATURE:

/ NAME/KEY: CDS

/ LOCATION: (91)...(1044)

/ NAME/KEY: misc feature

/ LOCATION: (1)...(1900)

/ OTHER INFORMATION: n = A,T,C or G

US-10-001-254-17

Query Match 99.8%; Score 907.4; DB 46; Length 1924;
 Best Local Similarity 99.9%; Pred. No. 7.6e-150;
 Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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1 ATGGCGCTATCCGGGTGCAACCCCGGCTCTGGAGAGAGATGCTGACTAC 60
91 ATGGCGCTATCCGGGTGCAACCCCGGCTCTGGAGAGAGATGCTGACTAC 150
61 TACGGGATGCTGCTTCAACCGTATGTTCCAGGTGTGGGGGCACTGACGAGTGC 120
151 TACGGGATGCTGCTTCAACCGTATGTTCCAGGTGTGGGGGCACTGACGAGTGC 210
121 GAGCTGAGCTCTGCTTCTGCTGATGAGGCTCTGCGCGCGAGGCTTAGCC 180
211 GAGCTGAGCTCTGCTTCTGCTGATGAGGCTCTGCGCGCGAGGCTTAGCC 270
181 CGGGCCCGAGGCTGTGCGCGAGCTGAGCGTGTGTGGGCAAGCCAGCAAGTGTGCGG 240
271 CGGGCCCGAGGCTGTGCGCGAGCTGAGCGTGTGTGGGCAAGCCAGCAAGTGTGCGG 330
241 AGCAACCTGGCGGCTGCTGGGCAACCTCTGCGGCTGCGCGCGCAAGCTGCTGCGG 300
331 AGCAACCTGGCGGCTGCTGGGCAACCTCTGCGGCTGCGCGCGCAAGCTGCTGCGG 390
301 CACCTGGCGCGCAACCGCGCGCGAGTGTCTCAGAACGCTATAGCTATGCACTCC 360
391 CACCTGGCGCGCAACCGCGCGCGAGTGTCTCAGAACGCTATAGCTATGCACTCC 450
361 AGCTTTTAAAGAGAGACAGAGGTAAGTGTGCTGCGCGCTGCGCAAGCAAGTTCTGCA 420
451 AGCTTTTAAAGAGAGACAGAGGTAAGTGTGCTGCGCGCTGCGCAAGCAAGTTCTGCA 510
421 AATTCTGAGAGGGTCAAGTGGGAGACAGAGCTCCCGGCAACCAAGCGGCAAGCGAGT 480
511 AATTCTGAGAGGGTCAAGTGGGAGACAGAGCTCCCGGCAACCAAGCGGCAAGCGAGT 570

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QY	481	CGGGGCGGGCCGAGTGTGTGTCAGAGCGGGCGGAGAGGGGCCCGCAGCCGACCCAG	54.0
Db	571	CGGGGCGGGCCGAGTGTGTGTGTCAGAGCGGGCGGAGAGGGGCCCGCAGCCGACCCAG	63.0
QY	541	CAGCAGTCAGAGCCCGCCAGACCTTCTCTGAAGGCAAGTGACTGTGATCCGAGCTC	60.0
Db	631	CAGCAGTCAGAGCCCGCCAGACCTTCTCTGAAGGCAAGTGACTGTGATCCGAGCTC	69.0
QY	601	CGGGTTCCAGCAGCACTATCTGCGAGCATGTGGCCAGCCTTGAGAGCAGGGCCGTGGGATCCCG	66.0
Db	691	CGGGTTCCAGCAGCACTATCTGCGAGCATGTGGCCAGCCTTGAGAGCAGGGCCGTGGGATCCCG	75.0
QY	661	CGGCCCCAGGCGCTGCGCGCGGAGCTGGAAGTGTGTGGCAGGCGCAACCGCAGTGTGCGC	72.0
Db	751	CGGCCCCAGGCGCTGCGCGCGGAGCTGGAAGTGTGTGGGAGGCGCAACCGCAGTGTGCGC	81.0
QY	721	TCAGGGAGCTGGGCTCTGTGTGTGTGAATCATCAAGTTCTCAGAGCTCTCTATCTGGAC	78.0
Db	811	TCAGGGAGCTGGGCTCTGTGTGTGTGAATCATCAAGTTCTCAGAGCTCTCTATCTGGAC	87.0
QY	781	GCCTTCTGGGGGCGACTACCTGAGTGGCGGCTGTCAGAGCCCTGGCGGGCGAGTTCCTG	84.0
Db	871	GCCTTCTGGGGGCGACTACCTGAGTGGCGGCTGTCAGAGCCCTGGCGGGCGAGTTCCTG	93.0
QY	841	ACTGAGGCCCTTGCAGAGGCTGTGGGCGGAGAGGCTGTTGCCTGTGATCAGTGTGGAT	90.0
Db	931	ACTGAGGCCCTTGCAGAGGCTGTGGGCGGAGAGGCTGTTGCCTGTGATCAGTGTGGAT	99.0
QY	901	GAGGCTGAC 909	
Db	991	GAGGCTGAC 999	

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RESULT 5
US-60-301-889-17
? Sequence 17, Application US/60301889
? GENERAL INFORMATION:
? APPLICANT: Reed, John C.
? APPLICANT: Godzik, Adam
? APPLICANT: Pawlowski, Krzysztof
? APPLICANT: Fiorentino, Loredana
? APPLICANT: Lee, Sug Hyung
? APPLICANT: Roth, Wilfred
? APPLICANT: Stenner-Lewen, Frank
? TITLE OF INVENTION: Novel Death Domain Proteins
? FILE REFERENCE: P-HJ 4718
? CURRENT APPLICATION NUMBER: US/60/301,889
? CURRENT FILING DATE: 2001-06-29
? NUMBER OF SEQ ID NOS: 62
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 17
? LENGTH: 1924
? TYPE: DNA
? ORGANISM: Homo sapien
? FEATURES:
? NAME/KEY: CDS
? LOCATION: (91)..(1044)
? NAME/KEY: misc_feature
? LOCATION: (1)..(1900)
? OTHER INFORMATION: n = A,T,C or G
US-60-301-889-17

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Query Match	99.8%	Score 907.4;	DB 100;	Length 1924;
Best Local Similarity	99.9%	Pred. No. 7.6e-150;		
Matches 908; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

QY 1 AATGGGCGCTATCCGGGCTGACCCCGGGCCCGCTGCTGGGAGGAGATGATGCTCCGTGACTAC 60
Db 91 AATGGGCGCTATCCGGGCTGACCCCGGGCCCGCTGCTGGGAGGAGATGATGCTCCGTGACTAC 150
QY 61 TACGGGATGCTGTCGCTTCAACGTATGTCGAGATGCTGTGGGCGGGCAACTGACCGGATGC 120
|||||

Db	151	TACGGGAATGCTGTGCCTTACCCGTAATGTTCCAGAGTGAGTGAGGCGGAGCACTGACCCGAGTGC	210
QY	121	GAGCTGGAAGCTCTCTGGCCTTTCTCTGCTGGATGAGGCTCTTGCGCGCGCCGCGAGGCTTAAGCC	180
Db	211	GAGCTGGAAGCTCTCTGGCCTTTCTCTGCTGGATGAGGCTCTCTGGCGCGCCGCGAGGCTTAAGCC	270
QY	181	CGGGCCCGCAGCGGGCTTGAAGCTCTCTGCTGGAGCTTGAGACGCGCGCGGGCAGTGGCGGAG	240
Db	271	CGGGCCCGCAGCGGGCTTGAAGCTCTCTGCTGGAGCTTGAGACGCGCGCGGGCAGTGGCGGAG	330
QY	241	AGCAACCTGCGAGCTCTGCGGGCAACTCTGCGCGTGTGGCCCGCCAGCACTGTGCGCG	300
Db	331	AGCAACCTGCGAGCTCTGCGGGCAACTCTGCGCGTGTGGCCCGCCAGCACTGTGCGCG	390
QY	301	CACCTGGGGCGCCAGAGCGGCGCGCGGCACAGTGTCTCCAGAACGCTAATGAGCACTCC	360
Db	391	CACCTGGGGCGCCAGAGCGGCGCGCGGCACAGTGTCTCCAGAACGCTAATGAGCACTCC	450
QY	361	AGCTTTCAAAAGAGCAGAGGGATGAGCTGCCTGCCTCGCTCGGACAGTCAAGCAATTTCTGCA	420
Db	451	AGCTTTCAAAAGAGCAGAGGGATGAGCTGCCTGCCTCGCTCGGACAGTCAAGCAATTTCTGCA	510
QY	421	AATTCTCAGCAGGGTCAGTGGGAGACAGGCTTCCCCCAACCAAGCGGCAAGCGGCGGAGT	480
Db	511	AATTCTCAGCAGGGTCAGTGGGAGACAGGCTTCCCCCAACCAAGCGGCAAGCGGCGGAGT	570
QY	481	CGGGGCGGGCCAGTGTGTGTGTGCACAGCGGCGGCGAGAGGGGGCCCGACCGCACCCGAG	540
Db	571	CGGGGCGGGCCAGTGTGTGTGTGCACAGCGGCGGCGAGAGGGGGCCCGACCGCACCCGAG	630
QY	541	CAGCAGTCAGAGCCCGCGCAGACCTTCTCTGAAGGCAAAAGTGAACCTGTGACATCCGACTC	600
Db	631	CAGCAGTCAGAGCCCGCGCAGACCTTCTCTGAAGGCAAAAGTGAACCTGTGACATCCGACTC	690
QY	601	CGGGTTCAGAGCAAGTACTGTCGAGCATGGGCCAGCCTTGGACAGGGCGCTTGGCATCCCGG	660
Db	691	CGGGTTCAGAGCAAGTACTGTCGAGCATGGGCCAGCCTTGGACAGGGCGCTTGGCATCCCGG	750
QY	661	CGGCCCCCAGGCGCTGCGCGCAGCTGAGCATGTGTTTGGGCAAGCCACCCGAGTGTGCGC	720
Db	751	CGGCCCCCAGGCGCTGCGCGCAGCTGAGCATGTGTTTGGGCAAGCCACCCGAGTGTGCGC	810
QY	721	TCAAGGAGCACTGGGCTCTGTGTGTGTGTGAACATCAAGTTCTCAGAGCTCTTCTAATCTGAGC	780
Db	811	TCAAGGAGCACTGGGCTCTGTGTGTGTGTGAACATCAAGTTCTCAGAGCTCTTCTAATCTGAGC	870
QY	781	GCGTTCCTGGGGGAGCACTACCTAGATGAGCGCGCTGCTGACAGGCCCTGGGGGCGGTCTCTG	840
Db	871	GCGTTCCTGGGGGAGCACTACCTAGATGAGCGCGCTGCTGACAGGCCCTGGGGGCGGTCTCTG	930
QY	841	ACTGAGGCGCTCTGCGAGAGGCTGTGGGCGCGGAGAGGCTGTTCGCTGCTGTGATCTGAT	900
Db	931	ACTGAGGCGCTCTGCGAGAGGCTGTGGGCGCGGAGAGGCTGTTCGCTGCTGTGATCTGAT	990
QY	901	GAGGCTGAC	909
Db	991	GAGGCTGAC	999

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RESULT 6
US-10-170-235-12745
; Sequence 12745, Application US/10170235
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
; TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
; FILE REFERENCE: CLO01380
; CURRENT APPLICATION NUMBER: US/10/170,235
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 42514
SEQ ID NO 12745
;
; LENGTH: 1959
; TYPE: DNA
;

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Db 969 GCCTTCTGGGGGCGACTACTAGTGGCCGCTGCTGCGAGGCGCTGCGGGGGGCTGTTCCTG 1028
 QY 841 ACTAGAGCCCTGCGAGAGGCTGTGGGCGGAGAGCTGTTCCGCTTGCTGCTCAGTGTGGAT 900
 Db 1029 ACTAGAGGCGCTGCGAGAGCTGTGTGGGCGGAGAGGCTGTTCCGCTTGCTGCTCAGTGTGGAT 1088
 QY 901 GAGGCTGAC 909
 Db 1089 GAGGCTGAC 1097

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RESULT 8
PCT-US00-26524B-339
Sequence 339, Application PC/TUS0026524B
GENERAL INFORMATION:
APPLICANT: Birse et. al.
TITLE OR INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
FILE REFERENCE: PA005FCT
CURRENT APPLICATION NUMBER: PCT/US00/26524B
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 339
LENGTH: 2045
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US00-26524B-339

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Query Match Similarity: 99.9%; Score 907.4; DB 1; Length 2045;
Best Local Similarity: 99.9%; Pred. No. 7,66-150;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCGCTATCCGGGTGCAGCCCGGCCCCGCTGCTGGAGAGAGATGATGCTGCTGCACTAC 60
Db 121 ATGGCGCTATCCGGGTGCAGCCCGGCCCCGCTGCTGGAGAGAGATGATGCTGCTGCACTAC 180
QY 61 TACGGGATGCTGTGCTTCACTTCACTTATTTTCCAGGTGTGTGGGCGGGCAACTGACCGAGTGC 120
Db 181 TACGGGATGCTGTGCTTCACTTCACTTATTTTCCAGGTGTGTGGGCGGGCAACTGACCGAGTGC 240
QY 121 GAGCTGAGAGCTCTGCGACCTTCTGCTGTGATGAGGCTCTTGCGCGCGCGGAGGCTTACCC 180
Db 241 GAGCTGAGAGCTCTGCGACCTTCTGCTGTGATGAGGCTCTTGCGCGCGCGGAGGCTTACCC 300
QY 181 CGGGCCCGCAGCGGCTAGAGCTCTGCTGAGCTGAGCGCGCGGCGCAGTGCAGCGAG 240
Db 301 CGGGCCCGCAGCGGCTAGAGCTCTGCTGAGCTGAGCGCGCGGCGCAGTGCAGCGAG 360
QY 241 AGCAACTGCGGCTGTGTTGGGCACTCTGCGGCTGTGCGCCGCAAGCACTGTGTCGG 300
Db 361 AGCAACTGCGGCTGTGTTGGGCACTCTGCGGCTGTGCGCCGCAAGCACTGTGTCGG 420
QY 301 CACCTGGGCGCAGCGGCGCGCGCAAGTCTCCAGAAACGTTAAGTTAAGGCACTTCC 360
Db 421 CACCTGGGCGCAGCGGCGCGCGCAAGTCTCCAGAAACGTTAAGTTAAGGCACTTCC 480
QY 361 AGCTTTCAAAGAGACAGAGGTTAGTCCGTCGCTCGCTCGGCAAGTCAAGCAGTTTCTCA 420
Db 481 AGCTTTCAAAGAGACAGAGGTTAGTCCGTCGCTCGCTCGGCAAGTCAAGCAGTTTCTCA 540
QY 421 AATTCTCAGCAGGCTCAGTGGGAGACAGGCTTCCCCCAACCAACGAGCGGCGAGT 480
Db 541 AATTCTCAGCAGGCTCAGTGGGAGACAGGCTTCCCCCAACCAACGAGCGGCGAGT 600
QY 481 CGGGCCCGGCGCAGTGTGTGTCCAGACGCGCGGAGAGAGGGGCCCGCAACCCAG 540
Db 601 CGGGCCCGGCGCAGTGTGTGTCCAGACGCGCGGAGAGAGGGGCCCGCAACCCAG 660

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QY	541	AAAGAGTCAGAGCCCGGCGAAGCTTCTCTGAAAGGCAAAAGTGAACCTGTGACATCCGGCTC	600
Db	661	CAGCAGTCAGAGCCCGGCGAAGCTTCTCTGAAAGGCAAAAGTGAACCTGTGACATCCGGCTC	720
QY	601	CGGGTTCGAGCAGAGTACTGTGAGCATGGGCGACGCTTGGAGCAGGGCGTGGCATCCCGG	660
Db	721	CGGGTTCGAGCAGAGTACTGTGAGCATGGGCGACGCTTGGAGCAGGGCGTGGCATCCCGG	780
QY	661	CGGCCCCAGAGCGCTGGCGCGGCGAGCTGAGCGTGTGTTGGGCAAGGCGACCCGACAGTGTCCGC	720
Db	781	CGGCCCCAGAGCGCTGGCGCGGCGAGCTGAGCGTGTGTTGGGCAAGGCGACCCGACAGTGTCCGC	840
QY	721	TCAAGGGGACCTGGGCTCTGTTGTTTGTGACATCAAGTTCTCAGAGCTCTCCTATCTGGAAC	780
Db	841	TCAAGGGACCTGGGCTCTGTTGTTTGTGACATCAAGTTCTCAGAGCTCTCCTATCTGGAAC	900
QY	781	GCTTCTTGGGGCGACTACTGAGTGGGCGCCCTGCTGAGGCGCCCTGGCGGGCGTGTCCYG	840
Db	901	GCTTCTTGGGGCGACTACTGAGTGGGCGCCCTGCTGAGGCGCCCTGGCGGGCGTGTCCYG	960
QY	841	ACTGAGGCCCCGCGAGAGGCTGTGTGGGCGGAGGCTGTTGGCTGCTGTGTCAAGTGTGAT	900
Db	961	ACTGAGGCCCCGCGAGAGGCTGTGTGGGCGGAGGCTGTTGGCTGCTGTGTCAAGTGTGAT	1020
QY	901	GAGGCTGAC 909	
Db	1021	GAGGCTGAC 1029	

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RESULT 9
US-09-669-445-2
; Sequence 2, Application US/09669445
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Apoptosis Related Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PTO02P1
; CURRENT APPLICATION NUMBER: US/09/669,445
; CURRENT FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US00/06642
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/126,018
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/139,638
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/149,449
; PRIOR FILING DATE: 1999-08-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2045
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-669-445-2

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Query Match	99.8%	Score 907.4	DB 30	Length 2045
Best Local Similarity	99.9%	Pred. No. 7,66-150		
Matches 908	Conservative 0	Mismatches 1	Indels 0	Gaps 0

QY	1	ATGGCGCTATCCGGAGTCGACCCCGGAGCCCGCTGCTGGAGAGAGATGAGTGCCTTGACTAC	60
DB	121	ATGGCGCTATCCGGAGTCGACCCCGGAGCCCGCTGCTGGAGAGAGATGAGTGCCTTGACTAC	180
QY	61	TACGGGATGCTGTGCTTACCGATATGTCAGGTGTGGCGGCGCACTGACCGAGTGC	120
DB	181	TACGGGATGCTGTGCTTACCGATATGTCAGGTGTGGCGGCGCACTGACCGAGTGC	240
QY	121	GAGCTGAGACTCTGCGCTTCTCTGCTGATGAGGCTCCTTGCGCGCCGCGAGGCTTACCC	180
DB	241	GAGCTGAGACTCTGCGCTTCTCTGCTGATGAGGCTCCTTGCGCGCCGCGAGGCTTACCC	300
QY	181	CGGGCCCGCAGCGGCTTAGACTCTCTGTGAGCTGAGAGCCCGCGGCGCAATGCGCGAG	240
DB	301	CGGGCCCGCAGCGGCTTAGACTCTCTGTGAGCTGAGAGCCCGCGGCGCAATGCGCGAG	360


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RESULT 11
US-10-100-683-2084
; Sequence 2084, Application US/10100683
; GENERAL INFORMATION:
; APPLICANT: Rosen, et al.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS900
; CURRENT APPLICATION NUMBER: US/10/100,683
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: US 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,845
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,599
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,632
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,892
; PRIOR FILING DATE: 1997-08-22
; Remaining Prior Application data removed - See file wrapper or PAM.
; NUMBER OF SEQ ID NOS: 13468
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2084
; LENGTH: 2045
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-100-683-2084

Query Match          99.8%; Score 907.4; DB 48; Length 2045;
Best Local Similarity 99.9%; Pred. No. 7.6e-150;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCGCTATCCGGGTCGACCCCGGCGCTGCTGGAGAGAGATGAGTCCCTGACTAC 60
DB 121 ATGGCGCTATCCGGGTCGACCCCGGCGCTGCTGGAGAGAGATGAGTCCCTGACTAC 180
QY 61 TACGGAGTCTGTGCTTCAACCGTATGTTGAGTGTGGGCGGCACTGACCGAGTGC 120
DB 181 TACGGAGTCTGTGCTTCAACCGTATGTTGAGTGTGGGCGGCACTGACCGAGTGC 240
QY 121 GAGCTGGAGTCTGTGCTTCTTCTGCTGATGAGGCTCTGCGCCCGCGAGGCTTAGCC 180
DB 241 GAGCTGGAGTCTGTGCTTCTTCTGCTGATGAGGCTCTGCGCCCGCGAGGCTTAGCC 300
QY 181 CGGGCCCGAGCGGCGCTTAAGAGCTCTGCTGAGTGAAGGCGCGCCCGAGGCTTAGCC 240
DB 301 CGGGCCCGAGCGGCGCTTAAGAGCTCTGCTGAGTGAAGGCGCGCCCGAGGCTTAGCC 360
QY 241 AGCAACTGTGGGCTGTGGGCAACTCTGCGGTGCTGGCGCCGCAAGCAAGCTGCTGCC 300
DB 361 AGCAACTGTGGGCTGTGGGCAACTCTGCGGTGCTGGCGCCGCAAGCAAGCTGCTGCC 420
QY 301 CACCTGGCGCGCAAGCGGCGCGCGCGAGTGTCTCCAGAAAGCTATAGCTTAGCACTTCC 360
DB 421 CACCTGGCGCGCAAGCGGCGCGCGCGAGTGTCTCCAGAAAGCTATAGCTTAGCACTTCC 480
QY 361 AGCTCTTCAAGAGAGAGAGGAGTGTGCTGCGCGCTGCGAGTCAAGCAATTTCTGCA 420
DB 481 AGCTCTTCAAGAGAGAGAGGAGTGTGCTGCGCGCTGCGAGTCAAGCAATTTCTGCA 540
QY 421 AATTCTCAGCAGGAGTGTGAGAGAGAGGCTTCCCGCAACCAAGCGGCGAGGAGT 480
DB 541 AATTCTCAGCAGGAGTGTGAGAGAGAGGCTTCCCGCAACCAAGCGGCGAGGAGT 600

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QY 481 CGGGCCCGAGCGGCTGTGCTGCTGAGAGGCGCGAGAGAGGCGCCCGAGCGCACTCCGAG 540
DB 601 CGGGCCCGAGCGGCTGTGCTGCTGAGAGGCGCGAGAGAGGCGCCCGAGCGCACTCCGAG 660
QY 541 CAGCAGTCAAGAGCGCGCAAGCTTCTCTGTAAGGCAAGTGAATCTGTGACATCCGCTC 600
DB 661 CAGCAGTCAAGAGCGCGCAAGCTTCTCTGTAAGGCAAGTGAATCTGTGACATCCGCTC 720
QY 601 CGGGTTCCAGCAGAGTACTGCGAGATGAGGCGCGAGCTTGGAGCAGAGCGGTGCAATCCGG 660
DB 721 CGGGTTCCAGCAGAGTACTGCGAGATGAGGCGCGAGCTTGGAGCAGAGCGGTGCAATCCGG 780
QY 661 CGGGCCCGAGCGGCTGTGCGCGAGCTGAGACGTTGTTGGGCAAGCGCACTGCTGCGC 720
DB 781 CGGGCCCGAGCGGCTGTGCGCGAGCTGAGACGTTGTTGGGCAAGCGCACTGCTGCGC 840
QY 721 TCAAGGAGACTGTGGCTGTGTTGTGATCAAGTTCTCAGAGCTTCTCTATCTGAGC 780
DB 841 TCAAGGAGACTGTGGCTGTGTTGTGATCAAGTTCTCAGAGCTTCTCTATCTGAGC 900
QY 781 GCTTCTGGGAGGACTACTGATGAGGCGCCCTGCTGCAAGCGCCGCGGCGGTTCCTG 840
DB 901 GCTTCTGGGAGGACTACTGATGAGGCGCCCTGCTGCAAGCGCCGCGGCGGTTCCTG 960
QY 841 ACTGAGGCGCTGCGAGAGGCTGTGGGCGGAGGCTGTTGCTGCTGCTGCTGAT 900
DB 961 ACTGAGGCGCTGCGAGAGGCTGTGGGCGGAGGCTGTTGCTGCTGCTGCTGAT 1020
QY 901 GAGGCTGAC 909
DB 1021 GAGGCTGAC 1029

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RESULT 12
US-10-106-698-349
; Sequence 349, Application US/10106698
; GENERAL INFORMATION:
; APPLICANT: Roben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: Patentin Ver. 3.0
; SEQ ID NO 349
; LENGTH: 2045
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-106-698-349

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Query Match          99.8%; Score 907.4; DB 48; Length 2045;
Best Local Similarity 99.9%; Pred. No. 7.6e-150;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCGCTATCCGGGTCGACCCCGGCGCTGCTGGAGAGAGATGAGTCCCTGACTAC 60
DB 121 ATGGCGCTATCCGGGTCGACCCCGGCGCTGCTGGAGAGAGATGAGTCCCTGACTAC 180
QY 61 TACGGAGTCTGTGCTTCAACCGTATGTTGAGTGTGGGCGGCACTGACCGAGTGC 120
DB 181 TACGGAGTCTGTGCTTCAACCGTATGTTGAGTGTGGGCGGCACTGACCGAGTGC 240
QY 121 GAGCTGGAGTCTGTGCTTCTTCTGCTGATGAGGCTCTGCGCCCGCGAGGCTTAGCC 180
DB 241 GAGCTGGAGTCTGTGCTTCTTCTGCTGATGAGGCTCTGCGCCCGCGAGGCTTAGCC 300

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QY 181 CCGGCCCCGAGCGGCTTAGAGCTCTGCTGAGCTGAGCGCCCGGCGAGTGCAG 240
Db 301 CCGGCCCCGAGCGGCTTAGAGCTCTGCTGAGCTGAGCGCCCGGCGAGTGCAG 360
QY 241 AGCAACTCGGCTGCTGAGGCACTCTGCGGCTGCGCCGCGCACTGCTGCGG 300
Db 361 AGCAACTCGGCTGCTGAGGCACTCTGCGGCTGCGCCGCGCACTGCTGCGG 420
QY 301 CACTGCGCGGCAAGCGGCGCGGCAAGTCTTCCAGAACTATAGTATGCACTCC 360
Db 421 CACTGCGCGGCAAGCGGCGCGGCAAGTCTTCCAGAACTATAGTATGCACTCC 480
QY 361 AGCTCTTCAAGAGAGCAGAGGGTACTCCCGCGCGCTGCGAGTCAAGCACTTCA 420
Db 481 AGCTCTTCAAGAGAGCAGAGGGTACTCCCGCGCGCTGCGAGTCAAGCACTTCA 540
QY 421 AATTCTCAGCAGAGTCTAGTGGAGACAGGCTCCCCCAACCAAGCGGCGAGGAGT 480
Db 541 AATTCTCAGCAGAGTCTAGTGGAGACAGGCTCCCCCAACCAAGCGGCGAGGAGT 600
QY 481 CCGGCGCGGCGGCTGCTGCTGCGAGCGGCGGAGAGGCGCCGCACTGCGAG 540
Db 601 CCGGCGCGGCGGCTGCTGCTGCGAGCGGCGGAGAGGCGCCGCACTGCGAG 660
QY 541 CAGCAGTCAAGAGCGGCGGCAAGCTTCTGTAAGGCAAGTCACTGTGACATCCGCTC 600
Db 661 CAGCAGTCAAGAGCGGCGGCAAGCTTCTGTAAGGCAAGTCACTGTGACATCCGCTC 720
QY 601 CCGGTTTCAGCAGAGTCTGAGCAGATGAGCGGCGGCTGAGCAGGCGGCTGAG 660
Db 721 CCGGTTTCAGCAGAGTCTGAGCAGATGAGCGGCGGCTGAGCAGGCGGCTGAG 780
QY 721 CCGGCCCCGAGCGGCTGCGGCGGCAAGTCTGTTGGGCAAGCGCAGTGTGCGC 720
Db 841 CCGGCCCCGAGCGGCTGCGGCGGCAAGTCTGTTGGGCAAGCGCAGTGTGCGC 840
QY 841 TCAAGGAGCTGAGGCTGCTGCTGTTGTGACATCAAGTCTCAGAGCTCTCTATCTGAC 780
Db 901 TCAAGGAGCTGAGGCTGCTGCTGTTGTGACATCAAGTCTCAGAGCTCTCTATCTGAC 900
QY 901 ACTGAGCGGCTGCGAGAGGCTGTGAGCGGCGGAGGCTGTGCTGCTGCTGAGT 900
Db 961 ACTGAGCGGCTGCGAGAGGCTGTGAGCGGCGGAGGCTGTGCTGCTGCTGAGT 1020
QY 901 GAGGCTGAC 909
Db 1021 GAGGCTGAC 1029

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; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,599
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,632
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13468
; SOFTWARE: Patencin Ver. 2.0
; SEQ ID NO: 2084
; LENGTH: 2045
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-001-793-2084

Query Match      99.8%; Score 907.4; DB 68; Length 2045;
Best Local Similarity 99.9%; Pred. No. 7,6e-150;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATGCGCTATCCGGGTCAACCCCGGCGGCTGCTGCTGAGAGAGATGAGTGCCTGACTAC 60
Db 121 AATGCGCTATCCGGGTCAACCCCGGCGGCTGCTGCTGAGAGAGATGAGTGCCTGACTAC 180
QY 61 TAACGGAGTCTGCTGCTTCAACCTATGTTTCAAGTGTGTGGGCGGCACTGACGAGTGC 120
Db 181 TAACGGAGTCTGCTGCTTCAACCTATGTTTCAAGTGTGTGGGCGGCACTGACGAGTGC 240
QY 121 GAGCTGAGCTCTGCTGCTTCTGCTGATGAGGCTCTGAGCGGCGGAGGCTTAC 180
Db 241 GAGCTGAGCTCTGCTGCTTCTGCTGATGAGGCTCTGAGCGGCGGAGGCTTAC 300
QY 241 GAGGCCCCGAGCGGCTTGAAGCTCTGCTGAGTGAAGCGGCGGCACTGCGCGAG 240
Db 301 GAGGCCCCGAGCGGCTTGAAGCTCTGCTGAGTGAAGCGGCGGCACTGCGCGAG 360
QY 301 AGCAACTGCGGCTGCTGAGGCACTCTGCTGAGGCTGAGCGGCGGCACTGCTGCGG 300
Db 421 AGCAACTGCGGCTGCTGAGGCACTCTGCTGAGGCTGAGCGGCGGCACTGCTGCGG 420
QY 421 CACTGAGCGGCAAGCGGCGGCAAGTCTTCAAGACGCTTATGAGTATGAGCACTCC 360
Db 541 CACTGAGCGGCAAGCGGCGGCAAGTCTTCAAGACGCTTATGAGTATGAGCACTCC 480
QY 541 AGCTCTTCAAGAGAGCAGAGGGTACTGCTGCGGCTGCGGCAAGTCAAGCACTTCA 420
Db 661 AGCTCTTCAAGAGAGCAGAGGGTACTGCTGCGGCTGCGGCAAGTCAAGCACTTCA 540
QY 661 AATTCTCAGCAGAGTCTAGTGGAGAGCAGGCTCCCCCAACCAAGCGGCGAGGAGT 480
Db 781 AATTCTCAGCAGAGTCTAGTGGAGAGCAGGCTCCCCCAACCAAGCGGCGAGGAGT 600
QY 781 CCGGCGCGGCGGCTGCTGCTGCGAGCGGCGGAGAGGCGCCGCACTGCGAG 540
Db 901 CCGGCGCGGCGGCTGCTGCTGCGAGCGGCGGAGAGGCGCCGCACTGCGAG 660
QY 901 CCGGTTTCAGCAGAGTCTGAGCAGATGAGCGGCGGCTGAGCAGGCGGCTGAG 780
Db 1021 CCGGTTTCAGCAGAGTCTGAGCAGATGAGCGGCGGCTGAGCAGGCGGCTGAG 900
QY 1021 CCGGCCCCGAGCGGCTGCTGCTGCGAGCGGCGGAGAGGCGCCGCACTGCGAG 540
Db 1141 CCGGCCCCGAGCGGCTGCTGCTGCGAGCGGCGGAGAGGCGCCGCACTGCGAG 660
QY 1141 CAGCAGTCAAGAGCGGCGGCAAGCTTCTGTAAGGCAAGTCACTGTGACATCCGCTC 600
Db 1261 CAGCAGTCAAGAGCGGCGGCAAGCTTCTGTAAGGCAAGTCACTGTGACATCCGCTC 720
QY 1261 CCGGTTTCAGCAGAGTCTGAGCAGATGAGCGGCGGCTGAGCAGGCGGCTGAG 780
Db 1381 CCGGTTTCAGCAGAGTCTGAGCAGATGAGCGGCGGCTGAGCAGGCGGCTGAG 900
QY 1381 CCGGCCCCGAGCGGCTGCTGCTGCGAGCGGCGGAGAGGCGCCGCACTGCGAG 540
Db 1501 CCGGCCCCGAGCGGCTGCTGCTGCGAGCGGCGGAGAGGCGCCGCACTGCGAG 660
QY 1501 CCGGTTTCAGCAGAGTCTGAGCAGATGAGCGGCGGCTGAGCAGGCGGCTGAG 780
Db 1621 CCGGTTTCAGCAGAGTCTGAGCAGATGAGCGGCGGCTGAGCAGGCGGCTGAG 900
QY 1621 TCAAGGAGCTGAGGCTGCTGCTGTTGTGACATCAAGTCTCAGAGCTCTCTATCTGAC 780
Db 1741 TCAAGGAGCTGAGGCTGCTGCTGTTGTGACATCAAGTCTCAGAGCTCTCTATCTGAC 900

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RESULT 13
US-11-001-793-2084
; Sequence 2084, Application US/11001793
; GENERAL INFORMATION:
; APPLICANT: Rosen, et al.
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS900
; CURRENT APPLICATION NUMBER: US/11/001,793
; CURRENT FILING DATE: 2004-12-02
; PRIOR APPLICATION NUMBER: US/10/100,683
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: US 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: US 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: US 60/056,845
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/043,580

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QY 781 GCCTTCGAGGCGCACTACCTGAGTGGGCGCCCTGCTGAGGCGCCCTGCGGGCGGCTTCTG 840
DB 901 GCCTTCGAGGCGCACTACCTGAGTGGGCGCCCTGCTGAGGCGCCCTGCGGGCGGCTTCTG 960
QY 841 ACTGAGCGCCCTGCGAGAGGCTGTGGGCGGGAGGCTGTTCGCTGTGTGTCACTGTGAT 900
DB 961 ACTGAGCGCCCTGCGAGAGGCTGTGGGCGGGAGGCTGTTCGCTGTGTGTCACTGTGAT 1020
QY 901 GAGGCTGAC 909
DB 1021 GAGGCTGAC 1029

RESULT 14
US-09-652-355-10438
Sequence 10438, Application US/09652355
GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew M.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1192-001
CURRENT APPLICATION NUMBER: US/09/652,355
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,136
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 11227
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10438
LENGTH: 2460
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(2460)
OTHER INFORMATION: n = A,T,C or G
US-09-652-355-10438

* Query Match 99.8%; Score 907.4; DB 29; Length 2460;
Best Local Similarity 99.9%; Pred. No. 7.5e-150;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCCCTATCCGGGTGAGACCCCGGCGCCGCTGCTGGAGAGAGATGCTGAGACTAC 60
DB 165 ATGGCCCTATCCGGGTGAGACCCCGGCGCCGCTGCTGGAGAGAGATGAGTCCCTGAGACTAC 224
QY 61 TACGGGATGCTGTGCTTCAACCTATGTTGAGGTGGTGGCGGCACTGACCGAGTGC 120
DB 225 TACGGGATGCTGTGCTTCAACCTATGTTGAGGTGGTGGCGGCACTGACCGAGTGC 284
QY 121 GAGCTGAGAGCTCTGCGCTTTCGCTGAGAGAGAGCTCTGCGCGCCCGAGAGCTTAGCC 180
DB 285 GAGCTGAGAGCTCTGCGCTTTCGCTGAGAGAGAGCTCTGCGCGCCCGAGAGCTTAGCC 344
QY 181 CGGGCCCGGAGCGGCTAGAGCTCTGCTGAGAGCTGAGAGCGCGGGGAGTGGCGAG 240
DB 345 CGGGCCCGGAGCGGCTAGAGCTCTGCTGAGAGCTGAGAGCGCGGGGAGTGGCGAG 404
QY 241 AGCAACCTGCGGCTGCTGGGGCACTCTGCGCGTGTGGCGCCCGCAACGACTGTGCGG 300
DB 405 AGCAACCTGCGGCTGCTGGGGCACTCTGCGCGTGTGGCGCCCGCAACGACTGTGCGG 464
QY 301 CACCTGCGCGGAGAGGGGCGCGCGGCAAGTCTCCAGAGAGCTATAGCTATGCACTCC 360
DB 465 CACCTGCGCGGAGAGGGGCGCGCGGCAAGTCTCCAGAGAGCTATAGCTATGCACTCC 524
QY 361 AGCTCTTCAAGAGAGCAGAGGTAAGTGCCTGCGCGTGGAGTCAAGCACTTCTGCA 420
DB 525 AGCTCTTCAAGAGAGCAGAGGTAAGTGCCTGCGCGTGGAGTCAAGCACTTCTGCA 584
QY 421 AATTTTCAGAGAGGTGATGGAGAGAGAGTCCCCCCCAACCAAGCGGCGAGCGAGT 480
DB 585 AATTTTCAGAGAGGTGATGGAGAGAGAGTCCCCCCCAACCAAGCGGCGAGCGAGT 644

QY 481 CGGGCCCGGCGCAGTGTGTGTGCAAGAGCGCGGAGAGAGGGGCCCCAGCGGACCCGAG 540
DB 645 CGGGCCCGGCGCAGTGTGTGTGCAAGAGCGCGGAGAGAGGGGCCCCAGCGGACCCGAG 704
QY 541 CAGCAGTCAAGAGCCCGCAGACCTTCTCTGAAAGGCAAGTGAAGCTGTGACATCCGGCTC 600
DB 705 CAGCAGTCAAGAGCCCGCAGACCTTCTCTGAAAGGCAAGTGAAGCTGTGACATCCGGCTC 764
QY 601 CGGGTTCAGAGCAGATGATCTGCGAGCATGGGCGCAGGCTTGGAGCAGGGCGTGGCATCCGG 660
DB 765 CGGGTTCAGAGCAGATGATCTGCGAGCATGGGCGCAGGCTTGGAGCAGGGCGTGGCATCCGG 824
QY 661 CGGGCCCGGCGCCTGGCGCGGAGCTGAGAGTGTGTTGGCGAGGCGCAGGAGTGTGGCG 720
DB 825 CGGGCCCGGCGCCTGGCGCGGAGCTGAGAGTGTGTTGGCGAGGCGCAGGAGTGTGGCG 884
QY 721 TCAAGGACCTGAGCTGTGTGTTGTGACATCAAGTTCTCAGAGCTTCTATCTGAGC 780
DB 885 TCAAGGACCTGAGCTGTGTGTTGTGACATCAAGTTCTCAGAGCTTCTATCTGAGC 944
QY 781 GCCTTCGAGGCGCACTACTGAGTGGCGCCCTGCTGCAAGCCCTGCGGGCGTGTCTG 840
DB 945 GCCTTCGAGGCGCACTACTGAGTGGCGCCCTGCTGCAAGCCCTGCGGGCGTGTCTG 1004
QY 841 ACTGAGCGCCCTGCGAGAGGCTGTGGGCGGGAGGCTGTGCGCTGCTGATGATGAT 900
DB 1005 ACTGAGCGCCCTGCGAGAGGCTGTGGGCGGGAGGCTGTGCGCTGCTGATGATGAT 1064
QY 901 GAGGCTGAC 909
DB 1065 GAGGCTGAC 1073

RESULT 15
US-09-652-814-9661
Sequence 9661, Application US/09652814
GENERAL INFORMATION:
APPLICANT: Holzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1191-001
CURRENT APPLICATION NUMBER: US/09/652,814
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,109
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 10797
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9661
LENGTH: 2460
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(2460)
OTHER INFORMATION: n = A,T,C or G
US-09-652-814-9661

* Query Match 99.8%; Score 907.4; DB 29; Length 2460;
Best Local Similarity 99.9%; Pred. No. 7.5e-150;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCCCTATCCGGGTGAGACCCCGGCGCCGCTGCTGGAGAGAGATGCTGAGACTAC 60
DB 165 ATGGCCCTATCCGGGTGAGACCCCGGCGCCGCTGCTGGAGAGAGATGCTGAGACTAC 224
QY 61 TACGGGATGCTGTGCTTCAACCTATGTTGAGGTGGTGGCGGCACTGACCGAGTGC 120
DB 225 TACGGGATGCTGTGCTTCAACCTATGTTGAGGTGGTGGCGGCACTGACCGAGTGC 284
QY 121 GAGCTGAGAGCTCTGCGCTTTCGCTGATGATGAGCTCTGCGCGCGCGGAGGCTTAGCC 180
DB 285 GAGCTGAGAGCTCTGCGCTTTCGCTGATGATGAGCTCTGCGCGCGCGGAGGCTTAGCC 344

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 12, 2005, 16:30:05 ; Search time 56 Seconds
(without alignments)
1767.946 Million cell updates/sec

Title: US-10-030-271-2

Perfect score: 1550
Sequence: 1 MALSGSTAPCWEDECDLYD.....LREAVGRKRVLLVSEAD 303

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	99.5	318	14	US-10-001-254-18
2	1543	99.5	326	14	US-10-296-539-1
3	1543	99.5	366	14	US-10-106-698-4626
4	1413	91.2	304	14	US-10-013-477-11
5	1404	90.6	319	9	US-09-925-302-758
6	1404	90.6	319	10	US-09-925-302-758
7	987	63.7	242	15	US-10-296-115-1220
8	614.5	39.6	318	9	US-09-935-223-4
9	614.5	39.6	318	9	US-09-733-167-1
10	608.5	39.3	318	9	US-09-935-223-6
11	608.5	39.3	318	9	US-09-733-167-3
12	545.5	35.2	217	9	US-09-799-777-26
13	514	33.2	101	14	US-10-001-254-8

14	422	27.2	210	9	US-09-733-167-6	Sequence 6, Appli
15	265.5	17.1	146	14	US-10-001-254-38	Sequence 36, Appl
16	227	14.6	99	14	US-10-001-254-36	Sequence 36, Appl
17	225.5	14.5	114	9	US-09-733-167-5	Sequence 5, Appli
18	224	14.5	99	14	US-10-001-254-37	Sequence 37, Appl
19	136	8.8	340	15	US-10-352-839-3	Sequence 3, Appli
20	135.5	8.7	163	16	US-10-437-963-106027	Sequence 106027, A
21	132	8.5	384	15	US-10-425-114-42732	Sequence 42732, A
22	120	7.7	182	16	US-10-437-963-116837	Sequence 116837, A
23	120	7.7	399	15	US-10-425-114-64272	Sequence 64272, A
24	119.5	7.7	19723	15	US-10-084-846A-5	Sequence 5, Appli
25	119	7.7	547	16	US-10-437-963-184154	Sequence 184154, A
26	118.5	7.6	459	16	US-10-437-963-186228	Sequence 186228, A
27	118	7.6	281	15	US-10-425-114-72807	Sequence 72807, A
28	117	7.5	247	16	US-10-437-963-164918	Sequence 164918, A
29	116.5	7.5	218	16	US-10-437-963-117951	Sequence 117951, A
30	116.5	7.5	649	16	US-10-437-963-117651	Sequence 117651, A
31	115	7.4	82	16	US-10-437-963-110001	Sequence 110001, A
32	114.5	7.4	126	16	US-10-767-701-33992	Sequence 33992, A
33	114.5	7.4	134	16	US-10-767-701-42899	Sequence 42899, A
34	114.5	7.4	741	16	US-10-437-963-193189	Sequence 193189, A
35	114.5	7.4	19608	15	US-10-084-846A-8	Sequence 8, Appli
36	114	7.4	134	16	US-10-437-963-185509	Sequence 185509, A
37	113.5	7.3	291	16	US-10-437-963-195777	Sequence 195777, A
38	113.5	7.3	599	15	US-10-094-749-1828	Sequence 1828, Ap
39	113.5	7.3	758	15	US-10-108-260A-2612	Sequence 2612, Ap
40	113	7.3	155	16	US-10-437-963-103601	Sequence 103601, A
41	112.5	7.3	240	16	US-10-437-963-190104	Sequence 190104, A
42	112.5	7.3	19652	15	US-10-084-846A-7	Sequence 7, Appli
43	111	7.2	178	16	US-10-437-963-203446	Sequence 203446, A
44	111	7.2	347	15	US-10-425-114-51867	Sequence 51867, A
45	110	7.1	539	15	US-10-425-114-39176	Sequence 39176, A

ALIGNMENTS

RESULT 1
US-10-001-254-18
; Sequence 18, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sung Hyung
; APPLICANT: Roth, Wilfried
; APPLICANT: Steiner-Llewen, Frank
; TITLE OF INVENTION: No. US20030049702A1e1 Death Domain Proteins
; FILE REFERENCE: P-IL 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-254-18
Query Match 99.5% Score 1543; DB 14; Length 318;
Best Local Similarity 99.7% Pred. No. 9.7e-12;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALSGSTAPCWEDECDLYDGMKSLHMFVVGQLTRECLELLAFLLDDEAPGAGGLA 60
DB 1 MALSGSTAPCWEDECDLYDGMKSLHMFVVGQLTRECLELLAFLLDDEAPGAGGLA 60

QY 61 RARSGLELLLELERRGQCGESNLRLLGQLRLVLAHDDLPHLARRRRVPSPERYSYGTS 120
DB 61 RARSGLELLLELERRGQCGESNLRLLGQLRLVLAHDDLPHLARRRRVPSPERYSYGTS 120
QY 121 SSSKRTGSCRRRRSSSSANSQCGQWETGSPPTKQRRSRGRPSGARRRRRGAPAPQ 180
DB 121 SSSKRTGSCRRRRSSSSANSQCGQWETGSPPTKQRRSRGRPSGARRRRRGAPAPQ 180
QY 181 QOSEPARPSSGKVTCDIRLRAVEYCEHGPALBEGVARRPQALAROLDVFGQATAVLR 240
DB 181 QOSEPARPSSGKVTCDIRLRAVEYCEHGPALBEGVARRPQALAROLDVFGQATAVLR 240
QY 241 SRDLGSVVCIDIKFSELSYLDAPFWGDYLSGALLQALRGVFLTEALREAVGRAVRLVSV 300
DB 241 SRDLGSVVCIDIKFSELSYLDAPFWGDYLSGALLQALRGVFLTEALREAVGRAVRLVSV 300
QY 301 EAD 303
DB 301 EAD 303

RESULT 2

US-10-296-539-1
; Sequence 1, Application US/10296539
; Publication No. US20030165933A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: TANG, Y. TOM
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: YUE, Henry
; APPLICANT: BURFORD, Neil
; APPLICANT: DING, Li
; APPLICANT: ELIJOT, Vicki S.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: BAUGHN, Mariah R.
; TITLE OF INVENTION: REGULATORS OF APOPTOSIS
; FILE REFERENCE: PI-0307 PCT
; CURRENT APPLICATION NUMBER: US/10/296,539
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: 60/209,407; 60/250,326
; PRIOR FILING DATE: 2000-06-01; 2000-11-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030165933A1 3102521CD1
US-10-296-539-1

Query Match 99.5%; Score 1543; DB 14; Length 326;
Best Local Similarity 99.7%; Pred. No. 1e-126;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALSGSTPAPCWEDECDLDYGMLSLHRMFEVVGQLTECELELLAFLLDEAPGAGGLA 60
DB 1 MALSGSTPAPCWEDECDLDYGMLSLHRMFEVVGQLTECELELLAFLLDEAPGAGGLA 60
QY 61 RARSGLELLLELERRGQCGESNLRLLGQLRLVLAHDDLPHLARRRRVPSPERYSYGTS 120
DB 61 RARSGLELLLELERRGQCGESNLRLLGQLRLVLAHDDLPHLARRRRVPSPERYSYGTS 120
QY 121 SSSKRTGSCRRRRSSSSANSQCGQWETGSPPTKQRRSRGRPSGARRRRRGAPAPQ 180
DB 121 SSSKRTGSCRRRRSSSSANSQCGQWETGSPPTKQRRSRGRPSGARRRRRGAPAPQ 180
QY 181 QOSEPARPSSGKVTCDIRLRAVEYCEHGPALBEGVARRPQALAROLDVFGQATAVLR 240
DB 181 QOSEPARPSSGKVTCDIRLRAVEYCEHGPALBEGVARRPQALAROLDVFGQATAVLR 240
QY 241 SRDLGSVVCIDIKFSELSYLDAPFWGDYLSGALLQALRGVFLTEALREAVGRAVRLVSV 300
DB 241 SRDLGSVVCIDIKFSELSYLDAPFWGDYLSGALLQALRGVFLTEALREAVGRAVRLVSV 300

DB 241 SRDLGSVVCIDIKFSELSYLDAPFWGDYLSGALLQALRGVFLTEALREAVGRAVRLVSV 300
QY 301 EAD 303
DB 301 EAD 303

RESULT 3

US-10-106-698-4626
; Sequence 4626, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 4626
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-698-4626

Query Match 99.5%; Score 1543; DB 14; Length 366;
Best Local Similarity 99.7%; Pred. No. 1.1e-126;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALSGSTPAPCWEDECDLDYGMLSLHRMFEVVGQLTECELELLAFLLDEAPGAGGLA 60
DB 41 MALSGSTPAPCWEDECDLDYGMLSLHRMFEVVGQLTECELELLAFLLDEAPGAGGLA 100
QY 61 RARSGLELLLELERRGQCGESNLRLLGQLRLVLAHDDLPHLARRRRVPSPERYSYGTS 120
DB 101 RARSGLELLLELERRGQCGESNLRLLGQLRLVLAHDDLPHLARRRRVPSPERYSYGTS 160
QY 121 SSSKRTGSCRRRRSSSSANSQCGQWETGSPPTKQRRSRGRPSGARRRRRGAPAPQ 180
DB 161 SSSKRTGSCRRRRSSSSANSQCGQWETGSPPTKQRRSRGRPSGARRRRRGAPAPQ 220
QY 181 QOSEPARPSSGKVTCDIRLRAVEYCEHGPALBEGVARRPQALAROLDVFGQATAVLR 240
DB 221 QOSEPARPSSGKVTCDIRLRAVEYCEHGPALBEGVARRPQALAROLDVFGQATAVLR 280
QY 241 SRDLGSVVCIDIKFSELSYLDAPFWGDYLSGALLQALRGVFLTEALREAVGRAVRLVSV 300
DB 281 SRDLGSVVCIDIKFSELSYLDAPFWGDYLSGALLQALRGVFLTEALREAVGRAVRLVSV 340
QY 301 EAD 303
DB 341 EAD 343

RESULT 4

US-10-013-477-11
; Sequence 11, Application US/10013477
; Publication No. US20030049732A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Apoptosis Related Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PTO02P1
; CURRENT APPLICATION NUMBER: US/10/013,477
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: 09/669,445
; PRIOR FILING DATE: 2000-09-25

;; PRIOR APPLICATION NUMBER: PCT/US00/06642
;; PRIOR FILING DATE: 2000-03-15
;; PRIOR APPLICATION NUMBER: 60/126, 018
;; PRIOR FILING DATE: 1999-03-24
;; PRIOR APPLICATION NUMBER: 60/139, 638
;; PRIOR FILING DATE: 1999-06-17
;; PRIOR APPLICATION NUMBER: 60/149, 449
;; PRIOR FILING DATE: 1999-08-18
;; SOFTWARE: Patent In Ver. 2.0
;; SEQ ID NO 11
;; LENGTH: 304
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-013-477-11

Query Match 91.2%; Score 1413; DB 14; Length 304;
Best Local Similarity 99.6%; Pred. No. 2,2e-115;
Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 MLSLHMFVVGQQLTECELELLAFLLDEAPGAAGLAARSGLELLLEERRGQCGESN 82
DB 1 MLSLHMFVVGQQLTECELELLAFLLDEAPGAAGLAARSGLELLLEERRGQCGESN 60
QY 83 LALLGQLRVLAHDLPLHARKRRRPPVSPERYSYGTSSSKRTGSCRRRRQSSSSANS 142
DB 61 LALLGQLRVLAHDLPLHARKRRRPPVSPERYSYGTSSSKRTGSCRRRRQSSSSANS 120
QY 143 OOGOMETGSPPTKORRSRGRSPGARRRRGAPAPPOOSPPARRSSGKTCIDRLRV 202
DB 121 OOGOMETGSPPTKORRSRGRSPGARRRRGAPAPPOOSPPARRSSGKTCIDRLRV 180
QY 203 RAEYCEHGFALQGVASRRRQALARQLDVFGQATAVLARSDIGSVVCDIKFSELSTLDAF 262
DB 181 RAEYCEHGFALQGVASRRRQALARQLDVFGQATAVLARSDIGSVVCDIKFSELSTLDAF 240
QY 263 WGDYLSGALLQALRGVFTLEALREAVGREAVRLVSVDEAD 303
DB 241 WGDYLSGALLQALRGVFTLEALREAVGREAVRLVSVDEAD 281

RESULT 5
US-09-925-302-758
;; Sequence 758, Application US/09925302
;; Patent No. US20020044941A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;; FILE REFERENCE: PA104
;; CURRENT APPLICATION NUMBER: US/09/925,302
;; CURRENT FILING DATE: 2001-08-10
;; PRIOR APPLICATION NUMBER: PCT/US00/05918
;; PRIOR FILING DATE: 2000-03-08
;; PRIOR APPLICATION NUMBER: 60/124, 270
;; PRIOR FILING DATE: 1999-03-12
;; NUMBER OF SEQ ID NOS: 896
;; SOFTWARE: Patent In Ver. 2.0
;; SEQ ID NO 758
;; LENGTH: 319
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-925-302-758

Query Match 90.6%; Score 1404; DB 9; Length 319;
Best Local Similarity 99.6%; Pred. No. 1.4e-114;
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALSGSTAPCWEDECDLDYGMLSLHMFVVGQQLTECELELLAFLLDEAPGAAGLA 60
DB 41 MALSGSTAPCWEDECDLDYGMLSLHMFVVGQQLTECELELLAFLLDEAPGAAGLA 100
QY 61 PARSGLELLLEERRGQCGESNLRLLGQLRVLAHDLPLHARKRRRPPVSPERYSYGT 120

DB 101 PARSGLELLLEERRGQCGESNLRLLGQLRVLAHDLPLHARKRRRPPVSPERYSYGT 160
QY 121 SSSKRTGSCRRRRQSSSSANSOOGOMETGSPPTKORRSRGRPGGARRRRGAPAPQ 180
DB 161 SSSKRTGSCRRRRQSSSSANSOOGOMETGSPPTKORRSRGRPGGARRRRGAPAPQ 220
QY 181 OOSEPARPSSGKTCIDRLRVRAEYCEHGFALQGVASRRRQALARQLDVFGQATAVLR 240
DB 221 OOSEPARPSSGKTCIDRLRVRAEYCEHGFALQGVASRRRQALARQLDVFGQATAVLR 280
QY 241 SRDLGSVVCDIKFSELSTLDAFWDYLSGALLQ 273
DB 281 SRDLGSVVCDIKFSELSTLDAFWDYLSGALLQ 313

RESULT 6
US-09-925-302-758
;; Sequence 758, Application US/09925302
;; Publication No. US20030064072A9
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;; FILE REFERENCE: PA104
;; CURRENT APPLICATION NUMBER: US/09/925,302
;; CURRENT FILING DATE: 2001-08-10
;; PRIOR APPLICATION NUMBER: PCT/US00/05918
;; PRIOR FILING DATE: 2000-03-08
;; PRIOR APPLICATION NUMBER: 60/124, 270
;; PRIOR FILING DATE: 1999-03-12
;; NUMBER OF SEQ ID NOS: 896
;; SOFTWARE: Patent In Ver. 2.0
;; SEQ ID NO 758
;; LENGTH: 319
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-925-302-758

Query Match 90.6%; Score 1404; DB 10; Length 319;
Best Local Similarity 99.6%; Pred. No. 1.4e-114;
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALSGSTAPCWEDECDLDYGMLSLHMFVVGQQLTECELELLAFLLDEAPGAAGLA 60
DB 41 MALSGSTAPCWEDECDLDYGMLSLHMFVVGQQLTECELELLAFLLDEAPGAAGLA 100
QY 61 PARSGLELLLEERRGQCGESNLRLLGQLRVLAHDLPLHARKRRRPPVSPERYSYGT 120
DB 101 PARSGLELLLEERRGQCGESNLRLLGQLRVLAHDLPLHARKRRRPPVSPERYSYGT 160
QY 121 SSSKRTGSCRRRRQSSSSANSOOGOMETGSPPTKORRSRGRPGGARRRRGAPAPQ 180
DB 161 SSSKRTGSCRRRRQSSSSANSOOGOMETGSPPTKORRSRGRPGGARRRRGAPAPQ 220
QY 181 OOSEPARPSSGKTCIDRLRVRAEYCEHGFALQGVASRRRQALARQLDVFGQATAVLR 240
DB 221 OOSEPARPSSGKTCIDRLRVRAEYCEHGFALQGVASRRRQALARQLDVFGQATAVLR 280
QY 241 SRDLGSVVCDIKFSELSTLDAFWDYLSGALLQ 273
DB 281 SRDLGSVVCDIKFSELSTLDAFWDYLSGALLQ 313

RESULT 7
US-10-296-115-1220
;; Sequence 1220, Application US/10296115
;; Publication No. US20040053248A1
;; GENERAL INFORMATION:
;; APPLICANT: Hyseq Inc
;; TITLE OF INVENTION: NO. US20040053248A1el Nucleic Acids and Polypeptides
;; FILE REFERENCE: 784PCT
;; CURRENT APPLICATION NUMBER: US/10/296,115
;; CURRENT FILING DATE: 2002-11-18
;; PRIOR APPLICATION NUMBER: US09/488,725

TITLE OF INVENTION: Compositions For And Methods Of Making The Same
FILE REFERENCE: TJU499
CURRENT APPLICATION NUMBER: US/09/935,223
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 09/723,450
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/276,993
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 08/859,167
PRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 318
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Novel Sequence
US-09-935-223-6

Query Match 39.3%; Score 608.5; DB 9; Length 318;
Best Local Similarity 43.5%; Pred. No. 6 4e-45;
Matches 131; Conservative 56; Mismatches 93; Indels 21; Gaps 5;

Qy 12 WEDECDLYGMLSHRMEVVGQUTCELEBLAFL-LDEAPGAAGIARASGLELL 70
Db 12 WPEERGEQEHGLYSLHRMFDIVGTHLTHRDVLSFLFVDVIDDHERGL--IRNGDFLL 69
Qy 71 ELERRGCGESNLRLIGQLRLVLAHDDLPHLARRRVRVSP---ERYSGTSSSKRTE 127
Db 70 ALERQGRCDENFRQVLDLRIITHDDLPLYTLKKRAVCDLDVKYLEETSIKYVTPR 129
Qy 128 GSCRRRRQSSSSANQCGMETGSPPTK-----RGRSRGPRSGARRRRGAPAPQOQ 182
Db 130 ALSDEPRPPQSKTVPPHYVPCPTSGSQMCKSRPARGRTTLLSQRRR----- 180
Qy 183 SEPAPSSSEKVTCDIRLRVRAEYCEHGPALRQGVASRRPQALRQLDVFGQATVLSR 242
Db 181 -KSVTPDPKQKQTCIRLRVRAEYCOHETALQGNVFSNKQDPLERQFERFNQANTLKS 239
Qy 243 DLGSVVCIDIKFSELSYLDAPFMDYLSGALLQALRGVPLTEALREAVGREAVRLVSVDA 302
Db 240 DLGSITCIDIKFSELSYLDAPFMDYLSGALLQALRGVPLTEALREAVGREAVRLVSVDE 299
Qy 303 D 303
Db 300 D 300

RESULT 11
US-09-733-167-3
Sequence 3, Application US/09733167
Patent No. US20020099009A1
GENERAL INFORMATION:
APPLICANT: Peter, Marcus
APPLICANT: Krammer, Peter
TITLE OF INVENTION: Protein for Regulation of Apoptosis
FILE REFERENCE: 4121-120
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: PCT/DE99/01712
PRIOR FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: German Patent Application No. US20020099009A1 198 25 621.3
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 318
TYPE: PRT
ORGANISM: Mus musculus
US-09-733-167-3

Query Match 39.3%; Score 608.5; DB 9; Length 318;

Best Local Similarity 43.5%; Pred. No. 6 4e-45;
Matches 131; Conservative 56; Mismatches 93; Indels 21; Gaps 5;

Qy 12 WEDECDLYGMLSHRMEVVGQUTCELEBLAFL-LDEAPGAAGIARASGLELL 70
Db 12 WPEERGEQEHGLYSLHRMFDIVGTHLTHRDVLSFLFVDVIDDHERGL--IRNGDFLL 69
Qy 71 ELERRGCGESNLRLIGQLRLVLAHDDLPHLARRRVRVSP---ERYSGTSSSKRTE 127
Db 70 ALERQGRCDENFRQVLDLRIITHDDLPLYTLKKRAVCDLDVKYLEETSIKYVTPR 129
Qy 128 GSCRRRRQSSSSANQCGMETGSPPTK-----RGRSRGPRSGARRRRGAPAPQOQ 182
Db 130 ALSDEPRPPQSKTVPPHYVPCPTSGSQMCKSRPARGRTTLLSQRRR----- 180
Qy 183 SEPAPSSSEKVTCDIRLRVRAEYCEHGPALRQGVASRRPQALRQLDVFGQATVLSR 242
Db 181 -KSVTPDPKQKQTCIRLRVRAEYCOHETALQGNVFSNKQDPLERQFERFNQANTLKS 239
Qy 243 DLGSVVCIDIKFSELSYLDAPFMDYLSGALLQALRGVPLTEALREAVGREAVRLVSVDA 302
Db 240 DLGSITCIDIKFSELSYLDAPFMDYLSGALLQALRGVPLTEALREAVGREAVRLVSVDE 299
Qy 303 D 303
Db 300 D 300

RESULT 12
US-09-799-777-26
Sequence 26, Application US/09799777
Patent No. US20020091244A1
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Cortley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baugh, Mariah
APPLICANT: Sather, Susan
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/799,777
FILING DATE: 06-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/002,485
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0459 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 217 amino acids
TYPE: amino acid
STRANDEDNESS: single


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; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: UTRSN0706
; CLONE: 1638407
; SEQUENCE DESCRIPTION: SEQ ID NO: 26 :
US-09-799-777-26

Query Match      35.2%; Score 545.5; DB 9; Length 217;
Best Local Similarity 79.5%; Pred. No. 1.3e-39;
Matches 116; Conservative 1; Mismatches 20; Indels 9; Gaps 2;

QY 164 PSGGARRRRRGAPAPQOQSEPARPSSEKVTCT-----DIRLRVRAEYCEHGPALRGV 217
DB 52 PDGGGEPQ---PHPSSSQSPDPPLAKAGDTVMGKQAKORDIRLVRALRYCEHGPALRGV 108
QY 218 ASRRPQALRQLDVFGQATAVLRSDIGSVVCDIKFSELSYLDAPWGDYLSGALLQALRG 277
DB 109 ASRRPQALRQLDVFGQATAVLRSDIGSVVCDIKFSELSYLDAPWGDYLSGALLQALRG 168
QY 278 VFLTEALREAVGRVAVRLVSVDEAD 303
DB 169 VFLTEALREAVGRVAVRLVSVDEAD 194

RESULT 13
US-10-001-254-8
; Sequence 8, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sug Hyung
; APPLICANT: Roch, Wilfred
; APPLICANT: Stenmer-Liwen, Frank
; TITLE OF INVENTION: No. US20030049702A1e1 Death Domain Proteins
; FILE REFERENCE: P-LJ 5037
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-254-8

Query Match      33.2%; Score 514; DB 14; Length 101;
Best Local Similarity 99.0%; Pred. No. 3e-37;
Matches 100; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 WEDECLDYGYGMLSHRMFEVVGQLTCELELLAFLLDEAGAGGAGARASGLLELLE 71
DB 1 WEDECLDYGYGMLSHRMFEVVGQLTCELELLAFLLDEAGAGGAGARASGLLELLE 60
QY 72 LERRGCGGSNRLIGQLLRVLRARDLPLRLARKRRRPVP 112
DB 61 LERRGCGGSNRLIGQLLRVLRARDLPLRLARKRRRPVP 101

RESULT 14
US-09-733-167-6
; Sequence 6, Application US/09733167
; Patent No. US20020099009A1
; GENERAL INFORMATION:
; APPLICANT: Peter, Marcus
; APPLICANT: Kramer, Peter
; TITLE OF INVENTION: Protein for Regulation of Apoptosis
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; FILE REFERENCE: 4121-120
; CURRENT APPLICATION NUMBER: US/09/733,167
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/DE99/01712
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: German Patent Application No. US20020099009A1 198 25 621.3
; PRIOR FILING DATE: 1998-06-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C-DEDD, which is a deletion mutant of human DEDD comprising amino
US-09-733-167-6
; OTHER INFORMATION: acids 109-318 of the naturally occurring huma DEDD.

Query Match      27.2%; Score 422; DB 9; Length 210;
Best Local Similarity 52.3%; Pred. No. 8.2e-29;
Matches 81; Conservative 30; Mismatches 34; Indels 10; Gaps 1;

QY 149 TGSPPTKRQRRSGRGSGARRRRRGAPAPQOQSEPARPSSEKVTCDIRLRVRAEYCE 208
DB 48 TSGPQMSKRPARRATGSGQRRK-----KSVTPPKKQTCDIRLRVRAEYCE 97
QY 209 HGPALGEGVASSRRQALRQLDVFGQATAVLRSDIGSVVCDIKFSELSYLDAPWGDYLS 268
DB 98 HETALQGVNSKQDPLERQERENQANTIKSDLSIICDIFSELSYLDAPWGDYIN 157
QY 269 GALLQALRGVFLTEALREAVGRVAVRLVSVDEAD 303
DB 158 GLLLEALKGVTFTSLKQAVGHEAIKLVNDEAD 192
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RESULT 15
US-10-001-254-38
; Sequence 38, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Godzik, Adam
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sug Hyung
; APPLICANT: Roch, Wilfred
; APPLICANT: Stenmer-Liwen, Frank
; TITLE OF INVENTION: No. US20030049702A1e1 Death Domain Proteins
; FILE REFERENCE: P-LJ 5037
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US/10/001,254
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Danio rerio
US-10-001-254-38

Query Match      17.1%; Score 265.5; DB 14; Length 146;
Best Local Similarity 43.5%; Pred. No. 2.7e-15;
Matches 64; Conservative 13; Mismatches 23; Indels 47; Gaps 4;

QY 12 WEDECLDYGYGMLSHRMFEVVGQLTCELELLAFLLDEA-----P 53
DB 1 WEDECLSYETELSHEIFEIVGQLTCECGE-VAFLDFTYPGKHPLDPGWETDLP 59
QY 54 GAAG-----GLARSGLELLLELERRGCGGSNRL 85
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Db	60	GPDGSPQANTPCPRILKSWORMQPKGCSIASRHRPKSGVELLELERRGYLSDANLRP	119
Qy	86	LGQLRVLARHDLPHILARKRRRPVSP	112
Db	120	LQQLRLITRHDVLPFVSQKGRVSP	146

Search completed: February 12, 2005, 16:35:32
Job time : 57 secs

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99	8	2.6	452	7	ABO75449	ABO75449 Pseudomon	172	7	2.3	16	6	ABU09743	Abu09743 N-myristo
100	8	2.6	462	3	AAY92344	Aay92344 Human can	173	7	2.3	16	7	ADBA7663	AdbA7663 Human HGP
101	8	2.6	474	2	AAR14676	Aar14676 Rabbit vi	174	7	2.3	16	8	ADRA4056	AdrA4056 Human HGP
102	8	2.6	493	7	ABO83717	ABO83717 Pseudomon	175	7	2.3	31	2	AAY02997	Aay02997 Fragment
103	8	2.6	520	6	ABU34144	ABU34144 Protein e	176	7	2.3	31	7	ADA07832	Ada07832 Human sec
104	8	2.6	599	7	ADF70409	ADF70409 Orphan re	177	7	2.3	31	8	ADNA1249	Adna1249 Novel hum
105	8	2.6	632	7	ADG75710	ADG75710 Human pro	178	7	2.3	40	4	AAO12076	Aao12076 Human pol
106	8	2.6	679	7	ABO76654	ABO76654 Pseudomon	179	7	2.3	41	4	ABG02584	Abg02584 Novel hum
107	8	2.6	679	7	ABO80204	ABO80204 Pseudomon	180	7	2.3	46	3	AAB34183	Aab34183 Gene 28 h
108	8	2.6	690	7	ABO83604	ABO83604 Pseudomon	181	7	2.3	48	3	AAB34513	Aab34513 Human sec
109	8	2.6	693	8	ADRO8900	ADr08900 Human pro	182	7	2.3	57	5	ABP33077	Abp33077 Human ORF
110	8	2.6	712	4	ABG00341	ABg00341 Novel hum	183	7	2.3	61	3	AAG33160	Aag33160 Arabidops
111	8	2.6	736	8	AD116342	ADi16342 Human pro	184	7	2.3	61	4	AAW22110	Aaw22110 Peptide #
112	8	2.6	748	3	AAAG31702	AAag31702 Arabidops	185	7	2.3	61	4	ABBA4515	Abba4515 Peptide #
113	8	2.6	783	3	ABM83777	ABm83777 Human dia	186	7	2.3	61	4	AAAB38563	AAab38563 Peptide #
114	8	2.6	805	4	ABG24026	ABg24026 Novel hum	187	7	2.3	61	4	ABBA27344	Abb27344 Protein #
115	8	2.6	810	7	ABO63231	ABo63231 Klebsiell	188	7	2.3	61	4	AAW78316	Aaw78316 Human bon
116	8	2.6	812	8	ABM84231	ABm84231 Human dia	189	7	2.3	61	4	AAW65701	Aaw65701 Human liv
117	8	2.6	828	8	ADN24077	ADn24077 Bacterial	190	7	2.3	61	4	ABG59924	Abg59924 Human liv
118	8	2.6	835	3	AAAG31412	AAag31412 Arabidops	191	7	2.3	61	5	ABG47342	Abg47342 Human pep
119	8	2.6	840	7	ADG75711	ADg75711 Human pro	192	7	2.3	64	4	ABG22428	Abg22428 Novel hum
120	8	2.6	847	6	ADA55477	ADa55477 Human pro	193	7	2.3	66	4	AAU41567	Aau41567 Proptonib
121	8	2.6	882	7	ADBE78996	ADe78996 Human pro	194	7	2.3	67	5	ABM38066	ABm38066 Proptonib
122	8	2.6	897	8	ABM84232	ABm84232 Human dia	195	7	2.3	67	5	AAO19126	Aao19126 Human cit
123	8	2.6	902	7	ADBE58718	ADe58718 Human pro	196	7	2.3	68	4	AAU64738	Aau64738 Proptonib
124	8	2.6	902	8	ADH09584	ADh09584 Human hos	197	7	2.3	68	6	ABM61257	ABm61257 Proptonib
125	8	2.6	908	8	ABM84230	ABm84230 Human dia	198	7	2.3	72	4	AAU46000	Aau46000 Proptonib
126	8	2.6	909	3	AAAG31701	AAag31701 Arabidops	199	7	2.3	72	6	ABM42519	ABm42519 Proptonib
127	8	2.6	914	3	AAAG31700	AAag31700 Arabidops	200	7	2.3	73	8	ABO60213	ABo60213 Human gen
128	8	2.6	929	3	AAAG31411	AAag31411 Arabidops	201	7	2.3	78	4	AAU59388	Aau59388 Proptonib
129	8	2.6	937	6	ABP59344	ABp59344 Arabidops	202	7	2.3	78	6	ABM55907	ABm55907 Proptonib
130	8	2.6	937	6	ABP59344	ABp59344 Arabidops	203	7	2.3	79	4	AAU43608	Aau43608 Proptonib
131	8	2.6	945	6	ABU92034	ABu92034 Human pro	204	7	2.3	79	6	ABM40127	ABm40127 Proptonib
132	8	2.6	949	8	ADH09583	ADh09583 Human hos	205	7	2.3	82	5	ABP09067	ABp09067 Human ORF
133	8	2.6	952	3	AAAY70014	AAay70014 Human pro	206	7	2.3	84	3	AAAG26049	AAg26049 Zea may
134	8	2.6	952	8	ADH09582	ADh09582 Human hos	207	7	2.3	85	4	AAU48994	Aau48994 Proptonib
135	8	2.6	952	8	ADH09316	ADh09316 Human USP	208	7	2.3	85	4	ABBI5294	ABb15294 Human net
136	8	2.6	952	8	ADP24284	ADp24284 PRO polyp	209	7	2.3	85	5	ABP64016	ABp64016 Human ORF
137	8	2.6	952	8	ADP97378	ADp97378 Human USP	210	7	2.3	85	6	ABM45513	ABm45513 Proptonib
138	8	2.6	963	7	ADJ68716	ADj68716 Human hea	211	7	2.3	86	4	AAU45772	Aau45772 Proptonib
139	8	2.6	963	8	ADH09586	ADh09586 Human hos	212	7	2.3	86	4	ABR00929	ABr00929 Gene 216
140	8	2.6	963	8	ADH09587	ADh09587 Human hos	213	7	2.3	86	6	ABM42291	ABm42291 Proptonib
141	8	2.6	963	8	ADL23951	ADl23951 Deubiquit	214	7	2.3	86	6	ABU55857	ABu55857 Human gen
142	8	2.6	989	7	ABO68689	ABo68689 Pseudomon	215	7	2.3	86	6	ADU35696	ADu35696 Human gen
143	8	2.6	1032	4	AAU01206	AAu01206 Human cas	216	7	2.3	86	8	ADL81524	ADl81524 Human gen
144	8	2.6	1032	5	AAU73247	AAu73247 Human pla	217	7	2.3	89	3	AAAG26065	AAg26065 Zea may
145	8	2.6	1032	5	AAAG79554	AAg79554 Human CAR	218	7	2.3	98	3	AAAB43733	Aab43733 Human can
146	8	2.6	1059	6	ABU12111	ABu12111 Human pro	219	7	2.3	99	4	AAU00391	AAu00391 Human sec
147	8	2.6	1066	4	ABG24025	ABg24025 Novel hum	220	7	2.3	99	5	ABP22275	ABp22275 Human ORF
148	8	2.6	1085	4	AAAB38692	AAab38692 Human pol	221	7	2.3	99	8	ADH89008	ADh89008 Human POL
149	8	2.6	1089	2	AAW82396	AAw82396 Human UBP	222	7	2.3	102	4	AAW94871	Aaw94871 Human rep
150	8	2.6	1089	4	AAAB3691	AAab3691 Human pol	223	7	2.3	103	3	AAAG00834	AAg00834 Human sec
151	8	2.6	1089	4	ABG23332	ABg23332 Novel hum	224	7	2.3	104	3	AAAG51165	AAg51165 Arabidops
152	8	2.6	1116	7	ABO75628	ABo75628 Pseudomon	225	7	2.3	110	4	AAU42088	AAu42088 Proptonib
153	8	2.6	1125	4	ABG21348	ABg21348 Novel hum	226	7	2.3	110	6	ABM38607	ABm38607 Proptonib
154	8	2.6	1127	4	AAAM40477	AAam40477 Human pol	227	7	2.3	110	6	AAE35272	AAe35272 Human P45
155	8	2.6	1127	4	AAAM40478	AAam40478 Human pol	228	7	2.3	113	2	AAAY36969	Aay36969 Antno act
156	8	2.6	1127	4	ADG32650	ADg32650 Human nov	229	7	2.3	113	4	ABG19394	ABg19394 Novel hum
157	8	2.6	1131	4	ABG21347	ABg21347 Novel hum	230	7	2.3	113	6	ABR00932	ABr00932 Gene 216
158	8	2.6	1142	4	ABG24027	ABg24027 Novel hum	231	7	2.3	113	6	ABU55860	ABu55860 Human gen
159	8	2.6	1274	5	AAU75578	AAu75578 Human ubi	232	7	2.3	113	8	ADJ36949	ADj36949 Human gen
160	8	2.6	1274	5	ADU70043	ADu70043 Human hea	233	7	2.3	113	8	ADL81527	ADl81527 Human gen
161	8	2.6	1292	7	ADCC30915	ADc30915 Human nov	234	7	2.3	115	6	ADAE5708	ADa5708 Human pro
162	8	2.6	1317	5	ABG32160	ABg32160 Novel hum	235	7	2.3	115	7	ADH85583	ADh85583 Enterococ
163	8	2.6	1388	4	ABG21344	ABg21344 Novel hum	236	7	2.3	116	4	AAU58632	AAu58632 Proptonib
164	8	2.6	1604	5	AAU82715	AAu82715 Antno aci	237	7	2.3	116	6	ABM55151	ABm55151 Proptonib
165	8	2.6	1700	7	ADCC10002	ADc10002 Human NOV	238	7	2.3	117	5	ADU17219	ADu17219 NOYX prot
166	8	2.6	1958	2	AAAB60620	AAab60620 Protein E	239	7	2.3	117	7	ADD45022	ADd45022 Human pro
167	8	2.6	5217	6	ABUW0675	ABuW0675 Photoxhab	240	7	2.3	118	7	ADD45018	ADd45018 Human mac
168	7	2.3	7	7	ABU09729	ABu09729 Novel hum	241	7	2.3	118	5	AAAB3048	AAa33048 Human mac
169	7	2.3	7	7	ADBA7649	ADbA7649 Human GPC	242	7	2.3	118	5	AD117220	ADi17220 Human NOV
170	7	2.3	7	8	ADRA40555	ADrA40555 Human HGP	243	7	2.3	118	5	AD117228	ADi17228 Human NOV
171	7	2.3	10	4	AAAG93538	AAg93538 Transcrip	244	7	2.3	123	2	AAW23891	AAw23891 Human E1b

245	7	2.3	124	4	AAU44043	Aau44043	Propionib	318	7	2.3	195	2	AAW83898	Aaw83898	Bovine in
246	7	2.3	124	5	AAW50525	Aaw50525	Sentinel	319	7	2.3	195	5	ABG32983	Abg32983	Bovine je
247	7	2.3	124	6	ABM40562	Abm40562	Propionib	320	7	2.3	195	5	ABO73033	AbO73033	Pseudomon
248	7	2.3	126	6	AAU51805	Aau51805	Propionib	321	7	2.3	197	7	ADC01496	AdC01496	Enterohae
249	7	2.3	126	6	ABM48324	Abm48324	Propionib	322	7	2.3	197	7	ABO77791	AbO77791	Pseudomon
250	7	2.3	127	7	ADe08938	AdE08938	Novel pro	323	7	2.3	200	5	ABG30870	AbG30870	P. yoellii
251	7	2.3	127	7	ADe08937	AdE08937	Novel pro	324	7	2.3	202	4	ABB64930	AbB64930	Drosophi1
252	7	2.3	128	4	AAU58056	Aau58056	Propionib	325	7	2.3	202	4	ABB67278	AbB67278	Drosophi1
253	7	2.3	128	6	ABM54575	Abm54575	Propionib	326	7	2.3	210	7	ABO63406	AbO63406	Klebsiell
254	7	2.3	130	4	AAU31276	Aau31276	Novel hum	327	7	2.3	212	4	AAG73899	AaG73899	Human col
255	7	2.3	131	7	ADe07849	AdE07849	Novel pro	328	7	2.3	212	7	ABO63529	AbO63529	Klebsiell
256	7	2.3	134	4	AAg73965	AaG73965	Human col	329	7	2.3	212	8	ADN13992	AdN13992	Human pro
257	7	2.3	134	7	ABO70316	AbO70316	Pseudomon	330	7	2.3	213	8	ADN19470	AdN19470	Human PRO
258	7	2.3	134	7	ABO77324	AbO77324	Pseudomon	331	7	2.3	214	7	ABO79049	AbO79049	Pseudomon
259	7	2.3	136	7	ABO75786	AbO75786	Pseudomon	332	7	2.3	214	8	ADP43674	AdP43674	Human PMM
260	7	2.3	142	7	ABO71511	AbO71511	Pseudomon	333	7	2.3	215	7	ABO68954	AbO68954	Pseudomon
261	7	2.3	147	3	AAH32633	AaH32633	Eucalyptu	334	7	2.3	217	2	AAH68556	AaH68556	Klebsiell
262	7	2.3	147	8	ADM87674	AdM87674	Human EST	335	7	2.3	220	2	AAH57361	AaH57361	Translati
263	7	2.3	150	4	AAU18305	Aau18305	Human end	336	7	2.3	220	3	AAH08246	AaH08246	Arabidops
264	7	2.3	151	4	AAU44529	Aau44529	Propionib	337	7	2.3	224	6	ADA48140	AdA48140	Rice prot
265	7	2.3	151	6	ABM41048	Abm41048	Propionib	338	7	2.3	224	8	ADR96071	AdR96071	Novel S.
266	7	2.3	153	4	AAU17322	Aau17322	Novel sig	339	7	2.3	225	6	ABU02036	AbU02036	S. pneumo
267	7	2.3	153	7	ADB94030	AdB94030	Human nov	340	7	2.3	225	8	ADK46786	AdK46786	Streptoco
268	7	2.3	154	8	ADR10124	AdR10124	Human pro	341	7	2.3	227	8	ADP43673	AdP43673	Human PMM
269	7	2.3	155	3	AAH33880	AaH33880	Zea maye	342	7	2.3	230	3	AAH08245	AaH08245	Arabidops
270	7	2.3	155	8	ADH22519	AdH22519	Human tra	343	7	2.3	237	5	ABG92821	AbG92821	Thermophi
271	7	2.3	159	6	ABM65418	Abm65418	Propionib	344	7	2.3	240	7	ABO68955	AbO68955	Pseudomon
272	7	2.3	160	7	ABO71712	AbO71712	Pseudomon	345	7	2.3	240	7	ABO68955	AbO68955	Pseudomon
273	7	2.3	160	8	AD16359	Ad16359	Human pro	346	7	2.3	241	8	ABM82437	AbM82437	Tumour-as
274	7	2.3	161	7	ABO63735	AbO63735	Klebsiell	347	7	2.3	241	8	ADN21995	AdN21995	Bacterial
275	7	2.3	163	8	ADP81260	AdP81260	Protein o	348	7	2.3	243	2	AAH37299	AaH37299	Amtno aci
276	7	2.3	165	4	ABR00933	AbR00933	Gene 216	349	7	2.3	243	3	ADN24753	AdN24753	Bacterial
277	7	2.3	165	6	ABU55861	AbU55861	Human gen	350	7	2.3	246	4	AAE00639	AaE00639	Human fib
278	7	2.3	165	8	ADJ36950	AdJ36950	Human gen	351	7	2.3	246	4	AAE00640	AaE00640	Human fib
279	7	2.3	165	8	ADL81528	AdL81528	Human gen	352	7	2.3	246	8	ADR86103	AdR86103	Aspergill
280	7	2.3	166	4	AAU16609	Aau16609	Human nov	353	7	2.3	246	8	ADS21739	AdS21739	Bacterial
281	7	2.3	166	4	AAU40009	Aau40009	Propionib	354	7	2.3	247	2	AAH31793	AaH31793	Human fib
282	7	2.3	166	6	ABM36528	Abm36528	Propionib	355	7	2.3	247	3	AAH42005	AaH42005	Arabidops
283	7	2.3	166	6	ABU55678	AbU55678	Human nov	356	7	2.3	247	3	AAH52568	AaH52568	Arabidops
284	7	2.3	166	8	ABM84271	Abm84271	Human dia	357	7	2.3	247	3	AAH44802	AaH44802	Zea maye
285	7	2.3	170	4	AAU20144	Aau20144	Human DNA	358	7	2.3	248	2	AAH31791	AaH31791	Human fib
286	7	2.3	170	5	ABG91393	AbG91393	Novel hum	359	7	2.3	248	5	ABH78096	AbH78096	Amtno aci
287	7	2.3	170	8	ABO58515	AbO58515	Human gen	360	7	2.3	249	7	ABO80226	AbO80226	Pseudomon
288	7	2.3	172	2	AAW09281	Aaw09281	Human mat	361	7	2.3	253	8	AD139286	Ad139286	S. hygro
289	7	2.3	172	2	AAW09280	Aaw09280	Human mat	362	7	2.3	253	8	AD139256	Ad139256	S. epider
290	7	2.3	172	2	AAH93959	AaH93959	Human tau	363	7	2.3	255	4	AAH82105	AaH82105	Pseudomon
291	7	2.3	172	2	AAW31700	Aaw31700	Human int	364	7	2.3	255	7	ABO62558	AbO62558	Klebsiell
292	7	2.3	172	2	AAW44108	Aaw44108	Mature hu	365	7	2.3	256	3	AAH17737	AaH17737	Arabidops
293	7	2.3	173	2	AAW74460	Aaw74460	Human int	366	7	2.3	259	4	AAU37467	AaU37467	Staphyloc
294	7	2.3	173	2	AAW74461	Aaw74461	Human int	367	7	2.3	259	6	ABM71340	AbM71340	Staphyloc
295	7	2.3	173	2	ADP05649	AdP05649	Bacterial	368	7	2.3	260	3	AAH17816	AaH17816	Arabidops
296	7	2.3	173	7	ADM04746	AdM04746	Human pro	369	7	2.3	260	4	AAH79851	AaH79851	Corynebac
297	7	2.3	173	7	ABO75581	AbO75581	Pseudomon	370	7	2.3	260	8	ADN73667	AdN73667	Thale cre
298	7	2.3	177	7	ABO78617	AbO78617	Pseudomon	371	7	2.3	263	3	AAH17815	AaH17815	Arabidops
299	7	2.3	177	8	ADG22530	AdG22530	Cyanophag	372	7	2.3	264	7	ABO72311	AbO72311	Pseudomon
300	7	2.3	178	3	AAH41424	AaH41424	Human ORF	373	7	2.3	265	7	ABO80404	AbO80404	Pseudomon
301	7	2.3	178	4	ABR00931	AbR00931	Gene 216	374	7	2.3	265	8	ADN25444	AdN25444	Bacterial
302	7	2.3	178	4	ABP09514	AbP09514	Human ORF	375	7	2.3	266	3	AAH78552	AaH78552	Human RGF
303	7	2.3	178	6	ABU55859	AbU55859	Human gen	376	7	2.3	266	3	AAH7858	AaH7858	Human RGF
304	7	2.3	178	8	ADJ36948	AdJ36948	Human gen	377	7	2.3	266	6	ABG74160	AbG74160	Human fib
305	7	2.3	178	8	ADL81526	AdL81526	Human gen	378	7	2.3	266	6	ABG73848	AbG73848	Human fib
306	7	2.3	179	7	ABO81658	AbO81658	Human gen	379	7	2.3	266	6	ABG72719	AbG72719	Recombina
307	7	2.3	184	8	ADN17366	AdN17366	Bacterial	380	7	2.3	266	6	ABG72713	AbG72713	Recombina
308	7	2.3	186	7	ABO83504	AbO83504	Pseudomon	381	7	2.3	267	1	AAH2964	AaH2964	Encoded b
309	7	2.3	188	5	ABH04638	AbH04638	Human tet	382	7	2.3	267	2	AAH48064	AaH48064	FCF-3 CDN
310	7	2.3	191	3	AAH08247	AaH08247	Arabidops	383	7	2.3	267	2	AAW22600	AaW22600	Human fib
311	7	2.3	194	3	AAH51164	AaH51164	Arabidops	384	7	2.3	267	4	AAH50709	AaH50709	Human fib
312	7	2.3	194	3	ABO78339	AbO78339	Pseudomon	385	7	2.3	267	4	AAH00645	AaH00645	Human fib
313	7	2.3	195	1	AAH30076	AaH30076	Sequence	386	7	2.3	267	4	AAH56551	AaH56551	Human fib
314	7	2.3	195	2	AAH04541	AaH04541	Bovine in	387	7	2.3	267	4	AAH50277	AaH50277	Human RGF
315	7	2.3	195	2	AAW09289	Aaw09289	Human com	388	7	2.3	267	5	AAH18810	AaH18810	Human RGF
316	7	2.3	195	2	AAW44107	Aaw44107	Human int	389	7	2.3	267	5	ABH99124	AbH99124	Human fib
317	7	2.3	195	2	AAW73227	Aaw73227	Bovine in	390	7	2.3	267	8	ADM94750	AdM94750	Human fib

391	7	2.3	268	2	AAR75703	Aar75703 Human FGF	464	7	2.3	285	8	ADM93510	Adm93510 Human NOV
392	7	2.3	268	2	AAR70813	Aar70813 FGF-5, 3/	465	7	2.3	285	8	ADM93512	Adm93512 Human NOV
393	7	2.3	268	2	AAR80780	Aar80780 Fibroblas	466	7	2.3	285	8	ADM93508	Adm93508 Human NOV
394	7	2.3	268	2	AAW75715	Aaw75715 Fibroblas	467	7	2.3	285	8	ADM93514	Adm93514 Human NOV
395	7	2.3	268	2	AAW53031	Aaw53031 Fibroblas	468	7	2.3	285	8	ADM93518	Adm93518 Human NOV
396	7	2.3	268	2	AAW08585	Aaw08585 Human FGF	469	7	2.3	289	8	ADU67796	Adu67796 T. thermo
397	7	2.3	268	2	AAW31792	Aaw31792 Human FGF	470	7	2.3	289	8	ADU66808	Adu66808 T. thermo
398	7	2.3	268	3	AAV32337	Aav32337 Human fib	471	7	2.3	289	8	ADK01086	Adk01086 DNA polym
399	7	2.3	268	3	AAV90414	Aav90414 FGF-5, SE	472	7	2.3	289	8	ADJ79305	Adj79305 T. thermo
400	7	2.3	268	3	AAAB10296	Aab10296 Fibroblas	473	7	2.3	289	8	ADJ84745	Adj84745 T. thermu
401	7	2.3	268	4	AAAB1660	Aab1660 GFP5 prot	474	7	2.3	289	8	ADM75533	Adm75533 DNA polym
402	7	2.3	268	4	AAE00636	Aae00636 Human MUS	475	7	2.3	289	8	ADM66200	Adm66200 T. thermo
403	7	2.3	268	4	AAE00642	Aae00642 Human fib	476	7	2.3	289	8	ADDO4253	Ado04253 T. thermo
404	7	2.3	268	4	AAE04405	Aae04405 Human fib	477	7	2.3	289	8	ADP82330	Adp82330 DNA polym
405	7	2.3	268	4	AAAB50701	Aab50701 Human fib	478	7	2.3	292	3	AAAG40208	Aag40208 Arabidops
406	7	2.3	268	4	AAAB5816	Aab5816 Human fib	479	7	2.3	295	5	ABBB55001	Abb55001 Human PRO
407	7	2.3	268	6	ABP54276	Abp54276 Human fib	480	7	2.3	295	5	ABBB5607	Abb5607 Human ang
408	7	2.3	268	6	ADA95451	Ada95451 Fibroblas	481	7	2.3	295	6	ABU56619	Abu56619 Lung canc
409	7	2.3	268	7	ADC34580	Adc34580 Human fib	482	7	2.3	295	7	ADD10659	Add10659 Human sec
410	7	2.3	268	7	ADD66124	Add66124 Fibroblas	483	7	2.3	295	7	ADD37412	Add37412 Human sec
411	7	2.3	268	7	ADH92004	Adh92004 Fibroblas	484	7	2.3	295	7	ADD37412	Add37412 Human sec
412	7	2.3	268	8	ADS20334	Ads20334 Fibroblas	485	7	2.3	295	7	ADN38796	Adn38796 Cancer/an
413	7	2.3	268	8	ADT97922	Adt97922 Human ker	486	7	2.3	295	8	ADPA1620	Adpa1620 Human sec
414	7	2.3	269	7	ABO79905	Abot79905 Pseudomon	487	7	2.3	295	8	ADPA3803	Adpa3803 Human PRO
415	7	2.3	271	6	ADA47978	Ada47978 Rice prot	488	7	2.3	295	8	ADK83148	Adk83148 Human PRO
416	7	2.3	272	8	ADN46632	Adn46632 Thermococ	489	7	2.3	296	6	ABO27185	Abot27185 Protein e
417	7	2.3	273	6	ABUL6404	Abul6404 Protein e	490	7	2.3	297	7	ABO70186	Abot70186 Pseudomon
418	7	2.3	273	7	ABO67947	Abot67947 Pseudomon	491	7	2.3	298	7	ADC87387	Adc87387 Human GPC
419	7	2.3	273	7	ABO82987	Abot82987 Pseudomon	492	7	2.3	299	8	ADJ76361	Adj76361 Marker ge
420	7	2.3	276	4	AAU37525	Aau37525 Staphyloc	493	7	2.3	304	4	AAW93719	Aaw93719 Human pol
421	7	2.3	278	4	AAAG6910	Aag6910 Arabidops	494	7	2.3	304	4	AAAB72383	Aab72383 Human car
422	7	2.3	278	4	AAE02480	Aae02480 Arabidops	495	7	2.3	304	4	AAAB72384	Aab72384 Murine ca
423	7	2.3	278	8	ADE37069	Ade37069 Plant yle	496	7	2.3	304	6	ABR58661	Abri58661 Human can
424	7	2.3	278	8	AD143863	Adi43863 Plant tra	497	7	2.3	304	8	ADJ75656	Adj75656 Marker ge
425	7	2.3	278	7	ADDO1839	Ado01839 Thalecres	498	7	2.3	304	8	ADJ13634	Adj13634 Human pro
426	7	2.3	279	7	ABO81782	Abot81782 Pseudomon	499	7	2.3	305	4	AAU55194	Aau55194 Enterococ
427	7	2.3	281	7	ADE28785	Ade28785 Human NOV	500	7	2.3	305	6	ABU29145	Abu29145 Protein e
428	7	2.3	281	7	ADE28777	Ade28777 Human NOV	501	7	2.3	306	4	AAU34399	Aau34399 Staphyloc
429	7	2.3	281	7	ADE28793	Ade28793 Human NOV	502	7	2.3	310	4	AAU34380	Aau34380 Staphyloc
430	7	2.3	281	7	ADE28799	Ade28799 Human NOV	503	7	2.3	312	3	AAAB13058	Aab13058 Cyclic pl
431	7	2.3	281	7	ADE28797	Ade28797 Human NOV	504	7	2.3	312	3	AAAB23255	Aab23255 Streptomy
432	7	2.3	281	7	ADE28789	Ade28789 Human NOV	505	7	2.3	312	7	ADBO8326	Adbo8326 Novel pro
433	7	2.3	281	7	ADE28787	Ade28787 Human NOV	506	7	2.3	313	7	ABO73121	Abot73121 Pseudomon
434	7	2.3	281	7	ADE28795	Ade28795 Human NOV	507	7	2.3	314	7	ABO70090	Abot70090 Pseudomon
435	7	2.3	281	7	ADE28791	Ade28791 Human NOV	508	7	2.3	318	6	ABU36529	Abu36529 Protein e
436	7	2.3	281	7	ABO69002	Abot69002 Pseudomon	509	7	2.3	318	6	ABR55201	Abri55201 Amino ac1
437	7	2.3	281	7	ABO76152	Abot76152 Pseudomon	510	7	2.3	319	7	ABO74811	Abot74811 Pseudomon
438	7	2.3	281	8	ADM93532	Adm93532 Human NOV	511	7	2.3	319	4	AAU63124	Aau63124 Propionib
439	7	2.3	281	8	ADM93538	Adm93538 Human NOV	512	7	2.3	319	6	ABM59643	Abm59643 Propionib
440	7	2.3	281	8	ADM93540	Adm93540 Human NOV	513	7	2.3	321	3	AAAG14409	Aag14409 Arabidops
441	7	2.3	281	8	ADM93542	Adm93542 Human NOV	514	7	2.3	321	7	ADH85922	Adh85922 Enterococ
442	7	2.3	281	8	ADM93544	Adm93544 Human NOV	515	7	2.3	322	4	AAU37394	Aau37394 Staphyloc
443	7	2.3	281	8	ADM93530	Adm93530 Human NOV	516	7	2.3	323	4	AAAG52567	Aag52567 Arabidops
444	7	2.3	281	8	ADM93534	Adm93534 Human NOV	517	7	2.3	323	3	AAAG42004	Aag42004 Arabidops
445	7	2.3	281	8	ADM93522	Adm93522 Human NOV	518	7	2.3	323	3	ABO00535	Abot00535 Novel hum
446	7	2.3	281	8	ADM93536	Adm93536 Human NOV	519	7	2.3	323	8	AD143585	Adi43585 Plant tra
447	7	2.3	283	4	AAAB68051	Aab68051 Amino ac1	520	7	2.3	323	8	ADDO03389	Ado003389 Thalecres
448	7	2.3	283	4	AAAG90222	Aag90222 C glutami	521	7	2.3	324	6	ABR42537	Abri42537 Clorobloc
449	7	2.3	284	3	AAAG17736	Aag17736 Arabidops	522	7	2.3	325	4	AAAB79411	Aab79411 Corynebac
450	7	2.3	284	6	ABU34729	Abu34729 Protein e	523	7	2.3	325	4	AAAG31986	Aag31986 C glutami
451	7	2.3	284	6	ADA48496	Ada48496 Rice prot	524	7	2.3	325	7	ADJ70753	Adj70753 Human hea
452	7	2.3	284	7	ADU11706	Adu11706 Rice prot	525	7	2.3	325	7	ABO79420	Abot79420 Pseudomon
453	7	2.3	284	7	ABO78826	Abot78826 Pseudomon	526	7	2.3	330	3	AAAG14408	Aag14408 Arabidops
454	7	2.3	285	7	ADE28767	Ade28767 Human NOV	527	7	2.3	330	7	ABO69827	Abot69827 Pseudomon
455	7	2.3	285	7	ADE28773	Ade28773 Human NOV	528	7	2.3	330	8	ADT61489	Adt61489 A. thalia
456	7	2.3	285	7	ADE28769	Ade28769 Human NOV	529	7	2.3	335	7	ADB70078	Adb70078 C. neofo
457	7	2.3	285	7	ADE28765	Ade28765 Human NOV	530	7	2.3	336	3	AAAG50996	Aag50996 Arabidops
458	7	2.3	285	7	ADE28763	Ade28763 Human NOV	531	7	2.3	336	3	AAAG19302	Aag19302 Arabidops
459	7	2.3	285	7	ADE28761	Ade28761 Human NOV	532	7	2.3	339	4	AAU16193	Aau16193 Human nov
460	7	2.3	285	7	ADE28771	Ade28771 Human NOV	533	7	2.3	339	6	ABU55262	Abu55262 Human nov
461	7	2.3	285	7	ADJ70889	Adj70889 Human hea	534	7	2.3	340	2	AAW31544	Aaw31544 Human cyt
462	7	2.3	285	8	ADM93516	Adm93516 Human NOV	535	7	2.3	340	2	AAW17081	Aaw17081 EPH famil
463	7	2.3	285	8	ADM93506	Adm93506 Human NOV	536	7	2.3	340	2	AAW33699	Aaw33699 AL-2-bhor

537	7	2.3	340	2	AAW10637	AAW10637 NLERK2 1i	610	7	2.3	391	6	ABU23338	ABU23338 Protein e
538	7	2.3	340	2	AAW46615	AAW46615 Human tpa	611	7	2.3	393	7	ADP05580	ADP05580 Bacterial
539	7	2.3	340	6	ABU07845	ABU07845 Human eph	612	7	2.3	396	6	ABU39851	ABU39851 Protein e
540	7	2.3	340	8	ADQ021436	Adq21436 Human ebf	613	7	2.3	396	8	ADI43318	ADI43318 Plant tta
541	7	2.3	345	6	ABP80534	ABP80534 N. gonorr	614	7	2.3	396	8	ADM48230	ADM48230 Polypepti
542	7	2.3	346	7	ABO73355	ABO73355 Pseudomon	615	7	2.3	397	8	ADS30416	ADS30416 Bacterial
543	7	2.3	348	4	AAAG82304	AAg82304 S. epider	616	7	2.3	399	7	ABO76293	ABO76293 Pseudomon
544	7	2.3	348	7	ABO76859	ABO76859 Pseudomon	617	7	2.3	399	8	ADJ48713	ADJ48713 OLI-aesoc
545	7	2.3	351	4	AAAG81622	AAg81622 S. epider	618	7	2.3	401	3	AAAB21014	AAb21014 Human nuc
546	7	2.3	355	4	ABBT0336	ABBT0336 Drosophil	619	7	2.3	402	7	ABOC9449	ABOC9449 Pseudomon
547	7	2.3	356	8	ADP43678	ADP43678 Human PMM	620	7	2.3	402	7	ABO71401	ABO71401 Pseudomon
548	7	2.3	357	8	ADR96379	ADR96379 Novel S.	621	7	2.3	405	8	ADR16080	ADR16080 Human ADA
549	7	2.3	359	3	AAAG19301	AAg19301 Arabidops	622	7	2.3	405	8	ADR30763	ADR30763 Human ADA
550	7	2.3	359	3	AAAG50995	AAg50995 Arabidops	623	7	2.3	413	7	ADG75124	ADG75124 Human her
551	7	2.3	359	8	ADQ02511	AdQ02511 Thalecres	624	7	2.3	413	8	ADR16133	ADR16133 Human ADA
552	7	2.3	359	8	ADN73397	ADn73397 Thale cre	625	7	2.3	413	8	ADR16883	ADR16883 Human wil
553	7	2.3	360	8	ADN21970	ADn21970 Bacterial	626	7	2.3	414	2	AAW72139	AAW72139 HSV-2 str
554	7	2.3	360	8	ADN24728	ADn24728 Bacterial	627	7	2.3	414	2	AAW72159	AAW72159 HSV-2 str
555	7	2.3	361	8	ADR18589	ADR18589 Rat GPCR	628	7	2.3	416	3	AAAG17735	AAg17735 Arabidops
556	7	2.3	366	2	AAAY38904	AAy38904 Neisseria	629	7	2.3	416	4	AAAG82654	AAg82654 S. epider
557	7	2.3	366	2	AAAY38907	AAy38907 Neisseria	630	7	2.3	416	6	ABU42635	ABU42635 Protein e
558	7	2.3	366	2	AAAY38905	AAy38905 Neisseria	631	7	2.3	416	6	ADR30804	ADR30804 Human ADA
559	7	2.3	366	6	ABP77026	ABP77026 N. gonorr	632	7	2.3	417	5	ABP40161	ABP40161 Stephyloc
560	7	2.3	366	6	ABO00421	ABO00421 Novel hum	633	7	2.3	417	8	ADSO7208	ADSO7208 Stephyloc
561	7	2.3	367	8	ADS25131	ADs25131 Bacterial	634	7	2.3	419	4	AAU48288	AAU48288 Propionib
562	7	2.3	368	6	ABU19639	ABu19639 Protein e	635	7	2.3	419	6	ABM44807	ABu44807 Propionib
563	7	2.3	368	8	ABO67236	ABO67236 Klebsiell	636	7	2.3	419	6	ABU43572	ABu43572 Protein e
564	7	2.3	368	8	ADJ77832	ADj77832 Rice lipa	637	7	2.3	421	4	AAU37252	AAU37252 Stephyloc
565	7	2.3	369	7	ADM05113	Adm05113 Human pro	638	7	2.3	421	4	AAU36595	AAU36595 Stephyloc
566	7	2.3	372	7	ABO78613	ABO78613 Pseudomon	639	7	2.3	421	4	AAU33833	AAU33833 Stephyloc
567	7	2.3	372	8	ADQ02844	ADQ02844 Thalecres	640	7	2.3	421	5	ABBT8317	ABBT8317 Amino aci
568	7	2.3	374	7	ABO73679	ABO73679 Pseudomon	641	7	2.3	421	6	ABU15882	ABU15882 Protein e
569	7	2.3	375	2	AAAY50008	AAy50008 Thermus t	642	7	2.3	421	6	ABM72095	ABM72095 Stephyloc
570	7	2.3	375	2	AAW48177	AAw48177 Thermus t	643	7	2.3	422	7	ABO70706	ABO70706 Pseudomon
571	7	2.3	375	7	ADH87967	ADh87967 Enterococ	644	7	2.3	422	7	ABO81879	ABO81879 Pseudomon
572	7	2.3	376	2	AAW64377	AAw64377 Mycobacte	645	7	2.3	423	3	AAU33567	AAU33567 Pseudomon
573	7	2.3	376	2	AAW85054	AAw85054 Beta subu	646	7	2.3	423	6	ABU15665	ABU15665 Protein e
574	7	2.3	376	2	AAW81744	AAw81744 M. tuberc	647	7	2.3	426	8	ADP29670	ADP29670 Human sec
575	7	2.3	376	2	AAAY39031	AAy39031 M. tuberc	648	7	2.3	426	8	ADP29657	ADP29657 Human sec
576	7	2.3	376	2	AAAY39174	AAy39174 M. tuberc	649	7	2.3	429	4	AAAG4551	AAg4551 Human sug
577	7	2.3	376	8	ADJ67878	ADj67878 T. thermo	650	7	2.3	429	7	ABO74810	ABO74810 Pseudomon
578	7	2.3	376	8	ADJ67877	ADj67877 T. thermo	651	7	2.3	432	6	ADA33668	ADA33668 Acinetoba
579	7	2.3	376	8	ADJ68089	ADJ68089 T. thermo	652	7	2.3	432	8	ADN22868	ADN22868 Bacterial
580	7	2.3	376	8	ADJ68090	ADJ68090 T. thermo	653	7	2.3	434	8	ADS25067	ADs25067 Bacterial
581	7	2.3	376	8	ADK01168	ADk01168 DNA polym	654	7	2.3	437	3	AAAY4930	AAy4930 Human sec
582	7	2.3	376	8	ADK01167	ADk01167 DNA polym	655	7	2.3	437	5	ABP65593	ABP65593 Bifidobac
583	7	2.3	376	8	ADJ79387	ADJ79387 T. thermo	656	7	2.3	439	4	ABG12185	ABG12185 Novel hum
584	7	2.3	376	8	ADJ79386	ADJ79386 T. thermo	657	7	2.3	439	8	ADH41603	ADH41603 Novel hum
585	7	2.3	376	8	ADJ84827	ADJ84827 T. thermo	658	7	2.3	440	7	ADH74167	ADH74167 Pseudomon
586	7	2.3	376	8	ADJ84826	ADJ84826 T. thermo	659	7	2.3	440	7	ABO81421	ABO81421 Pseudomon
587	7	2.3	376	8	ADM77614	ADM77614 DNA polym	660	7	2.3	444	7	ADOC94325	ADOC94325 E. faeciu
588	7	2.3	376	8	ADM77615	ADM77615 DNA polym	661	7	2.3	446	8	ADOC5661	ADOC5661 Novel hum
589	7	2.3	376	8	ADM66282	ADM66282 T. thermo	662	7	2.3	448	6	ABU70545	ABU70545 Human adi
590	7	2.3	376	8	ADM66281	ADM66281 T. thermo	663	7	2.3	448	7	ABO81484	ABO81484 Pseudomon
591	7	2.3	376	8	ADQ04334	ADQ04334 T. thermo	664	7	2.3	450	7	ABO83538	ABO83538 Pseudomon
592	7	2.3	376	8	ADQ04335	ADQ04335 T. thermo	665	7	2.3	454	2	AAW85046	AAW85046 Gamma sub
593	7	2.3	376	8	ADP82411	ADp82411 Thermus t	666	7	2.3	454	2	AAAY50005	AAy50005 Thermus t
594	7	2.3	376	8	ADP82412	ADp82412 DNA polym	667	7	2.3	454	8	ADJ67775	ADJ67775 T. thermo
595	7	2.3	379	8	ADRI6128	ADRI6128 Human ADA	668	7	2.3	454	8	ADJ67987	ADJ67987 T. thermo
596	7	2.3	379	8	ADRI6129	ADRI6129 Human ADA	669	7	2.3	454	8	ADK01065	ADK01065 DNA polym
597	7	2.3	379	8	ADRI6110	ADRI6110 Human ADA	670	7	2.3	454	8	ADJ79284	ADJ79284 T. thermo
598	7	2.3	379	8	ADRI6108	ADRI6108 Human ADA	671	7	2.3	454	8	ADJ84724	ADJ84724 T. thermo
599	7	2.3	379	8	ADRI6112	ADRI6112 Human ADA	672	7	2.3	454	8	ADM77512	ADM77512 DNA polym
600	7	2.3	379	8	ADRI6132	ADRI6132 Human ADA	673	7	2.3	454	8	ADM66179	ADM66179 T. thermo
601	7	2.3	379	8	ADRI6130	ADRI6130 Human ADA	674	7	2.3	454	8	ADQ04232	ADQ04232 T. thermo
602	7	2.3	379	8	ADRI6131	ADRI6131 Human ADA	675	7	2.3	454	8	ADP82309	ADP82309 DNA polym
603	7	2.3	379	8	ADRI6127	ADRI6127 Human ADA	676	7	2.3	455	2	AAW33698	AAW33698 AL-2-Long
604	7	2.3	379	8	ADRI6129	ADRI6129 Human ADA	677	7	2.3	456	7	ABO70671	ABO70671 Pseudomon
605	7	2.3	379	8	ADRI6110	ADRI6110 Human ADA	678	7	2.3	458	2	AAAS4834	AAAS4834 Human der
606	7	2.3	379	8	ADRI6108	ADRI6108 Human ADA	679	7	2.3	458	8	ADJ48714	ADJ48714 OLI-aesoc
607	7	2.3	383	8	ADRI30793	ADRI30793 Human ADA	680	7	2.3	458	8	ADM37054	ADM37054 Human alp
608	7	2.3	385	7	ADN19022	ADN19022 Bacterial	681	7	2.3	458	8	ADQ29176	ADQ29176 Mouse GPC
609	7	2.3	390	6	ABM67364	ABM67364 Pseudomon	682	7	2.3	459	7	ABO80782	ABO80782 Pseudomon

683	7	2.3	460	3	AAB54132	Aab54132	Human	pan	756	7	2.3	505	8	ADM93490	Adm93490	Human	NOV
684	7	2.3	461	7	ABO75710	AbO75710	Pseudomon		757	7	2.3	505	8	ADM93504	Adm93504	Human	NOV
685	7	2.3	462	8	ADM37052	AdM37052	Human alp		758	7	2.3	505	8	ADM93484	Adm93484	Human	NOV
686	7	2.3	464	2	AAW85045	Aaw85045	Gammia sub		759	7	2.3	506	7	ABO69644	AbO69644	Pseudomon	
687	7	2.3	464	2	AAV50004	Aav50004	Thermus t		760	7	2.3	507	7	ABO68722	AbO68722	Pseudomon	
688	7	2.3	464	8	ADJ67774	AdJ67774	T. thermo		761	7	2.3	508	4	AAW79842	Aaw79842	Human	pro
689	7	2.3	464	8	ADJ67986	AdJ67986	T. thermo		762	7	2.3	511	4	ABW65414	AbW65414	Human	pro
690	7	2.3	464	8	ADK01064	AdK01064	DNA polym		763	7	2.3	513	8	ADJ42667	AdJ42667	Plant	tra
691	7	2.3	464	8	ADJ79283	AdJ79283	T. thermo		764	7	2.3	513	8	ADDO02916	AdDO02916	Thalaeetes	
692	7	2.3	464	8	ADJ84723	AdJ84723	T. thermo		765	7	2.3	514	8	ADH41601	AdH41601	Novel hum	
693	7	2.3	464	8	ADM77511	AdM77511	DNA polym		766	7	2.3	515	2	AAW72076	Aaw72076	Novel-2 str	
694	7	2.3	464	8	ADM66178	AdM66178	T. thermo		767	7	2.3	515	3	AAW42510	Aaw42510	Human	ORF
695	7	2.3	464	8	ADO04231	AdO04231	T. thermo		768	7	2.3	515	8	ADN47628	AdN47628	Thermococ	
696	7	2.3	464	8	ADP82308	AdP82308	DNA polym		769	7	2.3	522	6	AAE35267	Aae35267	Human	P45
697	7	2.3	465	4	AAW95721	Aaw95721	Human pro		770	7	2.3	523	7	AAW78858	Aaw78858	Human	pro
698	7	2.3	465	5	ABW90332	AbW90332	Human pol		771	7	2.3	524	4	AAW36649	Aaw36649	Human	pol
699	7	2.3	465	5	ABW64595	AbW64595	Human alb		772	7	2.3	524	4	ADW28737	AdW28737	Human	NOV
700	7	2.3	465	5	AAE21637	Aae21637	Human gen		773	7	2.3	524	8	ADM93482	Adm93482	Human	NOV
701	7	2.3	465	8	ADL77862	AdL77862	Albumin f		774	7	2.3	526	4	AAW80094	Aaw80094	Human	pro
702	7	2.3	467	6	ABP76730	AbP76730	Streptomy		775	7	2.3	526	4	AAW80116	Aaw80116	Human	pro
703	7	2.3	468	7	ABO78829	AbO78829	Pseudomon		776	7	2.3	527	4	AAU64492	Aau64492	Proplionib	
704	7	2.3	469	5	AAU72939	Aau72939	Neisseria		777	7	2.3	527	5	ABW1194	AbW1194	Herbicida	
705	7	2.3	469	6	ADA54968	Ada54968	Human pro		778	7	2.3	527	6	ABW64701	AbW64701	Proplionib	
706	7	2.3	470	8	ADM26441	AdM26441	Hyperther		779	7	2.3	527	6	ABW61011	AbW61011	Proplionib	
707	7	2.3	470	8	ADL90192	AdL90192	Human enz		780	7	2.3	528	2	AAW05909	Aaw05909	Thermophi	
708	7	2.3	470	8	ADS41716	AdS41716	Bacterial		781	7	2.3	529	2	AAW85044	Aaw85044	Tau subun	
709	7	2.3	472	7	ABO83322	AbO83322	Pseudomon		782	7	2.3	529	2	AAW50003	Aaw50003	Thermus t	
710	7	2.3	476	8	ABO58882	AbO58882	Human gen		783	7	2.3	529	8	AAW50025	Aaw50025	Thermus t	
711	7	2.3	477	5	ABW93927	AbW93927	Herbicida		784	7	2.3	529	8	ADJ67772	AdJ67772	T. thermo	
712	7	2.3	477	7	ABO78770	AbO78770	Pseudomon		785	7	2.3	529	8	ADJ67984	AdJ67984	T. thermo	
713	7	2.3	479	4	AAW92879	Aaw92879	Human pro		786	7	2.3	529	8	ADK01062	AdK01062	DNA polym	
714	7	2.3	479	7	ADP76665	AdP76665	Novel hum		787	7	2.3	529	8	ADJ79281	AdJ79281	T. thermo	
715	7	2.3	480	7	ADP74132	AdP74132	Human nov		788	7	2.3	529	8	ADJ84721	AdJ84721	T. thermo	
716	7	2.3	482	7	ABO82746	AbO82746	Pseudomon		789	7	2.3	529	8	ADM77509	AdM77509	DNA polym	
717	7	2.3	484	7	ABO75503	AbO75503	Pseudomon		790	7	2.3	529	8	ADM66176	AdM66176	T. thermo	
718	7	2.3	485	7	ABE07854	AbE07854	Novel pro		791	7	2.3	529	8	ADDO4229	AdDO4229	T. thermo	
719	7	2.3	485	8	ABO58389	AbO58389	Human gen		792	7	2.3	529	8	ADP82306	AdP82306	Thermus t	
720	7	2.3	486	7	ABO82658	AbO82658	Pseudomon		793	7	2.3	537	8	ADP29732	AdP29732	Human sec	
721	7	2.3	490	7	ABO73969	AbO73969	Pseudomon		794	7	2.3	537	8	ADP29769	AdP29769	Human sec	
722	7	2.3	496	7	ABO77922	AbO77922	Pseudomon		795	7	2.3	537	8	ADP29752	AdP29752	Human sec	
723	7	2.3	499	7	ABO70875	AbO70875	Pseudomon		796	7	2.3	538	4	AAW41590	Aaw41590	Human	pol
724	7	2.3	501	7	ADW28781	AdW28781	Human NOV		797	7	2.3	543	7	ADD46553	AdD46553	Human	pro
725	7	2.3	501	7	ADW28783	AdW28783	Human NOV		798	7	2.3	547	4	AAW41435	Aaw41435	Human	pol
726	7	2.3	501	7	ADW28779	AdW28779	Human NOV		799	7	2.3	548	4	ABW59192	AbW59192	Drosophili	
727	7	2.3	501	7	ABO68984	AbO68984	Pseudomon		800	7	2.3	550	2	AAW98558	Aaw98558	H. pylori	
728	7	2.3	501	7	ABO81139	AbO81139	Pseudomon		801	7	2.3	552	5	ADJ16903	AdJ16903	Human	NOV
729	7	2.3	501	8	ABO68049	AbO68049	Pseudomon		802	7	2.3	553	4	AAW61323	Aaw61323	Human	tra
730	7	2.3	501	8	ADM93524	AdM93524	Human NOV		803	7	2.3	553	4	AAW39804	Aaw39804	Human	pol
731	7	2.3	501	8	ADM93526	AdM93526	Human NOV		804	7	2.3	553	4	AAW95285	Aaw95285	Human	pro
732	7	2.3	504	3	AAW16593	Aaw16593	Arabidops		805	7	2.3	553	8	ABO68683	AbO68683	Pseudomon	
733	7	2.3	505	4	ABG03717	AbG03717	Novel hum		806	7	2.3	554	8	ADN04972	AdN04972	Antibiot	
734	7	2.3	505	4	ABG03717	AbG03717	Novel hum		807	7	2.3	560	7	ABO77361	AbO77361	Pseudomon	
735	7	2.3	505	7	ADW28775	AdW28775	Human NOV		808	7	2.3	560	8	ABW85018	AbW85018	Human	tra
736	7	2.3	505	7	ADW28753	AdW28753	Human NOV		809	7	2.3	561	2	AAW63701	Aaw63701	Human	hsk
737	7	2.3	505	7	ADW28757	AdW28757	Human NOV		810	7	2.3	561	5	ADJ16582	AdJ16582	Human	NOV
738	7	2.3	505	7	ADW28739	AdW28739	Human NOV		811	7	2.3	561	8	ADN42236	AdN42236	Human	NOV
739	7	2.3	505	7	ADW28743	AdW28743	Human NOV		812	7	2.3	565	4	AAW39201	Aaw39201	Human	pol
740	7	2.3	505	7	ADW28747	AdW28747	Human NOV		813	7	2.3	566	5	ADH48764	AdH48764	NOV19 pro	
741	7	2.3	505	7	ADW28749	AdW28749	Human NOV		814	7	2.3	568	6	ABU43107	AbU43107	Protein e	
742	7	2.3	505	7	ADW28741	AdW28741	Human NOV		815	7	2.3	568	7	ADW07846	AdW07846	Novel pro	
743	7	2.3	505	7	ADW28751	AdW28751	Human NOV		816	7	2.3	568	7	ABO73715	AbO73715	Pseudomon	
744	7	2.3	505	7	ADW28745	AdW28745	Human NOV		817	7	2.3	568	7	ABG02057	AbG02057	Novel hum	
745	7	2.3	505	7	ADW28755	AdW28755	Human NOV		818	7	2.3	569	6	ABU21949	AbU21949	Protein e	
746	7	2.3	505	8	ADW28759	AdW28759	Human NOV		819	7	2.3	572	7	ABO75250	AbO75250	Pseudomon	
747	7	2.3	505	8	ADM93486	AdM93486	Human NOV		820	7	2.3	573	4	AAW79110	Aaw79110	Human	pro
748	7	2.3	505	8	ADM93488	AdM93488	Human NOV		821	7	2.3	574	4	AAW11086	Aaw11086	Arabidops	
749	7	2.3	505	8	ADM93500	AdM93500	Human NOV		822	7	2.3	574	4	ABG03206	AbG03206	Novel hum	
750	7	2.3	505	8	ADM93498	AdM93498	Human NOV		823	7	2.3	576	5	ABP39110	AbP39110	Staphyloc	
751	7	2.3	505	8	ADM93494	AdM93494	Human NOV		824	7	2.3	576	8	ADW07323	AdW07323	Staphyloc	
752	7	2.3	505	8	ADM93496	AdM93496	Human NOV		825	7	2.3	582	5	ABG61896	AbG61896	Prostate	
753	7	2.3	505	8	ADM93502	AdM93502	Human NOV		826	7	2.3	582	5	ABJ05557	AbJ05557	Breast ca	
754	7	2.3	505	8	ADM93520	AdM93520	Human NOV		827	7	2.3	582	5	ADM93509	Adm93509	Cancer/an	
755	7	2.3	505	8	ADM93492	AdM93492	Human NOV		828	7	2.3	582	7	ADM939575	AdM939575	Cancer/an	

829	7	2.3	582	7	ADN39535	Adh39535	Cancer/an	902	7	2.3	681	8	AD009782	AD009782	Rat SGLT
830	7	2.3	582	7	ADN39440	Adh39440	Cancer/an	903	7	2.3	681	8	AD009827	AD009827	Hamster S
831	7	2.3	585	7	ABU05348	Abu05348	Pancreas-	904	7	2.3	684	4	ABG14126	ABG14126	Human hum
832	7	2.3	585	8	ADH42375	Adh42375	Novel hum	905	7	2.3	684	6	ABJ37930	ABJ37930	NovX prot
833	7	2.3	587	7	ABO69534	AbO69534	Pseudomon	906	7	2.3	684	7	ABO83596	ABO83596	Pseudomon
834	7	2.3	588	4	AAB96513	Aab96513	Putative	907	7	2.3	686	8	ADP29724	ADP29724	Human sec
835	7	2.3	590	7	ABO70381	AbO70381	Pseudomon	908	7	2.3	687	6	ABR568332	ABR568332	NovX sec
836	7	2.3	591	4	ABG17270	Abg17270	Novel hum	909	7	2.3	688	6	ABU21490	ABU21490	Protein e
837	7	2.3	593	7	ABO74594	AbO74594	Pseudomon	910	7	2.3	688	8	ADP29389	ADP29389	Human sec
838	7	2.3	594	7	AAG15592	Aag15592	Arabidops	911	7	2.3	690	3	AAV50844	AAV50844	Human sec
839	7	2.3	596	6	AAE06614	Aae06614	Human pro	912	7	2.3	690	3	AAV50835	AAV50835	A. oryzae
840	7	2.3	596	6	AAE08088	Aae08088	Human tra	913	7	2.3	691	8	ADU54043	ADU54043	Bacterial
841	7	2.3	596	5	ABG31594	Abg31594	Human tra	914	7	2.3	694	6	ABU36802	ABU36802	Protein e
842	7	2.3	596	5	ABR80588	AbR80588	Human sbg	915	7	2.3	696	6	ADU55119	ADU55119	Human pro
843	7	2.3	596	5	AAO14199	Aao14199	Human tra	916	7	2.3	700	8	ABU00092	ABU00092	Human nov
844	7	2.3	596	5	AD116578	Ad116578	Human NOV	917	7	2.3	700	8	ADR30686	ADR30686	Mouse goo
845	7	2.3	596	6	ABR99498	AbR99498	Human aci	918	7	2.3	702	7	ABO82863	ABO82863	Pseudomon
846	7	2.3	596	6	ABU10299	Abu10299	Novel hum	919	7	2.3	703	3	AAH14781	AAH14781	Aspergill
847	7	2.3	596	6	ABU10300	Abu10300	Rabbit so	920	7	2.3	704	6	ABJ37934	ABJ37934	NOX prot
848	7	2.3	596	6	ADH42377	Adh42377	Novel hum	921	7	2.3	709	7	ADD01163	ADD01163	Human nuc
849	7	2.3	596	6	ADN42332	Adn42332	Novel hum	922	7	2.3	710	4	ABG20114	ABG20114	Novel hum
850	7	2.3	597	8	AD116900	Ad116900	Rabbit NO	923	7	2.3	712	2	AAW30749	AAW30749	Rat YTS21
851	7	2.3	597	8	ABM85015	Abm85015	Human dia	924	7	2.3	712	7	ADE56302	ADE56302	Rat Prote
852	7	2.3	598	8	ADH42373	Adh42373	Novel hum	925	7	2.3	715	7	ABO83994	ABO83994	Pseudomon
853	7	2.3	599	7	ABO71716	AbO71716	Pseudomon	926	7	2.3	716	3	AAG40451	AAG40451	Novel hum
854	7	2.3	599	7	ADU66342	AdU66342	Novel hum	927	7	2.3	720	5	ABP69719	ABP69719	Novel hum
855	7	2.3	600	4	AAB85503	Aab85503	Human pro	928	7	2.3	721	6	ABJ26419	ABJ26419	Aspergill
856	7	2.3	600	5	AAE24147	Aae24147	Human kin	929	7	2.3	722	7	ABO69735	ABO69735	Pseudomon
857	7	2.3	600	6	ABU37929	AbJ37929	NOX prot	930	7	2.3	724	7	ABO82969	ABO82969	Pseudomon
858	7	2.3	602	7	ABO81712	AbO81712	Pseudomon	931	7	2.3	726	8	ADR30684	ADR30684	Mouse goo
859	7	2.3	604	7	ADG74672	AdG74672	Human kin	932	7	2.3	731	8	ADP96881	ADP96881	C. albica
860	7	2.3	605	6	ABU24004	AbU24004	Protein e	933	7	2.3	733	8	ADN99796	ADN99796	Novel hum
861	7	2.3	606	8	ADE98284	Ade98284	Cancer-li	934	7	2.3	735	6	AAE37016	AAE37016	Human nuc
862	7	2.3	606	8	ABM85014	Abm85014	Human dia	935	7	2.3	738	6	AAE36065	AAE36065	Human tra
863	7	2.3	607	2	AAW09422	Aaw09422	Banana po	936	7	2.3	739	7	ADE08009	ADE08009	Novel pro
864	7	2.3	607	8	ABM84840	Abm84840	Human dia	937	7	2.3	741	4	AAE05188	AAE05188	Human dru
865	7	2.3	612	5	AD116580	Ad116580	Human NOV	938	7	2.3	743	6	ABJ37932	ABJ37932	NOX prot
866	7	2.3	612	8	ADH42379	Adh42379	Novel hum	939	7	2.3	745	6	AAE36064	AAE36064	Human tra
867	7	2.3	612	8	ADN42324	Adn42324	Human nov	940	7	2.3	746	8	AD009511	AD009511	Human gen
868	7	2.3	616	6	ABP57705	Abp57705	Saccharop	941	7	2.3	746	8	AD02537	AD02537	Protein e
869	7	2.3	632	7	ABO75844	AbO75844	Pseudomon	942	7	2.3	746	8	ADN21011	ADN21011	Bacterial
870	7	2.3	633	7	AAW93900	Aaw93900	Human pol	943	7	2.3	747	3	AAG40450	AAG40450	Arabidops
871	7	2.3	633	8	ADL32008	Adl32008	Human pro	944	7	2.3	749	7	AD121213	AD121213	Novel hum
872	7	2.3	633	8	ABM85017	Abm85017	Human dia	945	7	2.3	750	9	AAU01898	AAU01898	Mycobacte
873	7	2.3	635	7	ABO82900	AbO82900	Pseudomon	946	7	2.3	752	4	ABG28100	ABG28100	Novel hum
874	7	2.3	637	6	ABJ25819	AbJ25819	Aspergill	947	7	2.3	752	5	AAE15783	AAE15783	Human tra
875	7	2.3	643	6	ABR99497	AbR99497	Amino aci	948	7	2.3	760	5	AAE22157	AAE22157	Human TRN
876	7	2.3	643	8	ADU542943	Adu542943	Bacterial	949	7	2.3	760	7	ADE11758	ADE11758	Human sec
877	7	2.3	644	4	AAU33234	Aau33234	Novel hum	950	7	2.3	763	2	AAV24094	AAV24094	Mouse EPC
878	7	2.3	646	6	ABU20967	Abu20967	Protein e	951	7	2.3	768	5	ABP41137	ABP41137	Human ova
879	7	2.3	649	3	AAB12140	Aab12140	Hydrophob	952	7	2.3	787	7	ADR43728	ADR43728	Human pro
880	7	2.3	649	8	ABM85016	Abm85016	Human dia	953	7	2.3	787	8	ADH41599	ADH41599	Novel hum
881	7	2.3	650	5	ABR92769	AbR92769	HebIdicida	954	7	2.3	787	8	AD009512	AD009512	Human gen
882	7	2.3	655	7	ABO68366	AbO68366	Pseudomon	955	7	2.3	787	8	AD022538	AD022538	Protein e
883	7	2.3	658	7	ABO71749	AbO71749	Pseudomon	956	7	2.3	794	7	ADL10714	ADL10714	Human the
884	7	2.3	659	7	ABO81607	AbO81607	Pseudomon	957	7	2.3	797	8	ADP77181	ADP77181	KALPA. 2/
885	7	2.3	664	5	AAU85407	Aau85407	Human pro	958	7	2.3	801	5	ABP74123	ABP74123	Human TRI
886	7	2.3	664	5	ABR99496	AbR99496	Amino aci	959	7	2.3	802	5	AAH47105	AAH47105	First epi
887	7	2.3	672	7	ABO73661	AbO73661	Pseudomon	960	7	2.3	802	5	ABR78299	ABR78299	Amino aci
888	7	2.3	674	5	ABR93334	AbR93334	HebIdicida	961	7	2.3	802	7	ADH62503	ADH62503	Human MAP
889	7	2.3	674	5	ABU05342	AbU05342	Pancreas-	962	7	2.3	803	8	ADQ19759	ADQ19759	Human sof
890	7	2.3	674	5	ABU05347	AbU05347	Pancreas-	963	7	2.3	809	4	AAH41064	AAH41064	Human pol
891	7	2.3	674	5	ABU05346	Abu05346	Pancreas-	964	7	2.3	812	4	AAH47106	AAH47106	Second sp
892	7	2.3	674	6	AAE35063	Aae35063	Pancreas-	965	7	2.3	812	4	ABR00942	ABR00942	Gene 216
893	7	2.3	674	7	ADB85297	AdB85297	Human tra	966	7	2.3	812	5	ABR78300	ABR78300	Amino aci
894	7	2.3	674	8	AD009778	AdO09778	Human Na-	967	7	2.3	812	5	AAO14377	AAO14377	Human met
895	7	2.3	678	5	ABU05343	AbU05343	Pancreas-	968	7	2.3	812	5	AAU98885	AAU98885	Human pro
896	7	2.3	678	5	AD116902	Ad116902	Murine NO	969	7	2.3	812	6	ABU55870	ABU55870	Human 216
897	7	2.3	681	5	AD009780	AdO09780	Mouse SGL	970	7	2.3	812	7	ADH62505	ADH62505	Human MAP
898	7	2.3	681	5	AAO14202	Aao14202	Human tra	971	7	2.3	812	8	ADH41611	ADH41611	Novel hum
899	7	2.3	681	5	ABU05344	AbU05344	Pancreas-	972	7	2.3	812	8	ADJ36972	ADJ36972	Human gen
900	7	2.3	681	6	AAE36062	Aae36062	Human tra	973	7	2.3	812	8	ADL81550	ADL81550	Human gen
901	7	2.3	681	8	ADJ81711	AdJ81711	Human SMI	974	7	2.3	813	4	AAU29256	AAU29256	Human PRO


```
975 7 2.3 813 6 ABUS632 ABUS632 Human PRO
976 7 2.3 813 6 ABUS6180 ABUS6180 Novel hum
977 7 2.3 813 6 ABUS6495 ABUS6495 Human sec
978 7 2.3 813 6 ABUS6369 ABUS6369 Human sec
979 7 2.3 813 6 ABUS6759 ABUS6759 Human sec
980 7 2.3 813 6 ABUS6999 ABUS6999 Human sec
981 7 2.3 813 6 ABUS62938 ABUS62938 Human PRO
982 7 2.3 813 6 ABUS60059 ABUS60059 Human PRO
983 7 2.3 813 6 ABUS6308 ABUS6308 Human sec
984 7 2.3 813 6 ABUS6361 ABUS6361 Novel hum
985 7 2.3 813 6 ABUS62792 ABUS62792 Human sec
986 7 2.3 813 6 ABUS60869 ABUS60869 Human sec
987 7 2.3 813 6 ABUS602921 ABUS602921 Human sec
988 7 2.3 813 6 ABUS6075 ABUS6075 Human sec
989 7 2.3 813 6 ABUS64837 ABUS64837 Human sec
990 7 2.3 813 6 ABUS65810 ABUS65810 Human PRO
991 7 2.3 813 6 ABUS69970 ABUS69970 Novel hum
992 7 2.3 813 6 ABUS6185 ABUS6185 Novel hum
993 7 2.3 813 6 ABUS61891 ABUS61891 Novel hum
994 7 2.3 813 6 ABUS6584 ABUS6584 Human PRO
995 7 2.3 813 6 ABUS6425 ABUS6425 Human sec
996 7 2.3 813 6 ABUS67638 ABUS67638 Human sec
997 7 2.3 813 6 ABUS60666 ABUS60666 Human PRO
998 7 2.3 813 6 ABUS69584 ABUS69584 Human sec
999 7 2.3 813 6 ABUS69974 ABUS69974 Human sec
1000 7 2.3 813 6 ABUS6497 ABUS6497 Human sec
```

ALIGNMENTS

RESULT 1
AAB60386 standard; protein; 303 AA.

```
AC AAB60386;
XX
XX 24-APR-2001 (first entry)
DE Human apoptosis-associated factor NT2RM1000558 (portion), SEQ ID NO:2.
XX
XX Human; apoptosis-associated factor; NT2RM1000558; death effector domain;
KM DED; caspase family cleavage domain; pro-apoptotic; drug screening;
KM cell proliferation; ischaemic disease; chronic viral disease.
XX
OS Homo sapiens.
XX
XX WO200104300-A1.
XX
XX 18-JAN-2001.
XX
XX 06-JUL-2000; 2000WO-JP004516.
XX
XX 08-JUL-1999; 99JP-00194179.
XX 18-OCT-1999; 99US-0159586P.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Kawai Y, Miyoshi S, Satoh S;
PI WPI; 2001-138348/14.
XX
XX N-PSDB; AAF27407.
XX
XX Polynucleotide encoding an apoptosis-associated factor protein with death
PT effector domain and caspase family-cleavage domain, useful in regulating
PT diseases with cell proliferation.
XX
XX Claim 1; Page 43-44; 53pp; Japanese.
XX
XX The invention relates to a novel human apoptosis-associated factor
CC (AAB60386, AAB60387), designated NT2RM1000558, which contains a death
CC effector domain (DED) and a caspase family cleavage domain and is capable
CC of inducing apoptosis in cells. The invention also relates to nucleic
```

```
CC acids encoding the protein (AAF27407, AAF27408); variants of the protein
CC (particularly dominant negative variants); vectors and host cells
CC comprising a nucleic acid which encodes an apoptosis-associated factor
CC of the invention; the recombinant production of the protein; an antibody
CC against the protein; and methods of screening for compounds which can
CC regulate apoptosis. The apoptosis-related factor is useful in regulating
CC diseases associated with cell proliferation and in screening drug
CC candidates e.g., for regulating cell proliferation or cell death in
CC ischaemic diseases and chronic viral diseases. The present sequence
CC represents a substantial proportion of the human apoptosis-associated
CC factor NT2RM1000558
XX
SQ Sequence 303 AA;
Query Match 100.0%; Score 303; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 1,8e-264;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MALSGSTPAPCWEDECLDYGMLSLHMEVVGQUTTELELAFLLDEAPGAGLA 60
|||
1 MALSGSTPAPCWEDECLDYGMLSLHMEVVGQUTTELELAFLLDEAPGAGLA 60
Db 1
QY 61 RASGGLLELLELRGCGESNTLRLGQLRLVLAHDLPLHARKRRPVSPEYSYGT 120
|||
61 RASGGLLELLELRGCGESNTLRLGQLRLVLAHDLPLHARKRRPVSPEYSYGT 120
Db 61
QY 121 SSSKRTGSCRRRRQSSSSANSQGGWETGSPPTKGRGRGRRPGGARRRRGAPAPQ 180
|||
121 SSSKRTGSCRRRRQSSSSANSQGGWETGSPPTKGRGRGRRPGGARRRRGAPAPQ 180
Db 121
QY 181 QOSEPARPSEGGVTCIDIRLVAEYCEHPALGQVASRRPOLARQDLVFCQATVLR 240
|||
181 QOSEPARPSEGGVTCIDIRLVAEYCEHPALGQVASRRPOLARQDLVFCQATVLR 240
Db 181
QY 241 SRDLGSVCDIKFSELSYLDAPMGDYLSGALLQALRGVFTLALREAVGREAVLLVSD 300
|||
241 SRDLGSVCDIKFSELSYLDAPMGDYLSGALLQALRGVFTLALREAVGREAVLLVSD 300
Db 241
QY 301 EAD 303
|||
301 EAD 303
Db 301
```

RESULT 2

AAB60387 standard; protein; 326 AA.

```
ID AAB60387
XX
XX AAB60387;
XX
XX 24-APR-2001 (first entry)
DE Human apoptosis-associated factor NT2RM1000558, SEQ ID NO:4.
XX
XX Human; apoptosis-associated factor; NT2RM1000558; death effector domain;
KM DED; caspase family cleavage domain; pro-apoptotic; drug screening;
KM cell proliferation; ischaemic disease; chronic viral disease.
XX
XX Homo sapiens.
XX
XX WO200104300-A1.
XX
XX 18-JAN-2001.
XX
XX 06-JUL-2000; 2000WO-JP004516.
XX
XX 08-JUL-1999; 99JP-00194179.
XX 18-OCT-1999; 99US-0159586P.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Kawai Y, Miyoshi S, Satoh S;
PI WPI; 2001-138348/14.
XX
```


DR N-PSDB; AAF27408.
 XX Polynucleotide encoding an apoptosis-associated factor protein with death
 PT effector domain and caspase family-cleavage domain, useful in regulating
 PT diseases with cell proliferation.
 XX
 XX Claim 3; Page 47-48; 53pp; Japanese.
 XX
 CC The invention relates to a novel human apoptosis-associated factor
 CC (AAB60386, AAB60387), designated NT2RM1000558, which contains a death
 CC effector domain (DED) and a caspase family cleavage domain and is capable
 CC of inducing apoptosis in cells. The invention also relates to nucleic
 CC acids encoding the protein (AAF27407, AAF27408); variants of the protein
 CC (particularly dominant negative variants); vectors and host cells
 CC comprising a nucleic acid which encodes an apoptosis-associated factor
 CC of the invention; the recombinant production of the protein; an antibody
 CC against the protein; and methods of screening for compounds which can
 CC regulate apoptosis. The apoptosis-related factor is useful in regulating
 CC diseases associated with cell proliferation and in screening drug
 CC candidates e.g., for regulating cell proliferation or cell death in
 CC ischaemic diseases and chronic viral diseases. The present sequence
 CC represents the human apoptosis-associated factor NT2RM1000558
 XX
 XX Sequence 326 AA;
 SQ
 Query Match 100.0%; Score 303; DB 4; Length 326;
 Best Local Similarity 100.0%; Pred. No. 1.9e-264; Mismatches 0; Gaps 0;
 Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MALSGTAPACWEDECDYVGMISLHMFVEVGGQLTECELELLAFLIDEAPGAAGILA 60
 DB 1 MALSGTAPACWEDECDYVGMISLHMFVEVGGQLTECELELLAFLIDEAPGAAGILA 60
 QY 61 PARSGLELLERGGCGGSENLRLGQLRLVLAARDLPHLARRRRPVSPERYSGTSS 120
 DB 61 PARSGLELLERGGCGGSENLRLGQLRLVLAARDLPHLARRRRPVSPERYSGTSS 120
 QY 121 SSSKRTGSCRRRRSSSSANSQOGWETGSPPTKQRRSGRPGSGARRRRRGAPAPQ 180
 DB 121 SSSKRTGSCRRRRSSSSANSQOGWETGSPPTKQRRSGRPGSGARRRRRGAPAPQ 180
 QY 181 QOSEPARSSGKVTCDIRLRVRAVCEHGPALBEGVASSRRPOLARQLDVFGQATAVLR 240
 DB 181 QOSEPARSSGKVTCDIRLRVRAVCEHGPALBEGVASSRRPOLARQLDVFGQATAVLR 240
 QY 241 SRDGSVVCIDIKFSELSYLDAPFWDYLSGALLQALRGVFLTEALREAVRLLVSD 300
 DB 241 SRDGSVVCIDIKFSELSYLDAPFWDYLSGALLQALRGVFLTEALREAVRLLVSD 300
 QY 301 EAD 303
 DB 301 EAD 303
 RESULT 3
 AAB15551
 ID AAB15551 standard; protein; 304 AA.
 XX
 XX AAB15551;
 XX
 XX 28-FEB-2001 (first entry)
 XX
 XX Apoptosis related protein encoded by gene 1 clone HLDOK36.
 DE
 XX
 XX Cytostatic; antiinflammatory; immunosuppressive; antisclerotic; cardiatic;
 KW virucidal; anti-AIDS; vasotropic; anti-ischaemic; antiparkinsonian;
 KW anti-Alzheimer; gene therapy; human; apoptosis; fusion protein; cancer;
 KW colon; breast; prostate; melanoma; lymphoma; inflammation; herpes;
 KW autoimmune disorder; multiple sclerosis; viral infection.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO200056752-A2.
 PN

XX
 PD 28-SEP-2000.
 XX
 XX 15-MAR-2000; 2000WO-US006642.
 XX
 XX 24-MAR-1999; 99US-0126018P.
 XX
 XX 17-JUN-1999; 99US-0139638P.
 PR 17-JUN-1999; 99US-0139638P.
 PR 18-AUG-1999; 99US-0149449P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 PI Ruben SM, Ni J, Young PA;
 PT WPI; 2000-587660/55.
 DR N-PSDB; AAA95790.
 XX
 XX
 PT Nucleic acids encoding human apoptosis associated protein, useful for the
 PT prevention, treatment and diagnosis of e.g. Alzheimer's and Parkinson's
 PT disease, inflammation and ischemic injury.
 XX
 XX
 PS Claim 11; Page 252-253; 273pp; English.
 CC
 CC The invention relates to the isolation of genes encoding a human
 CC apoptosis-related proteins. The nucleotide sequences AAA95790-A95798
 CC encode the human apoptosis related proteins AAB15551-B15559. The genes
 CC can be used to generate fusion proteins by linking to the gene for the
 CC human immunoglobulin G Fc (IgG Fc) portion (AAA95799) for increasing the
 CC stability of the fusion protein as compared to the human protein only.
 CC The gene and encoded protein may be used in the prevention, treatment and
 CC diagnosis of diseases associated with inappropriate apoptosis associated
 CC protein expression, e.g. cancer (e.g. colon, breast and prostate cancer,
 CC melanomas and lymphomas), inflammation, autoimmune disorders (e.g.
 CC multiple sclerosis) and viral infections (e.g. herpes)
 XX
 XX Sequence 304 AA;
 SQ
 Query Match 73.9%; Score 224; DB 3; Length 304;
 Best Local Similarity 100.0%; Pred. No. 3.1e-193; Mismatches 0; Gaps 0;
 Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 80 ESNRLGQLRLVLAARDLPHLAKRRRPVSPERYSGTSSSKRTGSCRRRRSSSS 139
 DB 58 ESNRLGQLRLVLAARDLPHLAKRRRPVSPERYSGTSSSKRTGSCRRRRSSSS 117
 QY 140 ANSOOGWETGSPPTKQRRSGRPGSGARRRRRGAPAPQOSEPARSSGKVTCDIR 199
 DB 118 ANSOOGWETGSPPTKQRRSGRPGSGARRRRRGAPAPQOSEPARSSGKVTCDIR 177
 QY 200 LRVRAVCEHGPALBEGVASSRRPOLARQLDVFGQATVLRSDYGVVCDIKFSELSYL 259
 DB 178 LRVRAVCEHGPALBEGVASSRRPOLARQLDVFGQATVLRSDYGVVCDIKFSELSYL 237
 QY 260 DAFWGDYLSGALLQALRGVFLTEALREAVRLLVSDVDEAD 303
 DB 238 DAFWGDYLSGALLQALRGVFLTEALREAVRLLVSDVDEAD 281
 RESULT 4
 AAE24860
 ID AAE24860 standard; protein; 318 AA.
 XX
 XX AAE24860;
 XX
 XX 22-OCT-2002 (first entry)
 XX
 XX Human DED4 (death effector domain) protein.
 DE
 XX
 XX Human; death domain; DD; death effector domain; DED; Chlamydia infection;
 KW NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;
 KW inflammation; allergy; autoimmunity; allograft rejection; cell division;
 KW immune-based pathology; fibrosis; arthritis; graft versus host disease;
 KW immunosuppressive; gene therapy; antisense therapy.
 XX
 XX

OS Homo sapiens.
 XX Key Location/Qualifiers
 FH 53..74
 FT Region /note= "Nuclear localisation sequence"
 XX
 PN W0200240680-A2.
 XX
 PD 23-MAY-2002.
 XX
 PF 15-NOV-2001; 2001WO-US044844.
 XX
 PR 17-NOV-2000; 2000US-00715893.
 PR 29-JUN-2001; 2001US-0301889P.
 XX
 PA (BURN-) BURNHAM INST.
 XX
 PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W,
 PI Semmer-Liemen F;
 XX
 DR WPI; 2002-500222/53.
 DR N-PSDB; AAD40080.
 XX
 PT New polypeptide comprising a death domain or death effector domain,
 PT useful for discovery of drugs that suppress infection, inflammation,
 PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.
 XX
 PS Claim 3; Page 186-187; 209pp; English.
 XX
 CC The invention relates to an isolated polypeptide comprising a death
 CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention
 CC is useful for identifying a binding agent, preferably a protein or a drug
 CC that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC
 CC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or
 CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent and
 CC detecting the association of the domain and the candidate binding agent,
 CC by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or
 CC chemical crosslinking, nuclear magnetic resonance (NMR), mass
 CC spectroscopy (MS) and FPA. The invention is useful for modulating the
 CC level of a cell process such as cell proliferation, cell adhesion, cell
 CC stress response, responses to microbial infection and B cell
 CC immunoglobulin class switching, in particular apoptosis within a cell.
 CC Antibody specifically reactive with CTDD DD of C. trachomatis, C.
 CC muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the
 CC CTDD DD protein is useful for detecting a Chlamydia infection. The
 CC invention is useful for modulating the activity of oncogenic proteins,
 CC for treating a pathology caused by the oncogenic proteins and for
 CC treating bacterial infections by modulating the activity of bacterial
 CC proteins. The protein and antibody specific for it are useful for
 CC discovery of drugs that suppress infection, inflammation, allergy,
 CC sepsis, autoimmunity, allograft rejection and other diseases. The protein
 CC is useful for treating immune-based pathologies, pathologies associated
 CC with cell division, inflammatory diseases such as sepsis, fibrosis,
 CC arthritis, graft versus host disease. The invention is used in antisense
 CC therapy and gene therapy. The present sequence is human DED4 protein
 XX
 SQ Sequence 318 AA;
 Query Match 73.9%; Score 224; DB 5; Length 318;
 Best Local Similarity 100.0%; Pred. No. 3 2e-193;
 Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 80 ESNRLILGQLRLVLAARDLLPHLARKRRRPVSPERYSGTSSSKRTGSCRRRRQSSS 139
 DB 80 ESNRLILGQLRLVLAARDLLPHLARKRRRPVSPERYSGTSSSKRTGSCRRRRQSSS 139
 QY 140 ANSQGGWETGSPPTKQRGRSGRPGSGARRRRGAAGAQAQGGSEPRPSSSEGVTTDIR 199
 DB 140 ANSQGGWETGSPPTKQRGRSGRPGSGARRRRGAAGAQAQGGSEPRPSSSEGVTTDIR 199
 QY 200 LRVRAECCEGAPALDQGVASRRPQALAROLDVFGQAVAVRSRLGVSVDIKFSELSYL 259
 DB 200 LRVRAECCEGAPALDQGVASRRPQALAROLDVFGQAVAVRSRLGVSVDIKFSELSYL 259

QY 260 DAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 303
 DB 260 DAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 303
 RESULT 5
 ID AAE38903 standard; protein; 318 AA.
 XX
 AC AAE38903;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human DED4 protein.
 XX
 KW Human; death domain; DD; death effector domain; DED; cell proliferation;
 KW Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;
 KW neural growth factor receptor-interacting death domain; cell adhesion;
 KW vasotropic; microbial infection; inflammation; allograft rejection; CTDD;
 KW cell stress response; benign prostatic hypertrophy; antibacterial; NIDD;
 KW apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;
 KW neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;
 KW keloid.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 12..112
 FT /note= "Death effector domain of DED-4"
 FT Peptide 53..74
 FT /note= "Nuclear localisation sequence"
 XX
 PN US2003049702-A1.
 XX
 PD 13-MAR-2003.
 XX
 PF 15-NOV-2001; 2001US-00001254.
 XX
 PR 17-NOV-2000; 2000US-00715893.
 PR 17-NOV-2000; 2000US-0367360P.
 PR 29-JUN-2001; 2001US-0301889P.
 XX
 PA (REED/) REED J C.
 PA (GODZ/) GODZIK A.
 PA (PAWL/) PAWLOWSKI K.
 PA (FIOR/) FIORENTINO L.
 PA (LEES/) LEE S H.
 PA (ROTH/) ROTH W.
 PA (STEN/) STENNER-LIEMEN F.
 XX
 PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W,
 PI Semmer-Liemen F;
 XX
 DR WPI; 2002-500222/53.
 DR N-PSDB; AAD59062.
 XX
 PT New polypeptide comprising a death domain or death effector domain,
 PT useful for discovery of drugs that suppress infection, inflammation,
 PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.
 XX
 PS Claim 2; Page 44-45; 99pp; English.
 XX
 CC The present invention provides novel death domain (DD) and death effector
 CC domain (DED) proteins and nucleic acids encoding them. The invention also
 CC provides death domain containing protein such as Chlamydia trachomatis
 CC death domain containing protein (CTDD) DD and neural growth factor
 CC receptor-interacting death domain (NIDD) DD. The invention is useful for
 CC identifying a binding agent (e.g. protein or drug) that binds a DD, DED
 CC or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDD with a candidate
 CC binding agent and identifying an effective agent (e.g. protein or drug)
 CC that modulates the association of a DD, DED or NB-ARC domain with protein
 CC that binds the DD, DED or NB-ARC domain. The invention is also useful for

modulating the level of cell process such as apoptosis, cell adhesion, cell proliferation, cell stress responses, responses to microbial infection and B cell immunoglobulin class switching. DPs, DPs and NB-ARC domains and/or anti-DD, anti-DD or anti-NB-ARC domain antibodies are useful for discovery of drugs that suppress infection, autoimmunity, inflammation, allergy, allograft rejection, sepsis and other diseases. CC DD, DED or NB-ARC domain proteins are used to treat infection, allergy, autoimmunity, inflammation, allograft rejection, sepsis, keratinocyte hyperplasia, neoplasia, keloid, benign prostatic hypertrophy, fibrosis, inflammatory hyperplasia and smooth muscle cell proliferation in arteries following balloon angioplasty (restenosis). The invention is also used in antibody therapy and gene therapy. The present sequence is human DED4 CC protein. The DED4 gene is located on chromosome 19

XX Sequence 318 AA;

Query Match 73.9%; Score 224; DB 5; Length 318;
Best Local Similarity 100.0%; Pred. No. 3.2e-193;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 ESNRLIGQLRLVLRARHDLPHLARKRRRPPSPRYSYGTSSSKRTGSGRRRROSS 139
DB 80 ESNRLIGQLRLVLRARHDLPHLARKRRRPPSPRYSYGTSSSKRTGSGRRRROSS 139
QY 140 ANSOOGWETGSPPTKQRORSGRPSGARRRRGAPAPQOSEPARPSSEGVTCIDIR 199
DB 140 ANSOOGWETGSPPTKQRORSGRPSGARRRRGAPAPQOSEPARPSSEGVTCIDIR 199
QY 200 LRVAAECCEHPALGEGVARRRRPOLARQDLVFGQATVLRSDIGSVCDIKFSELSYL 259
DB 200 LRVAAECCEHPALGEGVARRRRPOLARQDLVFGQATVLRSDIGSVCDIKFSELSYL 259
QY 260 DAFNGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 303
DB 260 DAFNGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 303

RESULT 6
ABB07263
ID ABB07263 standard; protein; 326 AA.

XX ABB07263;
DT 26-MAR-2002 (first entry)
DE Human apoptosis regulator (APRG) polypeptide (Incyte ID. 3102521CD1).
XX APRG; apoptosis regulator; cytosolic; antiatherosclerotic; osteopathic;
KW antiatherosclerotic; hepatotropic; antipsoptic; antihelminthic; human;
KW antiallergic; antianemic; antiaesthetic; antithyroid; anti-HIV; cancer;
KW antiinflammatory; antidiabetic; antihypertensive; nephrotropic; ophthalmological;
KW immunosuppressive; dermatological; antitumor; antirheumatic; fungicide;
KW antitubercular; antibacterial; virucide; antiparasitic; protozoacide;
KW tranquilizer; vulnerary; gynecological; vasotropic; gene therapy.

XX Homo sapiens.

XX WO200192527-A2.

XX 06-DEC-2001.

XX 30-MAY-2001; 2001WO-US017581.

XX 01-JUN-2000; 2000US-0209407P.

XX 30-NOV-2000; 2000US-0250326P.

XX (INCYTE GENOMICS INC.

XX Tang YT, Azimzai Y, Yue H, Burford N, Ding L, Elliott VS;

XX Paterson C, Baughn MR;

XX WPI; 2002-114350/15.

XX N-PSDB; ABA94362.

XX Novel human apoptosis regulator polypeptides and polynucleotides for
PT diagnosing, preventing, treating cell proliferative, immunological and
PT reproductive disorders and for identifying modulators of therapeutic use.
PS Claim 1; Page 97-98; 103pp; English.

The invention provides human apoptosis regulator (APRG) polypeptides and polynucleotides. The APRG polypeptides, polynucleotides and modulators are useful for diagnosis, treatment and prevention of cell proliferative, immunological and reproductive disorders. The cell proliferative disorders include cancer, actinic keratosis, arteriosclerosis, attherosclerosis, bursitis, cirrhosis, hepatitis, psoriasis, and immunological disorders include acquired immunodeficiency syndrome (AIDS), adult respiratory distress syndrome, Addison's disease, ankylosing spondylitis, amyloidosis, allergies, anemia, osteoporosis, autoimmune hemolytic anemia, asthma, autoimmune thyroiditis, Crohn's disease, contact dermatitis, diabetes mellitus, gout, Graves' disease, glomerulonephritis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus, systemic sclerosis, ulcerative colitis, haemodialysis, urethritis, viral, bacterial, fungal, parasitic, protozoal, helminthic infections and trauma. Reproductive disorders include disorders of prolactin production, infertility, endometriosis, polycystic ovary syndrome, ectopic pregnancies, galactorrhea, abnormal sperm physiology, disruptions of spermatogenesis, cancer of testis and prostate, impotence, carcinoma of male breast and gynecomastia. The APRG polynucleotides are useful for creating knockin humanized animals or transgenic animals to model human disease and to detect and quantify gene expression in biopsied tissues in which expression of APRG is correlated with disease. CC APRG, fragments of it and antibodies specific for APRG are useful as CC elements on a microarray which is useful to monitor or measure protein- CC protein interactions, drug-target interactions and gene expression CC profiles. The present sequence represents a human APRG polypeptide

XX Sequence 326 AA;

Query Match 73.9%; Score 224; DB 5; Length 326;
Best Local Similarity 100.0%; Pred. No. 3.3e-193;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 ESNRLIGQLRLVLRARHDLPHLARKRRRPPSPRYSYGTSSSKRTGSGRRRROSS 139
DB 80 ESNRLIGQLRLVLRARHDLPHLARKRRRPPSPRYSYGTSSSKRTGSGRRRROSS 139
QY 140 ANSOOGWETGSPPTKQRORSGRPSGARRRRGAPAPQOSEPARPSSEGVTCIDIR 199
DB 140 ANSOOGWETGSPPTKQRORSGRPSGARRRRGAPAPQOSEPARPSSEGVTCIDIR 199
QY 200 LRVAAECCEHPALGEGVARRRRPOLARQDLVFGQATVLRSDIGSVCDIKFSELSYL 259
DB 200 LRVAAECCEHPALGEGVARRRRPOLARQDLVFGQATVLRSDIGSVCDIKFSELSYL 259
QY 260 DAFNGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 303
DB 260 DAFNGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 303

XX Homo sapiens.

XX ADCT9260 standard; protein; 326 AA.

XX ADCT9260;

XX 01-JAN-2004 (first entry)

XX Human DEDD2 protein SEQ ID NO:2.

XX human; death effector domains containing DNA-binding protein;

XX DED-containing DNA-binding protein; DEDD2; cell death; gene therapy;

XX cycostatic; cancer; chronic myeloid leukaemia.

XX Homo sapiens.

QY 230 DVEGQATAVLRSDLSGVCDIKFSELSYLDAPFMGDYLSGALLQALRGVFLTEALREAVG 289
DB 146 DVEGQATAVLRSDLSGVCDIKFSELSYLDAPFMGDYLSGALLQALRGVFLTEALREAVG 205
QY 290 REAVRLVSVDEAD 303
DB 206 REAVRLVSVDEAD 219
RESULT 11
ID ABB06038 standard; protein; 361 AA.
AC ABB06038;
XX
XX 10-MAY-2002 (first entry)
DE Human NS protein sequence SEQ ID NO:130.
XX
XX Human; cytostatic; osteopathic; gynaecological; neuroprotective;
KM antihemmatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;
KM vasotropic; antiarteriosclerotic; antiinflammatory; dermatological;
KM anorectic; muscular; antihypertensive; cardiovascular; anticoagulant;
KM antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiant;
KM anticonvulsant; antidiabetic; tranquilliser; antidepressant; neuroleptic;
KM gastrointestinal; virucide; anticancer; cerebroprotective; nootropic;
KM contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia;
KM endometriosis; degenerative disease; multiple sclerosis; psoriasis;
KM rheumatoid arthritis; catarract; restenosis; atherosclerosis; glaucoma;
KM inflammation; skin disorder; obesity; muscular dystrophy; AIDS;
KM infectility; cardiovascular disease; coagulation disease; hypertension;
KM ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration;
KM diabetes; anxiety; depression; schizophrenia; viral disease; stroke;
KM gastric ulcer; Alzheimer's disease.
XX
XX Homo sapiens.
OS
PN WO200206315-A2.
XX
XX 24-JAN-2002.
PD
XX 17-JUL-2001; 2001WO-II000653.
XX
XX 18-JUL-2000; 2000IL-00137345.
PR 15-DEC-2000; 2000IL-00140354.
XX
XX (COMP-) COMPUGEN LTD.
PI Mintz L, Freilich S, Bernstein J;
PI WPI; 2002-155037/20.
DR N-PSDB; ABL39692.
XX
XX One hundred and twenty eight novel nucleic acid sequences, useful for
PT treating and diagnosing e.g. cancer, asthma and Alzheimer's.
PS
XX Claim 6; Page 149-151; 290pp; English.
XX
XX ABL39691 to ABL39818 represent novel human nucleic acid sequences
CC encoding the proteins given in ABB06037 to ABB06164. The novel sequences
CC (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective,
CC antihemmatic, antiarthritic, antipsoriatic, ophthalmological, virucide,
CC vasotropic, antiarteriosclerotic, antiinflammatory, dermatological,
CC anorectic, muscular, anti-HIV, antihypertensive, cardiovascular, cardiant,
CC anticoagulant, antifibrinolytic, hypotension, antiasthmatic, cardiant,
CC immunomodulator, anticonvulsant, antidiabetic, tranquilliser, anticancer,
CC antidepressant, gastrointestinal, neuroleptic, cerebroprotective,
CC nootropic and contraceptive activities. The NS can be used in vaccines,
CC gene therapy and antitense therapy. Nucleic acid, expression vectors and
CC antibodies from the present invention can be used for treating and
CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
CC diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,

CC cataracts, restenosis, atherosclerosis, inflammation, skin disorders,
CC glaucoma, obesity, muscular dystrophy, AIDS, infectility, cardiovascular
CC disease, coagulation disease, ischaemia, hypertension, asthma, immune
CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,
CC depression, schizophrenia, viral disease, gastric ulcers, stroke,
CC Alzheimer's disease and as a contraceptive
XX
XX Sequence 361 AA;
SQ
Query Match 38.6%; Score 117; DB 5; Length 361;
Best Local Similarity 100.0%; Pred. No. 1,1e-96;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 175 AAPAPQOSEPARPSSEGVTCIDIRVRAEYCEHGPALGQVARRPOLARQOLDVFGQ 234
DB 202 AAPAPQOSEPARPSSEGVTCIDIRVRAEYCEHGPALGQVARRPOLARQOLDVFGQ 261
QY 235 ATAVLRSDLSGVCDIKFSELSYLDAPFMGDYLSGALLQALRGVFLTEALREAVG 291
DB 262 ATAVLRSDLSGVCDIKFSELSYLDAPFMGDYLSGALLQALRGVFLTEALREAVG 318
RESULT 12
ID ABB06039 standard; protein; 368 AA.
AC ABB06039;
XX
XX 10-MAY-2002 (first entry)
DE Human NS protein sequence SEQ ID NO:131.
XX
XX Human; cytostatic; osteopathic; gynaecological; neuroprotective;
KM antihemmatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;
KM vasotropic; antiarteriosclerotic; antiinflammatory; dermatological;
KM anorectic; muscular; antihypertensive; cardiovascular; anticoagulant;
KM antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiant;
KM anticonvulsant; antidiabetic; tranquilliser; antidepressant; neuroleptic;
KM gastrointestinal; virucide; anticancer; cerebroprotective; nootropic;
KM contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia;
KM endometriosis; degenerative disease; multiple sclerosis; psoriasis;
KM rheumatoid arthritis; catarract; restenosis; atherosclerosis; glaucoma;
KM inflammation; skin disorder; obesity; muscular dystrophy; AIDS;
KM infectility; cardiovascular disease; coagulation disease; hypertension;
KM ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration;
KM diabetes; anxiety; depression; schizophrenia; viral disease; stroke;
KM gastric ulcer; Alzheimer's disease.
XX
XX Homo sapiens.
OS
PN WO200206315-A2.
XX
XX 24-JAN-2002.
PD
XX 17-JUL-2001; 2001WO-II000653.
XX
XX 18-JUL-2000; 2000IL-00137345.
PR 15-DEC-2000; 2000IL-00140354.
XX
XX (COMP-) COMPUGEN LTD.
PI Mintz L, Freilich S, Bernstein J;
PI WPI; 2002-155037/20.
DR N-PSDB; ABL39693.
XX
XX One hundred and twenty eight novel nucleic acid sequences, useful for
PT treating and diagnosing e.g. cancer, asthma and Alzheimer's.
PS
XX Claim 6; Page 151-152; 290pp; English.
XX
XX ABL39691 to ABL39818 represent novel human nucleic acid sequences
CC encoding the proteins given in ABB06037 to ABB06164. The novel sequences

CC (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective,
 CC antineumatic, antiarthritic, antiporiatic, ophthalmological, vitucide,
 CC vasotropic, antiaeriosclerotic, antinflammatory, dermatological,
 CC anorectic, muscular, anti-HIV, antifertility, cardiovascular,
 CC anticonvulsant, antidiabetic, hypotension, transilliser, cardiant,
 CC immunomodulator, anticonvulsant, antidiabetic, tranquilliser, antituber,
 CC antidepressant, gastroenteric, neuroleptic, cerebroprotective,
 CC neurotic and contraceptive activities. The NS can be used in vaccines,
 CC gene therapy and antisense therapy. Nucleic acids, expression vectors and
 CC antinodules from the present invention can be used for treating and
 CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
 CC diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,
 CC cataracts, restenosis, atherosclerosis, inflammation, skin disorders,
 CC glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular
 CC disease, coagulation disease, ischaemia, hypertension, asthma, immune
 CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,
 CC depression, schizophrenia, viral disease, gastric ulcers, stroke,
 CC Alzheimer's disease and as a contraceptive

CC
 XX
 SQ Sequence 368 AA;

Query Match 38.6%; Score 117; DB 5; Length 368;
 Best Local Similarity 100.0%; Pred. No. 1.1e-96;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 APAPOQSQSPAPSSSGKVTCDIRLRVRAVCEHGPALGCVASRRPOLARQIDVFGQ 234
 DB 209 APAPOQSQSPAPSSSGKVTCDIRLRVRAVCEHGPALGCVASRRPOLARQIDVFGQ 268

QY 235 ATAVALRSRDIGSVVCDIKFSELSYLDAPMGDYLSGALLQALRGVLTALREAVGRE 291
 DB 269 ATAVALRSRDIGSVVCDIKFSELSYLDAPMGDYLSGALLQALRGVLTALREAVGRE 325

RESULT 13

AAE24855 ID AAE24855 standard; protein; 101 AA.

XX AAE24855;

XX 22-OCT-2002 (first entry)

DE Human DED4 DED (death effector domain) protein.

KM Human; death domain; DD; death effector domain; DED; Chlamydia infection;
 KM NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;
 KM inflammation; allergy; autoimmunity; allograft rejection; cell division;
 KM immune-based pathology; fibrosis; arthritis; graft versus host disease;
 KM immunosuppressive; gene therapy; antisense therapy.

OS Homo sapiens.

XX WO200240680-A2.

XX 23-MAY-2002.

XX 15-NOV-2001; 2001MO-US044844.

XX 17-NOV-2000; 2000US-00715893.

XX 29-JUN-2001; 2001US-0301889P.

XX (BURN-) BURHAM INST.

PI Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;

PI Steiner-Liwen F;

DR WPI; 2002-500222/53.

DR N-PSDB; AAD40075.

PT New polypeptide comprising a death domain or death effector domain,
 PT useful for discovery of drugs that suppress infection, inflammation,
 PT allergy, sepsis, autoimmunity, allograft rejection and other diseases.

PS Claim 1; Page 175; 209P; English.

XX The invention relates to an isolated polypeptide comprising a death
 CC domain (DD), death effector domain (DED) or NB-ARC domain. The invention
 CC is useful for identifying a binding agent, preferably a protein or a drug
 CC that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC
 CC domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or
 CC NIDD (NGFR-interacting Death Domain), with a candidate binding agent and
 CC detecting the association of the domain and the candidate binding agent,
 CC by yeast two hybrid assay, immunoprecipitation, SPA, ultraviolet (UV) or
 CC chemical crosslinking, nuclear magnetic resonance (NMR), mass
 CC spectroscopy (MS) and FPA. The invention is useful for modulating the
 CC level of a cell process such as cell proliferation, cell adhesion, cell
 CC stress responses, responses to microbial infection and B cell
 CC immunoglobulin class switching, in particular apoptosis within a cell.
 CC Antibody specifically reactive with CTDD DD of C. trachomatis, C.
 CC muridarum, C. pneumoniae, and C. psittaci or a nucleic acid encoding the
 CC CTDD DD protein is useful for detecting a Chlamydia infection. The
 CC invention is useful for modulating the activity of oncogenic proteins,
 CC for treating a pathology caused by the oncogenic proteins and for
 CC treating bacterial infections by modulating the activity of bacterial
 CC proteins. The protein and antibody specific for it are useful for
 CC discovery of drugs that suppress infection, inflammation, allergy,
 CC sepsis, autoimmunity, allograft rejection and other diseases. The protein
 CC is useful for treating immune-based pathologies, pathologies associated
 CC with cell division, inflammatory diseases such as sepsis, fibrosis,
 CC arthritis, graft versus host disease. The invention is used in antisense
 CC therapy and gene therapy. The present sequence is human DED4 DED protein

XX
 SQ Sequence 101 AA;

Query Match 22.1%; Score 67; DB 5; Length 101;
 Best Local Similarity 100.0%; Pred. No. 4.3e-52;
 Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 WEDECDIDYYGMLSLRMPFVVGQUTRECELELAFLDEAPAGAGLARAGLEELLE 71
 DB 1 WEDECDIDYYGMLSLRMPFVVGQUTRECELELAFLDEAPAGAGLARAGLEELLE 60

QY 72 LERRGQC 78

DB 61 LERRGQC 67

RESULT 14

AAE38898 ID AAE38898 standard; protein; 101 AA.

XX AAE38898;

XX 18-DEC-2003 (first entry)

DE Human DED4 DED protein.

KM Human; death domain; DD; death effector domain; DED; cell proliferation;
 KM Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;
 KM neural growth factor receptor-interacting death domain; cell adhesion;
 KM vasotropic; microbial infection; inflammation; allograft rejection; CTDD;
 KM cell stress response; benign prostatic hypertrophy; antibacterial; NIDD;
 KM apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;
 KM neoplasia; restenosis; immunosuppressive; antibody therapy; cytostatic;
 KM keloid.

OS Homo sapiens.

XX US2003049702-A1.

XX 13-MAR-2003.

XX 15-NOV-2001; 2001US-00001254.

XX 17-NOV-2000; 2000US-00715893.

XX 17-NOV-2000; 2000US-0367360P.

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OM protein - protein search, using sw model

Run on: February 12, 2005, 15:25:44 ; Search time 74 Seconds
(without alignments)
1583.627 Million cell updates/sec

Title: US-10-030-271-2
Perfect score: 1550
Sequence: 1 MALSGSTAPPCWEDECDLY.....LREAVGREAVRLVSVDEAD 303

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneeqp19808:*
2: geneeqp19908:*
3: geneeqp20008:*
4: geneeqp20018:*
5: geneeqp20028:*
6: geneeqp20038:*
7: geneeqp20048:*
8: geneeqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1550	100.0	303	4 AAB60386	Aab60386 Human apo
2	1550	100.0	326	4 AAB60387	Aab60387 Human apo
3	1543	99.5	318	5 AAE24860	Aae24860 Human DED
4	1543	99.5	318	5 AAE38903	Aae38903 Human DED
5	1543	99.5	326	5 AAB07263	Abb07263 Human apo
6	1543	99.5	326	7 ADC79260	Adc79260 Human DED
7	1543	99.5	366	4 AAG73852	Aag73852 Human DED
8	1413	91.2	304	3 AAB15551	Aab15551 Apoptosis
9	1404	90.6	319	3 AAB58420	Aab58420 Lung canc
10	1090.5	70.4	361	5 ABB06038	Abb06038 Human NS
11	1090.5	70.4	368	5 ABB06039	Abb06039 Human NS
12	987	63.7	242	4 AAM25705	Aam25705 Human pro
13	950.5	61.3	277	4 AAM39805	Aam39805 Human pro
14	854	55.1	217	4 AAM41591	Aam41591 Human pro
15	622.5	40.2	318	4 AAB94040	Aab94040 Human pro
16	614.5	39.6	318	2 AAW90108	Aaw90108 Human FLA
17	614.5	39.6	318	2 AAY51022	Aay51022 Human DED
18	614.5	39.6	318	5 AAE26087	Aae26087 Human FLA
19	613.5	39.6	318	4 AAB93016	Aab93016 Human pro
20	608.5	39.3	318	2 AAW90109	Aaw90109 Mouse FLA
21	608.5	39.3	318	3 AAY51023	Aay51023 Murine DE
22	608.5	39.3	318	5 AAE26088	Aae26088 Mouse FLA
23	514	33.2	101	5 AAE24855	Aae24855 Human DED
24	514	33.2	101	5 AAE38898	Aae38898 Human DED
25	136	8.8	340	3 AAY84360	Aay84360 Amino aci

26	136	8.8	397	8 ADP24485	Adp24485 PRO poly
27	135.5	8.7	398	7 ABO72356	Abot72356 Pseudomon
28	124	8.0	289	7 ABO77445	Abot77445 Pseudomon
29	124	8.0	599	7 ABO68504	Abot68504 Pseudomon
30	123.5	8.0	404	7 ABO84268	Abot84268 Pseudomon
31	122	7.9	450	7 ABO83695	Abot83695 Pseudomon
32	121.5	7.8	182	7 ABO84091	Abot84091 Pseudomon
33	120	7.7	165	7 ABO73027	Abot73027 Pseudomon
34	119.5	7.7	1041	7 ABO76891	Abot76891 Pseudomon
35	119	7.7	891	7 ABO81878	Abot81878 Pseudomon
36	119	7.7	1938	6 ABE76679	Abep76679 Streptomy
37	117.5	7.6	334	7 ABO78408	Abot78408 Pseudomon
38	117.5	7.6	372	7 ABO74480	Abot74480 Pseudomon
39	117	7.5	549	7 ABO69003	Abot69003 Pseudomon
40	117	7.5	589	7 ABO73107	Abot73107 Pseudomon
41	116.5	7.5	407	7 ABO71933	Abot71933 Pseudomon
42	116.5	7.5	557	7 ABO79337	Abot79337 Pseudomon
43	116	7.5	735	7 ABO83426	Abot83426 Pseudomon
44	115.5	7.5	574	7 ABO70112	Abot70112 Pseudomon
45	115.5	7.5	582	7 ABO77436	Abot77436 Pseudomon

ALIGNMENTS

RESULT 1	AAB60386	standard; protein; 303 AA.
ID	AAB60386	
XX	24-APR-2001	(first entry)
XX	Human apoptosis-associated factor NT2RM1000558 (portion), SEQ ID NO:2.	
XX	Human, apoptosis-associated factor; NT2RM1000558; death effector domain; DED; caspase family cleavage domain; pro-apoptotic; drug screening; cell proliferation; ischaemic disease; chronic viral disease.	
XX	Homo sapiens.	
OS	WO200104300-A1.	
XX	18-JAN-2001.	
XX	06-JUL-2000; 2000WO-JP004516.	
XX	08-JUL-1999; 99JP-00194179.	
XX	18-OCT-1999; 99US-0159586P.	
XX	(HELI-) HELIX RES INST.	
XX	Ota T, Isogai T, Nishikawa T, Kawai Y, Miyoshi S, Satoh S; WPI; 2001-138348/14.	
XX	N-PSDB; AAF27407.	
PT	Polynucleotide encoding an apoptosis-associated factor protein with death effector domain and caspase family-cleavage domain, useful in regulating diseases with cell proliferation.	
PT	Claim 1; Page 43-44; 53pp; Japanese.	
XX	The invention relates to a novel human apoptosis-associated factor (AAB60386, AAB60387), designated NT2RM1000558, which contains a death effector domain (DED) and a caspase family cleavage domain and is capable of inducing apoptosis in cells. The invention also relates to nucleic acids encoding the protein (AAF27407, AAF27408); variants of the protein (particularly dominant negative variants); vectors and host cells comprising a nucleic acid which encodes an apoptosis-associated factor of the invention; the recombinant production of the protein; an antibody against the protein; and methods of screening for compounds which can regulate apoptosis. The apoptosis-related factor is useful in regulating	

CC diseases associated with cell proliferation and in screening drug
 CC candidates e.g., for regulating cell proliferation or cell death in
 CC ischemic diseases and chronic viral diseases. The present sequence
 CC represents a substantial proportion of the human apoptosis-associated
 CC factor NT2RM1000558
 CC XX

Sequence 303 AA;

Query Match 100.0%; Score 1550; DB 4; Length 303;
 Best Local Similarity 100.0%; Pred. No. 1e-144; Indels 0; Gaps 0;
 Matches 303; Conservative 0; Mismatches 0;

QY 1 MALSGSTPAPCWEDECDIYYGMLSLHMFVVGQLTCELELAFLLDEAPGAGGLA 60
 Db 1 MALSGSTPAPCWEDECDIYYGMLSLHMFVVGQLTCELELAFLLDEAPGAGGLA 60
 QY 61 PARSGLELLELERRGCGESNRLGQLRVLARHDLPHLAKRRRPPVPERYSYGT 120
 Db 61 PARSGLELLELERRGCGESNRLGQLRVLARHDLPHLAKRRRPPVPERYSYGT 120
 QY 121 SSSKRTGSCRRRRQSSSSANSQCGQMTGSPPTKQGRSGRSGARRRRGAPAPQ 180
 Db 121 SSSKRTGSCRRRRQSSSSANSQCGQMTGSPPTKQGRSGRSGARRRRGAPAPQ 180
 QY 121 SSSKRTGSCRRRRQSSSSANSQCGQMTGSPPTKQGRSGRSGARRRRGAPAPQ 180
 Db 181 QOSEPARSSSEKVTCDIRLVRAYCEHGPALBEGVASRRPQALAROLDVFGQATAVLR 240
 QY 181 QOSEPARSSSEKVTCDIRLVRAYCEHGPALBEGVASRRPQALAROLDVFGQATAVLR 240
 Db 181 QOSEPARSSSEKVTCDIRLVRAYCEHGPALBEGVASRRPQALAROLDVFGQATAVLR 240
 QY 241 SRDLGSVVCDIKFSELSYLDAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSD 300
 Db 241 SRDLGSVVCDIKFSELSYLDAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSD 300
 QY 301 EAD 303
 Db 301 EAD 303

RESULT 2

AAB60387
 ID AAB60387 standard; protein; 326 AA.

AAB60387;

24-APR-2001 (first entry)

Human apoptosis-associated factor NT2RM1000558, SEQ ID NO.4.

Human; apoptosis-associated factor; NT2RM1000558; death effector domain;

KW DED; caspase family cleavage domain; pro-apoptotic; drug screening;

KW cell proliferation; ischemic disease; chronic viral disease.

XX Homo sapiens.

XX MO200104300-A1.

XX 18-JAN-2001.

XX 06-JUL-2000; 2000WO-JP004516.

XX 08-JUL-1999; 99JP-00194179.

XX 18-OCT-1999; 99US-0159586P.

XX (HELI-) HELIX RES INST.

XX Oca T, Isogai T, Nishikawa T, Kawai Y, Miyoshi S, Satoh S;

XX WPI, 2001-138348/14.

XX N-PSDB; AAF27408.

XX Polynucleotide encoding an apoptosis-associated factor protein with death

XX effector domain and caspase family-cleavage domain, useful in regulating

XX diseases with cell proliferation.

PS Claim 3; Page 47-48; 53pp; Japanese.

XX The invention relates to a novel human apoptosis-associated factor
 CC (AAB60386, AAB60387), designated NT2RM1000558, which contains a death
 CC effector domain (DED) and a caspase family cleavage domain and is capable
 CC of inducing apoptosis in cells. The invention also relates to nucleic
 CC acids encoding the protein (AAF27407, AAF27408); variants of the protein
 CC (particularly dominant negative variants); vectors and host cells
 CC comprising a nucleic acid which encodes an apoptosis-associated factor
 CC of the invention; the recombinant production of the protein; an antibody
 CC against the protein; and methods of screening for compounds which can
 CC regulate apoptosis. The apoptosis-related factor is useful in regulating
 CC diseases associated with cell proliferation and in screening drug
 CC candidates e.g., for regulating cell proliferation or cell death in
 CC ischemic diseases and chronic viral diseases. The present sequence
 CC represents the human apoptosis-associated factor NT2RM1000558
 CC XX

Sequence 326 AA;

Query Match 100.0%; Score 1550; DB 4; Length 326;
 Best Local Similarity 100.0%; Pred. No. 1.e-144; Indels 0; Gaps 0;
 Matches 303; Conservative 0; Mismatches 0;

QY 1 MALSGSTPAPCWEDECDIYYGMLSLHMFVVGQLTCELELAFLLDEAPGAGGLA 60
 Db 1 MALSGSTPAPCWEDECDIYYGMLSLHMFVVGQLTCELELAFLLDEAPGAGGLA 60
 QY 61 PARSGLELLELERRGCGESNRLGQLRVLARHDLPHLAKRRRPPVPERYSYGT 120
 Db 61 PARSGLELLELERRGCGESNRLGQLRVLARHDLPHLAKRRRPPVPERYSYGT 120
 QY 121 SSSKRTGSCRRRRQSSSSANSQCGQMTGSPPTKQGRSGRSGARRRRGAPAPQ 180
 Db 121 SSSKRTGSCRRRRQSSSSANSQCGQMTGSPPTKQGRSGRSGARRRRGAPAPQ 180
 QY 121 SSSKRTGSCRRRRQSSSSANSQCGQMTGSPPTKQGRSGRSGARRRRGAPAPQ 180
 Db 181 QOSEPARSSSEKVTCDIRLVRAYCEHGPALBEGVASRRPQALAROLDVFGQATAVLR 240
 QY 181 QOSEPARSSSEKVTCDIRLVRAYCEHGPALBEGVASRRPQALAROLDVFGQATAVLR 240
 Db 181 QOSEPARSSSEKVTCDIRLVRAYCEHGPALBEGVASRRPQALAROLDVFGQATAVLR 240
 QY 241 SRDLGSVVCDIKFSELSYLDAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSD 300
 Db 241 SRDLGSVVCDIKFSELSYLDAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSD 300
 QY 301 EAD 303
 Db 301 EAD 303

RESULT 3

AAE24860
 ID AAE24860 standard; protein; 318 AA.

AAE24860;

22-OCT-2002 (first entry)

Human DED4 (death effector domain) protein.

Human; death domain; DD; death effector domain; DED; Chlamydia infection;

KW NB-ARC domain; apoptosis; oncogenic protein; bacterial infection; sepsis;

KW inflammation; allergy; autoimmunity; allograft rejection; cell division;

KW immune-based pathology; fibrosis; arthritis; graft versus host disease;

KW immunosuppressive; gene therapy; anticense therapy.

XX Homo sapiens.

XX Key

XX Region

XX WO200240680-A2.

XX 23-MAY-2002.

Location/Qualifiers
 53..74
 /note="Nuclear localisation sequence"

XX 15-NOV-2001; 2001WO-US044844.
 XX PF
 XX 17-NOV-2000; 2000US-00715893.
 PR 29-JUN-2001; 2001US-0301889P.
 XX PR
 XX (BURN-) BURNHAM INST.
 XX PA
 XX Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
 PI Stenner-Liewen F;
 XX WPI, 2002-500222/53.
 XX DR N-PSDB; AAD40080.
 XX DR

New polypeptide comprising a death domain or death effector domain,
 useful for discovery of drugs that suppress infection, inflammation,
 allergy, sepsis, autoimmunity, allograft rejection and other diseases.

Claim 3; Page 186-187; 209pp; English.

The invention relates to an isolated polypeptide comprising a death
 domain (DD), death effector domain (DED) or NB-ARC domain. The invention
 is useful for identifying a binding agent, preferably a protein or a drug
 that binds a DD, DED or NB-ARC domain, by contacting a DD, DED or NB-ARC
 domain from DAP3, IRAK4, CTDD (Chlamydia trachomatis DD protein), DED4 or
 NIDD (NGFR-interacting Death Domain), with a candidate binding agent and
 detecting the association of the domain and the candidate binding agent,
 by yeast two hybrid assay, immunoprecipitation, SPR, ultraviolet (UV) or
 chemical crosslinking, nuclear magnetic resonance (NMR), mass
 spectroscopy (MS) and FPA. The invention is useful for modulating the
 level of a cell process such as cell proliferation, cell adhesion, cell
 stress responses, responses to microbial infection, cell apoptosis, cell
 immunoglobulin class switching, in particular apoptosis within a cell.
 Antibody specifically reactive with CTDD DD of C. trachomatis, C.
 muridarum, C. pneumoniae, and C. peitraci or a nucleic acid encoding the
 CTDD DD protein is useful for detecting a Chlamydia infection. The
 invention is useful for modulating the activity of oncogenic proteins,
 for treating a pathology caused by the oncogenic proteins and for
 treating bacterial infections by modulating the activity of bacterial
 proteins. The protein and antibody specific for it are useful for
 discovery of drugs that suppress infection, inflammation, allergy,
 sepsis, autoimmunity, allograft rejection and other diseases. The protein
 is useful for treating immune-based pathologies, pathologies associated
 with cell division, inflammatory diseases such as sepsis, fibrosis,
 arthritis, graft versus host disease. The invention is used in antisense
 therapy and gene therapy. The present sequence is human DED4 protein

Sequence 318 AA;

Query Match 99.5%; Score 1543; DB 5; Length 318;
 Best Local Similarity 99.7%; Pred. No. 5, 5e-144;

Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALSGTAPPCWEEBDCLDYGYMLSHRMFEVVGQLTCELELLAFLIDEAPGAAGGLA 60
 DB 1 MALSGTAPPCWEEBDCLDYGYMLSHRMFEVVGQLTCELELLAFLIDEAPGAAGGLA 60
 QY 61 PARSGLELLELERRGGCGESNLRLGQLRLTAHHDLPHARRRRVSPERSYSGS 120
 DB 61 PARSGLELLELERRGGCGESNLRLGQLRLTAHHDLPHARRRRVSPERSYSGS 120
 QY 121 SSSKRTGSSCRRRSSSSANSQCGWETGSPPTKRQRSSRPPSGARRRRRGAAPAPQ 180
 DB 121 SSSKRTGSSCRRRSSSSANSQCGWETGSPPTKRQRSSRPPSGARRRRRGAAPAPQ 180
 QY 181 QOSEPARPSSBQKTCIDRLRLVRAVECEHPALGEGVARSRRPQALARQLDVGQATAVLR 240
 DB 181 QOSEPARPSSBQKTCIDRLRLVRAVECEHPALGEGVARSRRPQALARQLDVGQATAVLR 240
 QY 241 SRDLGSVVCIDIKFSELSYDAFWGDTLGGALLQALRGVLTALAEAVGREAVRLVVD 300
 DB 241 SRDLGSVVCIDIKFSELSYDAFWGDTLGGALLQALRGVLTALAEAVGREAVRLVVD 300

QY 301 EAD 303
 DB 301 EAD 303

RESULT 4
 ID AAE38903
 AA AAE38903 standard; protein; 318 AA.

AAE38903;

18-DEC-2003 (first entry)

Human DED4 protein.

Human; death Domain; DD; death effector domain; DED; cell proliferation;
 Chlamydia trachomatis death domain containing protein; fibrosis; sepsis;
 neural growth factor receptor-interacting death domain; cell adhesion;
 vasotropic; microbial infection; inflammation; allograft rejection; CTDD;
 cell stress response; benign prostatic hypertrophy; antibacterial; NIDD;
 apoptosis; infection; autoimmunity; allergy; hyperplasia; gene therapy;
 keloid; restenosis; immunosuppressive; antibody therapy; cytostatic;
 Homo sapiens.

Key Location/Qualifiers
 FT Domain 12..112
 FT Peptide /note="Death effector domain of DED-4"
 FT 53..74
 FT /note="Nuclear localisation sequence"

US2003049702-A1.

13-MAR-2003.

15-NOV-2001; 2001US-00001254.

17-NOV-2000; 2000US-00715893.

17-NOV-2000; 2000US-0367360P.

29-JUN-2001; 2001US-0301889P.

(REED/) REED J C.
 (GODZ/) GODZIK A.
 (PAWL/) PAWLOWSKI K.
 (FIOR/) FIORENTINO L.
 (LEES/) LEE S H.
 (ROTH/) ROTH W.
 (STEN/) STENNER-LIEWEN F.

Reed JC, Godzik A, Pawlowski K, Fiorentino L, Lee SH, Roth W;
 PI Stenner-Liewen F;

WPI, 2002-500222/53.
 N-PSDB; AAD59062.

New polypeptide comprising a death domain or death effector domain,
 useful for discovery of drugs that suppress infection, inflammation,
 allergy, sepsis, autoimmunity, allograft rejection and other diseases.

Claim 2; Page 44-45; 99pp; English.

The present invention provides novel death Domain (DD) and death effector
 domain (DED) proteins and nucleic acids encoding them. The invention also
 provides death domain containing protein such as Chlamydia trachomatis
 death domain containing protein (CTDD) DD and neural growth factor
 receptor-interacting death domain (NIDD) DD. The invention is useful for
 identifying a binding agent (e.g. protein or drug) that binds a DD, DED
 or NB-ARC domain from DAP3, IRAK4, CTDD, DED4 or NIDD with a candidate
 binding agent and identifying an effective agent (e.g. protein or drug)
 that modulates the association of a DD, DED or NB-ARC domain with protein
 that binds the DD, DED or NB-ARC domain. The invention is also useful for
 modulating the level of cell process such as apoptosis, cell adhesion,

ADCT9260
ID ADCT9260 standard; protein; 326 AA.
XX
AC ADCT9260;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human DEDD2 protein SEQ ID NO:2.
XX
KW human; death effector domains containing DNA-binding protein;
KW DED-containing DNA-binding protein; DEDD2; cell death; gene therapy;
KW cytostatic; cancer; chronic myeloid leukaemia.
XX
OS Homo sapiens.
XX
PN WO2003054195-A1.
XX
PD 03-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-JP013371.
XX
PR 20-DEC-2001; 2001JP-00387854.
XX
PR 18-JUL-2002; 2002JP-00209458.
XX
PA (MORG) MORINAGA MILK IND CO LTD.
XX
PI Suzu S, Hageshita H, Nomaguchi K, Yamada M, Hayasawa H;
XX
DR WPI: 2003-569246/53.
XX
DR N-PSDB; ADCT9259.
XX
PT DNA encoding cell death proteins for treatment of kidney, large intestine
XX
PS and prostate cancers and leukemia.
XX
PS Claim 1; Page 20-21; 26pp; Japanese.
XX
CC The present sequence represents a human death effector domains (DED)
CC containing DNA-binding protein (DEDD) protein, designated DEDD2, that
CC causes cell death. Also described: (1) primer and probe for investigation
CC of the DEDD2 gene; and (2) reagents for gene therapy. DEDD2 has
CC cytostatic activity. DEDD2 can be used in the diagnosis and treatment of
CC cancers of the kidney, large intestine and prostate, and acute and
CC chronic myeloid leukaemia.
XX
SQ Sequence 326 AA;
Query Match 99.5%; Score 1543; DB 7; Length 326;
Best Local Similarity 99.7%; Pred. No. 5.7e-144;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MALSGSTPAPCWEDECDLDYGMLSLHMFVVGQLTECELELLAFLDPAAGLA 60
DB 1 MALSGSTPAPCWEDECDLDYGMLSLHMFVVGQLTECELELLAFLDPAAGLA 60
QY 61 PARSGLELLLELRGGCGESNLRLGQLAVLARHDLPLHAKRRRPVSPERYSYGTS 120
DB 61 PARSGLELLLELRGGCGESNLRLGQLAVLARHDLPLHAKRRRPVSPERYSYGTS 120
QY 121 SSSKRTGSCRRRRSSSSANSQOQWETGSPPTKRRSRGPRSGARRRRGAPAPQ 180
DB 121 SSSKRTGSCRRRRSSSSANSQOQWETGSPPTKRRSRGPRSGARRRRGAPAPQ 180
QY 181 QOSEPARPSSEKVTCDIRLVRVRAEYCEHGPALGEGVARSRRPQALARQDVGQATAVLR 240
DB 181 QOSEPARPSSEKVTCDIRLVRVRAEYCEHGPALGEGVARSRRPQALARQDVGQATAVLR 240
QY 241 SSDLGAVCDIKFSELSYDAFWGYLSGALLQALRGVFLTEALREAVGREAARLLVSD 300
DB 241 SDDLGVAVCDIKFSELSYDAFWGYLSGALLQALRGVFLTEALREAVGREAARLLVSD 300
QY 301 EAD 303
DB 301 EAD 303

RESULT 7
AAG73852
ID AAG73852 standard; protein; 366 AA.
XX
AC AAG73852;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen protein SEQ ID NO:4616.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US026524.
XX
PR 29-SEP-1999; 99US-0157137P.
XX
PR 03-NOV-1999; 99US-0163280P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI: 2001-235357/24.
XX
DR N-PSDB; AAG73283.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX
PT useful for preventing, diagnosing and/or treating colorectal cancers.
XX
PS Claim 11; Page 6413-6414; 9803pp; English.
XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene therapy
CC and vaccine production. N and P may be used in the prevention, diagnosis
CC and treatment of diseases associated with inappropriate P expression. For
CC example, N and P may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of P by expressing inactive proteins or to
CC supplement the patient's own production of P. Additionally, N may be used
CC to produce the colon cancer-associated P, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P
CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027
CC to 1052, 7921 and 7922
XX
SQ Sequence 366 AA;
Query Match 99.5%; Score 1543; DB 4; Length 366;
Best Local Similarity 99.7%; Pred. No. 6.6e-144;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MALSGSTPAPCWEDECDLDYGMLSLHMFVVGQLTECELELLAFLDPAAGLA 60
DB 41 MALSGSTPAPCWEDECDLDYGMLSLHMFVVGQLTECELELLAFLDPAAGLA 100
QY 61 PARSGLELLLELRGGCGESNLRLGQLAVLARHDLPLHAKRRRPVSPERYSYGTS 120
DB 101 PARSGLELLLELRGGCGESNLRLGQLAVLARHDLPLHAKRRRPVSPERYSYGTS 160
QY 121 SSSKRTGSCRRRRSSSSANSQOQWETGSPPTKRRSRGPRSGARRRRGAPAPQ 180

Db 161 SSKRTGSGCRRRRSSANSQGGWETGSPPTKQRRSGRSGGARRRRRCAPAPQ 220
QY 181 QQSEPARPSSEKVTCDIRLRVRAVECEHPALVEQVARSRRPQALARQLDVFGQATAVLR 240
Db 221 QQSEPARPSSEKVTCDIRLRVRAVECEHPALVEQVARSRRPQALARQLDVFGQATAVLR 280
QY 241 SRDLSGVVCDIKFSELSYLDAFWGDYLSGALLQALRGVFLTEALREAVGREAVLLVSD 300
Db 281 SRDLSGVVCDIKFSELSYLDAFWGDYLSGALLQALRGVFLTEALREAVGREAVLLVSD 340
QY 301 EAD 303
Db 341 EAD 343

RESULT 8
AAB15551
ID AAB15551 standard; protein; 304 AA.
AC AAB15551;
XX
XX 28-FEB-2001 (first entry)

XX Apoptosis related protein encoded by gene 1 clone HLD0K36.
XX
XX Cytostatic; antiinflammatory; immunosuppressive; antisclerotic; cardiant;
XX anti-AIDS; vasotropic; anti-ischaemic; antiparkinsonian;
XX anti-Alzheimer; gene therapy; human; apoptosis; fusion protein; cancer;
XX colon; breast; prostate; melanoma; lymphoma; inflammation; herpes;
XX autoimmune disorder; multiple sclerosis; viral infection.

OS Homo sapiens.
XX
XX WO200056752-A2.
XX
XX 28-SEP-2000.

PF 15-MAR-2000; 2000WO-US006642.
XX
XX 24-MAR-1999; 99US-0126018P.
XX 17-JUN-1999; 99US-0139638P.
XX 18-AUG-1999; 99US-0149449P.

XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Ni J, Young PA;
XX
XX WPI; 2000-587660/55.
XX N-PSDB; AAA95790.

XX Nucleic acids encoding human apoptosis associated protein, useful for the
XX prevention, treatment and diagnosis of e.g. Alzheimer's and Parkinson's
XX disease, inflammation and ischemic injury.
XX
XX Claim 11; Page 252-253; 273pp; English.

XX The invention relates to the isolation of genes encoding 9 human
XX apoptosis-related proteins. The nucleotide sequences AAA95790-A95798
XX encode the human apoptosis related proteins AAB15551-B15559. The genes
XX can be used to generate fusion proteins by linking to the gene for the
XX human immunoglobulin G Fc (IgG Fc) portion (AAA95799) for increasing the
XX stability of the fusion protein as compared to the human protein only.
XX The gene and encoded protein may be used in the prevention, treatment and
XX diagnosis of diseases associated with inappropriate apoptosis associated
XX protein expression, e.g. cancer (e.g. colon, breast and prostate cancer,
XX melanomas and lymphomas), inflammation, autoimmune disorders (e.g.
XX multiple sclerosis) and viral infections (e.g. herpes)

XX Sequence 304 AA;
SQ

Query Match 91.2%; Score 1413; DB 3; Length 304;
Best Local Similarity 99.6%; Pred. No. 3.9e-11;
Matches 280; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 MSLHMEFVVGQLTCECELELAFLLDEAPGAAGGLARASGLLELLEERRQCGESN 82
Db 1 MSLHMEFVVGQLTCECELELAFLLDEAPGAAGGLARASGLLELLEERRQCGESN 60
QY 83 LRLIGQLRLVLAARDLLPHLARRRRPVSPERYSGTSSSKTTEGSCRRRROSSANS 142
Db 61 LRLIGQLRLVLAARDLLPHLARRRRPVSPERYSGTSSSKTTEGSCRRRROSSANS 120
QY 143 QCGWETGSPPTKQRRSRPFGSGARRRRGAPAPQOQSEPARPSSEKVTCDIRLRV 202
Db 121 QCGWETGSPPTKQRRSRPFGSGARRRRGAPAPQOQSEPARPSSEKVTCDIRLRV 180
QY 203 RAECYCEHPALVEQVARSRRPQALARQLDVFGQATAVLRSDLSGVCDIKFSELSYDAF 262
Db 181 RAECYCEHPALVEQVARSRRPQALARQLDVFGQATAVLRSDLSGVCDIKFSELSYDAF 240
QY 263 WGDYLSGALLQALRGVFLTEALREAVGREAVRLIVSYDEAD 303
Db 241 WGDYLSGALLQALRGVFLTEALREAVGREAVRLIVSYDEAD 281

RESULT 9
AAB58420
ID AAB58420 standard; protein; 319 AA.
AC AAB58420;
XX
XX 14-MAR-2001 (first entry)

XX Lung cancer associated polypeptide sequence SEQ ID 758.
XX
XX Human, lung cancer associated protein; neuroprotective; cytoskeletal;
XX cardioactive; immunomodulatory; muscular active; vulnerary;
XX gastrointestinal; nephrotoxic; antiinfective; gynecological;
XX antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
XX proliferative disorder; wound healing; infectious disease.

OS Homo sapiens.
XX
XX WO200055180-A2.
XX
XX 21-SEP-2000.

PF 08-MAR-2000; 2000WO-US005918.
XX
XX 12-MAR-1999; 99US-0124270P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (ROSE/) ROSEN C A.

XX Ruben SM;
XX
XX WPI; 2000-587514/55.
XX N-PSDB; AAF18296.

XX Lung cancer associated gene sequences, referred to as lung cancer
XX antigeins, useful for treatment, prevention, and diagnosis of disorders
XX such as lung cancer.
XX
XX Claim 11; Page 1275-1276; 1425pp; English.

XX Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
XX associated proteins represented in AAB58106 - AAB58548. Lung cancer
XX associated proteins and polynucleotide sequences, their agonists, and
XX antagonists may have neuroprotective; cytoskeletal; cardioactive;
XX immunomodulatory; muscular active general; vulnerary; gastrointestinal
XX general; nephrotoxic; antiinfective; gynecological; or antibacterial
XX activity. The invention also includes antibodies specific for the protein
XX or polynucleotide sequences. The lung cancer associated polynucleotide
XX sequences may be used for detection of lung cancer, chromosome
XX identification, as chromosome markers, and for numerous other diagnostic
XX or research purposes. The proteins may be used to treat disorders such as

CC neural, immune, muscular, reproductive, gastrointestinal, pulmonary,
CC cardiovascular, renal, and proliferative disorders. The proteins may also
CC be used in the treatment of wounds and infectious diseases.
CC Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are
CC used in the course of the invention for the identification and
CC characterization of the polynucleotide and protein sequences
XX

SQ Sequence 319 AA;

Query Match 90.6%; Score 1404; DB 3; Length 319;
Best Local Similarity 99.6%; Pred. No. 3.2e-130;
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALSGSTAPPCWBEDECDLYGMLSLHMFVVGQLTCELELLAFLDDEAPGAAGLA 60
DB 41 MALSGSTAPPCWBEDECDLYGMLSLHMFVVGQLTCELELLAFLDDEAPGAAGLA 100
QY 61 RARSGLELLELERRGQCESNRLGQLRLVLRHDLPLHARKRRRVPSPERSYGT 120
DB 101 RARSGLELLELERRGQCESNRLGQLRLVLRHDLPLHARKRRRVPSPERSYGT 160
QY 121 SSSKRTGSCRRRRSSSSANSQOGWETGSPPTKRORSRGRPSGARRRRRGAAPAQ 180
DB 161 SSSKRTGSCRRRRSSSSANSQOGWETGSPPTKRORSRGRPSGARRRRRGAAPAQ 220
QY 181 QOSEPARPSESEKVTCDIRLVRABYCEHGPALBEGVASRRPOALARQLDVFGQATAVLR 240
DB 221 QOSEPARPSESEKVTCDIRLVRABYCEHGPALBEGVASRRPOALARQLDVFGQATAVLR 280
QY 241 SSDLGSVCDIKFSELSYLDAPFWGDLGSLALQ 273
DB 281 SDDLGSVCDIKFSELSYLDAPFWGDLGSLALQ 313

RESULT 10
ABBO6038
ID ABB06038 standard; protein; 361 AA.

XX 10-MAY-2002 (first entry)

DE Human NS protein sequence SEQ ID NO:130.

XX Human; cytosolic; osteopathic; gynaecological; neuroprotective;
KW antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;
KW vasotropic; antiarteriosclerotic; antiinflammatory; dermatological;
KW anorectic; muscular; antinfertility; cardiovascular; anticoagulant;
KW antifibrinolytic; hypotension; antiaesthetic; immunomodulator; cardiac;
KW anticonvulsant; antidiabetic; tranquiliser; antidepressant; auroleptic;
KW gastroenteric; virucide; antitumor; cerebroprotective; nootropic;
KW endometriosis; degenerative disease; multiple sclerosis; psoriasis;
KW rheumatoid arthritis; cataract; stenosis; atherosclerosis; glaucoma;
KW inflammation; skin disorder; obesity; muscular dystrophy; AIDS;
KW infertility; cardiovascular disease; coagulation disease; hypertension;
KW ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration;
KW diabetes; anxiety; depression; schizophrenia; viral disease; stroke;
KW gastric ulcer; Alzheimer's disease.

XX Homo sapiens.

OS WO200206315-A2.

XX 24-JAN-2002.

XX 17-JUL-2001; 2001WO-IL000653.

XX 18-JUL-2000; 2000IL-00137345.

XX 15-DEC-2000; 2000IL-00140354.

XX (COMP-) COMPUGEN LTD.

PI Mintz L, Freilich S, Bernstein J;
XX WPI; 2002-155037/20.
DR N-PsDB; ABL39692.

PT One hundred and twenty eight novel nucleic acid sequences, useful for
PT treating and diagnosing e.g. cancer, asthma and Alzheimer's.

XX Claim 6, Page 149-151; 290pp; English.

CC ABL39691 to ABL38818 represent novel human nucleic acid sequences
CC encoding the proteins given in ABB06037 to ABB06164. The novel sequences
CC (Ns) can have cytosolic, osteopathic, gynaecological, neuroprotective,
CC antirheumatic, antiarthritic, antipsoriatic, ophthalmological, virucide,
CC vasotropic, antiarteriosclerotic, antiinflammatory, dermatological,
CC anorectic, muscular, anti-HIV, antinfertility, cardiovascular,
CC anticonvulsant, antifibrinolytic, hypotension, antiaesthetic, cardiac,
CC immunomodulator, anticonvulsant, antidiabetic, tranquiliser, antitumor,
CC antidepressant, gastrointestinal, auroleptic, cerebroprotective,
CC nootropic and contraceptive activities. The NS can be used in vaccines,
CC gene therapy and antisense therapy. Nucleic acids, expression vectors and
CC antibodies from the present invention can be used for treating and
CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
CC diseases, dyslexia, multiple sclerosis, rheumatoid arthritis, psoriasis,
CC cataracts, stenosis, atherosclerosis, inflammation, skin disorders,
CC glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular
CC disease, coagulation disease, ischaemia, hypertension, diabetes, asthma, immune
CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,
CC depression, schizophrenia, viral disease, gastric ulcers, stroke,
CC Alzheimer's disease and as a contraceptive
XX

SQ Sequence 361 AA;

Query Match 70.4%; Score 1090.5; DB 5; Length 361;
Best Local Similarity 73.9%; Pred. No. 4.3e-99;
Matches 229; Conservative 11; Mismatches 31; Indels 39; Gaps 4;

QY 1 MALSGSTAPPCWBEDECDLYGMLSLHMFVVGQLTCELELLAFLDDEAPGAAGLA 60
DB 29 MALSGSTAPPCWBEDECDLYGMLSLHMFVVGQLTCELELLAFLDDEAPGAAGLA 88
QY 61 RARSGLELLELERRGQCESNRLGQLRLVLRHDLPLHARKRRRVPSPERSYGT 120
DB 89 RARSGLELLELERRGQCESNRLGQLRLVLRHDLPLHARKRRRVPSPERSYGT 133
QY 121 SSSKRTGSCRRRRSSSSANSQOGWETGSPPTKRORSRGRPSGARRRRRGAAPAQ 168
DB 134 SSSKRTGSCRRRRSSSSANSQOGWETGSPPTKRORSRGRPSGARRRRRGAAPAQ 188
QY 169 SSSKRTGSCRRRRSSSSANSQOGWETGSPPTKRORSRGRPSGARRRRRGAAPAQ 221
DB 189 SSSKRTGSCRRRRSSSSANSQOGWETGSPPTKRORSRGRPSGARRRRRGAAPAQ 248
QY 222 PQLARQLDVFGQATAVLRSDLSVCDIKFSELSYLDAPFWGDLGSLALQALRGVFLT 281
DB 249 PQLARQLDVFGQATAVLRSDLSVCDIKFSELSYLDAPFWGDLGSLALQALRGVFLT 308
QY 282 EALREAVGRE 291
DB 309 EALREAVGRE 318

RESULT 11

ABBO6039
ID ABB06039 standard; protein; 368 AA.

XX 10-MAY-2002 (first entry)

XX Human NS protein sequence SEQ ID NO:131.

XX Human; cytosolic; osteopathic; gynaecological; neuroprotective;

KW antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;
 KW vasotropic; antiarteriosclerotic; antiinflammatory; dermatological;
 KW anorectic; muscular; antinfertility; cardiovascular; anticoagulant;
 KW antifibrinolytic; hypotension; antiaesthetic; immunomodulator; cardiant;
 KW anticonvulsant; antidiabetic; tranquilizer; antidepressant; antiepileptic;
 KW gastroenteric; virucide; antitumor; cerebroprotective; nootropic;
 KW contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia;
 KW endometriosis; degenerative disease; multiple sclerosis; psoriasis;
 KW rheumatoid arthritis; cataract; restenosis; muscular dystrophy; AIDS;
 KW inflammation; skin disorder; obesity; coagulation disease; hypertension;
 KW intercellular; cardiovascular disease; epilepsy; angina; neurodegeneration;
 KW diabetes; anxiety; depression; schizophrenia; viral disease; stroke;
 KW gastric ulcer; Alzheimer's disease.
 KM Homo sapiens.
 XX
 OS
 PN MO200206315-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 17-JUL-2001; 2001WO-IL000653.
 XX
 PR 18-JUL-2000; 2000IL-00137345.
 XX
 PR 15-DEC-2000; 2000IL-00140354.
 XX
 PA (COMP-) COMPUGEN LTD.
 XX
 PI Mintz L, Freilich S, Bernstein J;
 XX
 DR WPI: 2002-155037/20.
 XX
 DR N-PSDB; ABL39693.
 XX
 PS One hundred and twenty eight novel nucleic acid sequences, useful for
 PT treating and diagnosing e.g. cancer, asthma and Alzheimer's.
 PT
 Claim 6, Page 151-152; 290pp; English.
 CC ABL39691 to ABL39818 represent novel human nucleic acid sequences
 CC encoding the proteins given in ABB06037 to ABB06164. The novel sequences
 CC (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective,
 CC antirheumatic, antiarthritic, antipsoriatic, ophthalmological, virucide,
 CC vasotropic, antiarteriosclerotic, antiinflammatory, dermatological,
 CC anorectic, muscular, anti-HIV, antinfertility, cardiovascular,
 CC anticoagulant, antifibrinolytic, hypotension, antiaesthetic, cardiant,
 CC immunomodulator, anticonvulsant, antidiabetic, tranquilizer, antitumor,
 CC antidepressant, gastroenteric, antiepileptic, cerebroprotective,
 CC nootropic and contraceptive activities. The NS can be used in vaccines,
 CC gene therapy and antitense therapy. Nucleic acids, expression vectors and
 CC antibodies from the present invention can be used for treating and
 CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
 CC diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,
 CC cataracts, restenosis, atherosclerosis, inflammation, skin disorders,
 CC glaucoma, obesity, muscular dystrophy, AIDS, intercellular, cardiovascular
 CC disease, coagulation disease, ischaemia, hypertension, asthma, immune
 CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,
 CC depression, schizophrenia, viral disease, gastric ulcers, stroke,
 CC Alzheimer's disease and as a contraceptive
 CC
 XX
 XX Sequence 368 AA:
 XX
 Query Match 70.4%; Score 1090.5; DB 5; Length 368;
 Best Local Similarity 73.9%; Pred. No. 4.4e-99;
 Matches 229; Conservative 11; Mismatches 31; Indels 39; Gaps 4;
 QY 1 MALSGSTPAPCWEDECDIYYGMLSLRMEFVVGQGLTECELELLAFLDPAAGAGLA 60
 DB 36 MALSGSTPAPCWEDECDIYYGMLSLRMEFVVGQGLTECELELLAFLDPAAGAGYA 95
 QY 61 PARSGLELLLERRGCGGSENLALGQLAVLARHDLPLAKRRRPVPEKSYGTS 120
 DB 96 PARSGLELLLERRGCGGSENLALGQLAVLARHDLPLAKRRRPVPEKSYGTS 140

QY 121 SSSKTEGSCRRRRROSSSSANSOQO-----WETGSPPTKR-----QRSSRGRRSGCA-- 168
 DB 141 -----AAGCCLQALIMAPPALORGRVAVANGSAGVAGILSRFGSGQAPPPQSGTAES 195
 QY 169 -----RRRRRGAAPAPQOQSEPPAPSSSEKTYTCOIRLVRAEYCEHGFALFGVASRR 221
 DB 196 GPANWQGTAAERAPAPAPQOQSEPPAPSSSEKTYTCOIRLVRAEYCEHGFALFGVASRR 255
 QY 222 PQLAROLDVFGQATVATRSRDIGSVVCDIKFSELSYLDAPWGDYLSGALLQALRGVFLT 281
 DB 256 PQLAROLDVFGQATVATRSRDIGSVVCDIKFSELSYLDAPWGDYLSGALLQALRGVFLT 315
 QY 282 EALREAVGRE 291
 DB 316 EALREAVGRE 325
 RESULT 12
 ID AAM25705
 ID AAM25705 standard; protein; 242 AA.
 AC AAM25705;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Human protein sequence SEQ ID NO.1220.
 XX
 KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
 KW antinfertility; antirheumatic; antiarthritic; immunosuppressive;
 KW antibacterial; endocrine; cardiant; central nervous system; vitruide;
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antiaesthetic; anaemia;
 KW antiagregant; haemostatic; vulnerary; antitumor; antidiabetic; cytostatic;
 KW dermatological; antiallergic; antiaesthetic; antiparkinsonian; infection;
 KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
 KW immunostimulant; gene therapy; antitense therapy; vaccine; inflammation;
 KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
 KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
 KW neurological disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200153455-A2.
 XX
 PD 26-JUL-2001.
 XX
 PF 22-DEC-2000; 2000WO-US035017.
 XX
 PR 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI: 2001-457603/49.
 DR N-PSDB; AAM99646.
 XX
 PT Isolated human polynucleotides encoding polypeptides, useful for the
 PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
 XX
 PS Claim 20; Page 253; 1217pp; English.
 XX
 CC AAM99166 to AAM9994 encode the human proteins given in AAM25225 to
 CC AAM25963. The proteins can have activities based on the tissues and cells
 CC they are expressed in, such as: antinflammatory; antirheumatic;
 CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
 CC central nervous system; vitruide; anti-HIV; fungicide; antimutagen;
 CC cardiovascular; antiaesthetic; antiagregant; haemostatic; vulnerary;

PN MO200153312-A1.
 XX 26-JUL-2001.
 XX 26-DEC-2000; 2000WO-US034263.
 XX 23-DEC-1999; 99US-00471275.
 XX 21-JAN-2000; 2000US-00488725.
 XX 25-APR-2000; 2000US-00552317.
 XX 20-JUN-2000; 2000US-00598042.
 XX 19-JUL-2000; 2000US-00620312.
 XX 03-AUG-2000; 2000US-00653450.
 XX 14-SEP-2000; 2000US-00662191.
 XX 19-OCT-2000; 2000US-00693036.
 XX 29-NOV-2000; 2000US-00727344.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA,
 PI Zhou F, Goodrich R, Drmanac RT;
 XX WPI; 2001-442253/47.
 DR N-PSDB; AAI60747.
 XX Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.
 PT Example 2; SEQ ID NO 6522; 10078bp; English.
 XX The invention relates to human nucleic acids (AA157798-AA161369) and the
 CC encoded polypeptides (CYA36642-AA42213) with neurotrophic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localized neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilization of the activities such as: immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemia and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification
 XX Sequence 217 AA;
 SQ
 Query Match 55.1%; Score 854; DB 4; Length 217;
 Best Local Similarity 90.5%; Pred. No. 5.9e-76;
 Matches 171; Conservative 2; Mismatches 10; Indels 6; Gaps 2;
 QY 1 MALSGSTPAPCWEDEDCDYGYGMLSHRFEVVGQUTCECELLAFLIDEAPGANGGUA 60
 DB 30 MALSGSTPAPCWEDEDCDYGYGMLSHRFEVVGQUTCECELLAFLIDEAPGANGGUA 89
 QY 61 PARSGELLEERRRQCGGGSNRLGQLRLVLAARDLLPHLARKRRRPVSPERYSGTS 120
 DB 90 PARSGELLEERRRQCGGGSNRLGQLRLVLAARDLLPHLARKRRRPVSPERYSGTS 149
 QY 121 SSSKRTGSCRRRRSSSSNANSOQGWETGSPPTKQRRSRGPPSGARRRRRG-APAP 179
 DB 150 SSSKRTGSCRRRRSSSSNANSOQGWETGSPPTKQRRSRGPPSGARRRRRGPPHPS 204
 QY 180 QOQSEPPAP 188
 DB 205 SSGSPDLP 213
 RESULT 15
 AAB94040
 ID AAB94040 standard; protein; 318 AA.
 XX

AC AAB94040;
 XX 26-JUN-2001 (first entry)
 DT Human protein sequence SEQ ID NO:14195.
 DE Human protein sequence SEQ ID NO:14195.
 XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 KM Homo sapiens.
 OS EP1074617-A2.
 XX EP1074617-A2.
 XX 07-FEB-2001.
 XX 28-JUL-2000; 2000EP-00116126.
 XX 29-JUL-1999; 99JP-00248036.
 XX 27-AUG-1999; 99JP-00300253.
 XX 11-JAN-2000; 2000JP-00118776.
 XX 02-MAY-2000; 2000JP-00183767.
 XX 09-JUN-2000; 2000JP-00241899.
 XX (HELI-) HELIX RES INST.
 XX Ora T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WPI; 2001-318749/34.
 XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-
 PT length cDNAs defined in the specification, and for the detection and/or
 PT diagnosis of the abnormality of the proteins encoded by the full-length
 PT cDNAs.
 PS Claim 8; SEQ ID NO 14195; 2537bp + Sequence listing; English.
 XX The present invention describes primer sets for synthesizing 5602 full-
 CC length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dr primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification; where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention
 XX Sequence 318 AA;
 SQ
 Query Match 40.2%; Score 622.5; DB 4; Length 318;
 Best Local Similarity 45.2%; Pred. No. 8.4e-53;
 Matches 136; Conservative 54; Mismatches 90; Indels 21; Gaps 6;
 QY 12 WEDECDYGYGMLSHRFEVVGQUTCECELLAFLIDEAPGANGGUA 70
 DB 12 WPEHGEQEHGGLYSLRWFVDIVGTHLTHRDVLTSLFVDIVDHERGL--INRGDFLL 69
 QY 71 ELERRQCGGSNRLGQLRLVLAARDLLPHLARKRRRPVSP---BRYSGTS---SSK 124
 DB 70 ALERQRCGGSNRFVQLRLITTRHDLPLVYTLKRRRAVCPDLVKKLEETISRYVTR 129


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Qy 125 RTGSCRRRRGSSSSANSQOQO--WETGSPPTKORRSRGRPSGGARRRRRGAPAPQOQ 182
Db 130 ALSDPEPRPPQPSKTVPPHYPVVCCPTSGPQWCSKRPARGATLGSQRKR----- 180
Qy 183 SEPARPSSEKVTCDIRLVRRAEYCEHGPALQGVASRRRQALRQLDVFGQATVLRSR 242
Db 181 -KPVTPDPEKEKQTCIRLVRRAEYCOHETALQGNVFSNRQDPLEROFERFNOANTILKSR 239
Qy 243 DLGSVVCDIKFSELSYLDAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEA 302
Db 240 DLGSITICDIKFSELSYLDAFWGDYINGSLLEALKGVFTDSLKQAVGHEATKLLVNVDBE 299
Qy 303 D 303
Db 300 D 300

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OM protein - protein search, using sw model

Run on: February 12, 2005, 16:31:06 ; Search time 72 Seconds
(without alignments)
2155.000 Million cell updates/sec

Title: US-10-030-271-2
Perfect score: 303
Sequence: 1 MALSGSTPAFCWEDECLDY.....LREAVGRAVLLVSVDAD 303

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 1000 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	224	73.9	326	1 DED2_HUMAN	Q8WKF8 homo sapien
2	117	38.6	330	1 DED2_MOUSE	Q8QZV0 mus musculu
3	23	7.6	168	2 Q8BRM9	Q8BRM9 mus musculu
4	14	4.6	369	2 Q919M3	Q919M3 brachydanto
5	13	4.3	318	1 DEDD_HUMAN	Q75618 homo sapien
6	13	4.3	318	1 DEDD_MOUSE	Q92113 mus musculu
7	13	4.3	318	1 DEDD_RAT	Q92113 mus musculu
8	13	4.3	404	2 Q6DH2	Q6DH2 brachydanto
9	11	3.6	243	2 Q6GNZ8	Q6GNZ8 xenopus lae
10	10	3.3	218	2 Q91W13	Q91W13 molluscum c
11	10	3.3	235	2 Q98222	Q98222 molluscum c
12	10	3.3	244	2 Q6DHV2	Q6DHV2 brachydanto
13	9	3.0	127	2 Q9Y9Y9	Q9Y9Y9 aeropyrum p
14	9	3.0	222	2 Q671V3	Q671V3 oryza sativ
15	9	3.0	227	2 Q706G3	Q706G3 anopheles g
16	9	3.0	241	2 Q6MBX0	Q6MBX0 parachlamy
17	9	3.0	385	2 Q6M204	Q6M204 corynebacte
18	9	3.0	395	2 Q8NLT5	Q8NLT5 corynebacte
19	9	3.0	478	2 Q82HT1	Q82HT1 streptomyce
20	9	3.0	629	2 Q871T5	Q871T5 neurospora
21	9	3.0	5835	2 Q631K8	Q631K8 burkholderi
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23	8	2.6	75	2 Q8UHG7	Q8UHG7 agrobacteri
24	8	2.6	93	2 Q9FLF2	Q9FLF2 enterococcu
25	8	2.6	101	2 Q6UPP9	Q6UPP9 human immun
26	8	2.6	105	2 Q92KN5	Q92KN5 rhizobium m
27	8	2.6	106	2 Q86VG6	Q86VG6 homo sapien
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29	8	2.6	125	2 Q9BRA0	Q9BRA0 homo sapien
30	8	2.6	125	2 Q9DZU5	Q9DZU5 mus musculu
31	8	2.6	129	2 Q6S3U5	Q6S3U5 oryza sativ

32	8	2.6	134	2 Q7GVZ3	Q7GVZ3 giardia lam
33	8	2.6	142	2 Q6ERC3	Q6ERC3 oryza sativ
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35	8	2.6	159	2 Q6H586	Q6H586 oryza sativ
36	8	2.6	161	2 Q94EB4	Q94EB4 oryza sativ
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39	8	2.6	165	2 Q7XGH6	Q7XGH6 oryza sativ
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45	8	2.6	197	2 Q0S575	Q0S575 mycobacteri
46	8	2.6	197	2 Q7U0W4	Q7U0W4 mycobacteri
47	8	2.6	223	2 Q84R51	Q84R51 oryza sativ
48	8	2.6	224	2 Q6SA89	Q6SA89 mycobacteri
49	8	2.6	224	2 Q6SA92	Q6SA92 mycobacteri
50	8	2.6	224	2 Q6SA93	Q6SA93 mycobacteri
51	8	2.6	224	2 Q69644	Q69644 mycobacteri
52	8	2.6	224	2 Q744E3	Q744E3 mycobacteri
53	8	2.6	224	2 Q7TVY9	Q7TVY9 mycobacteri
54	8	2.6	224	2 Q9CB91	Q9CB91 mycobacteri
55	8	2.6	225	2 Q744Y5	Q744Y5 mycobacteri
56	8	2.6	227	2 Q8RON9	Q8RON9 corynebacte
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59	8	2.6	227	2 Q8FTU1	Q8FTU1 corynebacte
60	8	2.6	229	2 Q6S3P9	Q6S3P9 oryza sativ
61	8	2.6	231	2 Q8N922	Q8N922 homo sapien
62	8	2.6	245	2 Q67UJ2	Q67UJ2 oryza sativ
63	8	2.6	248	2 Q86SM7	Q86SM7 homo sapien
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66	8	2.6	282	1 P811_YEAST	P811_YEAST
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68	8	2.6	324	2 Q92178	Q92178 lactococcus
69	8	2.6	332	2 Q6SXM6	Q6SXM6 oryza sativ
70	8	2.6	339	1 HXD9_MOUSE	HXD9_MOUSE
71	8	2.6	342	1 HXD9_HUMAN	HXD9_HUMAN
72	8	2.6	342	2 Q86ST1	Q86ST1 homo sapien
73	8	2.6	346	2 Q73WZ9	Q73WZ9 mycobacteri
74	8	2.6	352	2 Q6Z1A4	Q6Z1A4 oryza sativ
75	8	2.6	354	2 Q6ZK44	Q6ZK44 oryza sativ
76	8	2.6	356	2 Q91314	Q91314 aeromonas h
77	8	2.6	361	2 Q7TMA4	Q7TMA4 mus musculu
78	8	2.6	363	2 Q69949	Q69949 streptomyce
79	8	2.6	364	2 Q8PCN1	Q8PCN1 xanthomonas
80	8	2.6	369	2 Q8BPE0	Q8BPE0 xanthomonas
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82	8	2.6	392	2 Q7MXU4	Q7MXU4 porphyromon
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92	8	2.6	520	2 Q73YQ3	Q73YQ3 mycobacteri
93	8	2.6	528	2 Q8U666	Q8U666 agrobacteri
94	8	2.6	573	2 Q994E5	Q994E5 porcine ade
95	8	2.6	579	2 Q755M9	Q755M9 ashyia goss
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97	8	2.6	632	2 Q7OLF5	Q7OLF5 hordeum vul
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99	8	2.6	678	2 Q82NS2	Q82NS2 streptomyce
100	8	2.6	685	2 Q9P0N9	Q9P0N9 asospirillum
101	8	2.6	693	2 Q829A5	Q829A5 streptomyce
102	8	2.6	701	2 Q6FBA3	Q6FBA3 acinetobact
103	8	2.6	761	1 PQOF_KLEPN	PQOF_KLEPN
104	8	2.6	814	2 Q9ETL8	Q9ETL8 caenorhabdi

105	8	2.6	846	2	Q6PD17	Q6PD17 mus musculus
106	8	2.6	847	2	Q6TNV2	Q6TNV2 brachydanio
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110	8	2.6	881	2	Q9VT99	Q9VT99 drosophila
111	8	2.6	887	2	Q9ZS86	Q9ZS86 arabidopsis
112	8	2.6	890	2	Q81MT7	Q81MT7 oryza sativ
113	8	2.6	901	2	Q9C585	Q9C585 arabidopsis
114	8	2.6	908	2	Q7ZVL4	Q7ZVL4 brachydanio
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116	8	2.6	910	2	Q93Y01	Q93Y01 arabidopsis
117	8	2.6	924	2	Q22207	Q22207 arabidopsis
118	8	2.6	928	2	Q9T0B6	Q9T0B6 arabidopsis
119	8	2.6	934	2	Q6P5E8	Q6P5E8 mus musculus
120	8	2.6	937	2	Q9T0B8	Q9T0B8 arabidopsis
121	8	2.6	950	2	Q9PWC6	Q9PWC6 gallus gall
122	8	2.6	951	2	Q8H557	Q8H557 oryza sativ
123	8	2.6	952	2	Q9R085	Q9R085 rattus norv
124	8	2.6	953	2	Q80TY6	Q80TY6 mus musculus
125	8	2.6	963	1	UBP4_HUMAN	Q1107 homo sapien
126	8	2.6	973	2	Q8AVB6	Q8AVB6 xenopus lae
127	8	2.6	981	1	UB15_HUMAN	Q9Y4E8 homo sapien
128	8	2.6	981	1	UB15_MOUSE	Q8T5H1 mus musculus
129	8	2.6	981	1	Q80UK9	Q80UK9 mus musculus
130	8	2.6	1004	2	Q82JMS	Q82JMS streptomyce
131	8	2.6	1005	2	Q6W5R0	Q6W5R0 streptomyce
132	8	2.6	1021	1	CARA_MOUSE	P58660 mus musculus
133	8	2.6	1028	1	Q9ZS85	Q9ZS85 arabidopsis
134	8	2.6	1032	1	CARA_HUMAN	Q9BWT7 homo sapien
135	8	2.6	1044	2	Q7QVN9	Q7QVN9 giardia lam
136	8	2.6	1093	2	Q872P9	Q872P9 neurospora
137	8	2.6	1095	2	Q913U4	Q913U4 pseudomonas
138	8	2.6	1098	2	Q7R1Z8	Q7R1Z8 plasmodium
139	8	2.6	1132	2	Q813U1	Q813U1 plasmodium
140	8	2.6	1406	1	UBP6_HUMAN	P35125 homo sapien
141	8	2.6	1604	1	UB32_HUMAN	Q8NFA0 homo sapien
142	8	2.6	1733	1	VN1A_PRIVKA	P33385 pseudorabie
143	8	2.6	1790	2	Q8W0J4	Q8W0J4 oryza sativ
144	8	2.6	1958	2	Q69340	Q69340 suid herpes
145	8	2.6	5216	1	Q7N239	Q7N239 photorhabd
146	8	2.3	35	2	SMS_LAMFL	Q9PXR0 lampetra fl
147	7	2.3	47	2	Q23578	Q23578 caenorhabdi
148	7	2.3	52	2	Q61I02	Q61I02 drosophila
149	7	2.3	55	2	Q842D8	Q842D8 oryza sativ
150	7	2.3	56	2	Q6K5W3	Q6K5W3 oryza sativ
151	7	2.3	57	2	Q7NWK2	Q7NWK2 chromobacte
152	7	2.3	58	2	Q621W3	Q621W3 burkholderi
153	7	2.3	64	2	Q621W3	Q621W3 human cytom
154	7	2.3	64	2	Q6UDZ9	Q6UDZ9 human cytom
155	7	2.3	70	2	Q7M6G6	Q7M6G6 human cytom
156	7	2.3	73	2	Q84039	Q84039 mycobacteri
157	7	2.3	73	2	Q84039	Q84039 oryza sativ
158	7	2.3	73	2	Q8W0B8	Q8W0B8 oryza sativ
159	7	2.3	74	2	Q6YZR4	Q6YZR4 oryza sativ
160	7	2.3	75	2	Q7PWT3	Q7PWT3 anopheles g
161	7	2.3	81	2	Q8EUP5	Q8EUP5 xanthomonas
162	7	2.3	85	2	Q6P5U4	Q6P5U4 homo sapien
163	7	2.3	86	2	Q6P5U4	Q6P5U4 oryza sativ
164	7	2.3	87	2	Q6YUQ4	Q6YUQ4 oryza sativ
165	7	2.3	88	2	Q901H7	Q901H7 human immun
166	7	2.3	90	2	Q67TMS	Q67TMS oryza sativ
167	7	2.3	90	2	Q851Q7	Q851Q7 oryza sativ
168	7	2.3	90	2	Q8H4N9	Q8H4N9 oryza sativ
169	7	2.3	91	2	Q7Z7E4	Q7Z7E4 homo sapien
170	7	2.3	92	2	Q9S1X9	Q9S1X9 streptomyce
171	7	2.3	93	2	Q7SLV1	Q7SLV1 human immun
172	7	2.3	93	2	Q8ANAO	Q8ANAO human immun
173	7	2.3	94	2	Q6K7I2	Q6K7I2 oryza sativ
174	7	2.3	94	2	Q7SUI7	Q7SUI7 human immun
175	7	2.3	94	2	Q7SUG3	Q7SUG3 human immun
176	7	2.3	95	2	Q6YTB7	Q6YTB7 oryza sativ
177	7	2.3	95	2	Q8AMV7	Q8AMV7 human immun
178	7	2.3	96	2	Q8T9V4	Q8T9V4 aedes aegypt
179	7	2.3	96	2	Q6JCC9	Q6JCC9 human immun
180	7	2.3	97	2	Q6Z2G4	Q6Z2G4 oryza sativ
181	7	2.3	98	2	Q68QJ9	Q68QJ9 human immun
182	7	2.3	99	2	Q90BQ9	Q90BQ9 human immun
183	7	2.3	99	2	Q98X72	Q98X72 human immun
184	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
185	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
186	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
187	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
188	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
189	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
190	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
191	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
192	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
193	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
194	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
195	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
196	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
197	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
198	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
199	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
200	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
201	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
202	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
203	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
204	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
205	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
206	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
207	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
208	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
209	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
210	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
211	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
212	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
213	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
214	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
215	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
216	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
217	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
218	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
219	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
220	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
221	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
222	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
223	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
224	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
225	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
226	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
227	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
228	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
229	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
230	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
231	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
232	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
233	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
234	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
235	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
236	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
237	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
238	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
239	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
240	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
241	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
242	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
243	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
244	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
245	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
246	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
247	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
248	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
249	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun
250	7	2.3	99	2	Q68QJ6	Q68QJ6 human immun

251	7	2.3	143	2	069PH1	069ph1 oryza sativ	324	7	2.3	204	2	09H6X1	09h6x1 homo sapien
252	7	2.3	144	2	08BDJ6	08bdj6 shewanella	325	7	2.3	205	2	08A5M4	08a5m4 bacteroides
253	7	2.3	144	2	06ADL8	06adl8 leifsonia x	326	7	2.3	204	2	08BDR1	08bdr1 homo sapien
254	7	2.3	147	2	09AMT7	09amt7 oryza sativ	327	7	2.3	206	2	07TTH1	07tth1 mycobacteri
255	7	2.3	147	2	07NK38	07nk38 gloeobacter	328	7	2.3	207	2	09RUG1	09rug1 deinococcus
256	7	2.3	148	2	098B53	098b53 cyprinus ca	329	7	2.3	206	2	09L432	09l432 xanthomonas
257	7	2.3	150	2	07Z7E5	07z7e5 homo sapien	330	7	2.3	207	2	08P9K6	08p9k6 xanthomonas
258	7	2.3	150	2	07XXP0	07xyp0 chlorarachn	331	7	2.3	208	2	06H6A1	06h6a1 oryza sativ
259	7	2.3	152	2	05Z549	05z549 plasmid pps	332	7	2.3	210	2	06S4X7	06s4x7 oryza sativ
260	7	2.3	152	2	08YMH3	08ymh3 anabaena sp	333	7	2.3	211	2	06Z801	06z801 oryza sativ
261	7	2.3	153	2	09Y9Z9	09y9z9 aeropyrum p	334	7	2.3	211	2	08RE54	08re54 fusobacteri
262	7	2.3	154	2	06ZR76	06zr76 homo sapien	335	7	2.3	212	1	YLB1_ARCFU	YLB1_ARCFU
263	7	2.3	155	2	09YAL6	09yal6 aeropyrum p	336	7	2.3	213	1	H1X_HUMAN	H1X_HUMAN
264	7	2.3	157	2	07P239	07p239 chromobacte	337	7	2.3	213	2	08GTM2	08gtm2 homo sapien
265	7	2.3	158	2	0742M7	0742m7 mycobacteri	338	7	2.3	215	2	0842J2	0842j2 brassica ol
266	7	2.3	160	2	08HXB4	08hxb4 macaca faec	339	7	2.3	215	2	08Y2Y9	08y2y9 ralatonia b
267	7	2.3	160	2	06YVW7	06yv7 oryza sativ	340	7	2.3	217	2	087YK8	087yk8 pseudomonas
268	7	2.3	162	2	06BD40	06bd40 drosophila	341	7	2.3	218	2	09DWH9	09dwh9 rat cytoleg
269	7	2.3	167	2	07QUG1	07qug1 giardia lam	342	7	2.3	219	2	09X7G3	09x7g3 methylolact
270	7	2.3	168	2	09CW76	09cw76 mus musculu	343	7	2.3	223	2	09D5P3	09d5p3 mus musculu
271	7	2.3	168	2	07MSU7	07msu7 mouse adeno	344	7	2.3	224	1	TPMB_CHLTR	TPMB_CHLTR
272	7	2.3	170	2	09NBF9	09nbf9 philodina r	345	7	2.3	224	2	06Z9S6	06z9s6 oryza sativ
273	7	2.3	172	2	08LIU5	08liu5 oryza sativ	346	7	2.3	225	2	097PNO	097pno streptococc
274	7	2.3	172	2	07SV41	07sv41 physcomitre	347	7	2.3	225	2	08DP06	08dp06 streptococc
275	7	2.3	173	2	08N8Z9	08n8z9 homo sapien	348	7	2.3	227	2	08ZBU9	08zbu9 streptomyce
276	7	2.3	174	2	066K41	066k41 homo sapien	349	7	2.3	228	2	08LMC8	08lmc8 oryza sativ
277	7	2.3	174	2	0656U7	0656u7 oryza sativ	350	7	2.3	228	2	06JYH8	06jyh8 uncultured
278	7	2.3	174	2	063S59	063s59 burkholderi	351	7	2.3	231	2	08LHQ0	08lhu0 oryza sativ
279	7	2.3	178	2	08TCH5	08tch5 homo sapien	352	7	2.3	231	2	08GRN2	08grn2 oryza sativ
280	7	2.3	179	2	07Z7E3	07z7e3 homo sapien	353	7	2.3	231	2	06LFT7	06lft7 photobacter
281	7	2.3	180	2	09ZMF5	09zmf5 oryza sativ	354	7	2.3	231	2	08B100	08b100 chimpanzee
282	7	2.3	180	2	06CMV2	06cmv2 kluveromyc	355	7	2.3	233	2	08PBA5	08pba5 xanthomonas
283	7	2.3	180	2	07Z7E1	07z7e1 homo sapien	356	7	2.3	233	2	06DCP9	06dcp9 xenopus lae
284	7	2.3	180	2	098E78	098e78 rhizobium l	357	7	2.3	234	2	048418	048418 bacteriopia
285	7	2.3	182	2	06K310	06k310 oryza sativ	358	7	2.3	234	2	07Y292	07y292 phage phi 4
286	7	2.3	183	2	08WT05	08wt05 plasmodium	359	7	2.3	236	2	06Z3M7	06z3m7 oryza sativ
287	7	2.3	183	2	08LI61	08li61 oryza sativ	360	7	2.3	236	2	07RMS9	07rms9 neurospora
288	7	2.3	184	1	GCH1_AQUAE	066603 aquifex aeo	361	7	2.3	236	2	06YV10	06yv10 oryza sativ
289	7	2.3	184	2	069JZ0	069jz0 oryza sativ	362	7	2.3	237	2	08SBS7	08sbs7 oryza sativ
290	7	2.3	184	2	06YXR8	06yxr8 oryza sativ	363	7	2.3	237	2	07G668	07g668 oryza sativ
291	7	2.3	184	2	08Z0U3	08z0u3 streptomyce	364	7	2.3	238	1	PYRE_COCTM	PYRE_COCTM
292	7	2.3	184	2	0640T0	0640t0 xenopus tro	365	7	2.3	240	2	06G500	06g500 oryza sativ
293	7	2.3	186	1	ATPD_CYAPA	048082 cyanophora	366	7	2.3	240	2	07X185	07x185 oryza sativ
294	7	2.3	187	2	07R1F5	07r1f5 giardia lam	367	7	2.3	240	2	09LDM2	09ldm2 oryza sativ
295	7	2.3	187	2	09XVX5	09xvx5 caenorhabdi	368	7	2.3	240	2	08ZFC5	08zfc5 streptomyce
296	7	2.3	188	2	069PQ2	069pq2 oryza sativ	369	7	2.3	241	2	08PMU4	08pmu4 xanthomonas
297	7	2.3	188	2	0675Y1	0675y1 symbiodacte	370	7	2.3	244	2	08LMA7	08lma7 oryza sativ
298	7	2.3	189	2	09LH28	09lh28 oryza sativ	371	7	2.3	246	1	NDP_DEIRA	NDP_DEIRA
299	7	2.3	190	2	06YX18	06yx18 oryza sativ	372	7	2.3	246	2	08ZAC3	08zac3 streptomyce
300	7	2.3	191	2	086D99	086d99 caenorhabdi	373	7	2.3	246	2	06ZYK2	06zyk2 pyrobaculum
301	7	2.3	192	2	07MR58	07mr58 wolfinella s	374	7	2.3	247	2	07PM81	07pm81 anopheles g
302	7	2.3	193	2	084PC6	084pc6 oryza sativ	375	7	2.3	249	1	MSX1_CHICK	MSX1_CHICK
303	7	2.3	195	1	IN01_BOVIN	P07352 boe laurus	376	7	2.3	250	2	09HFS1	09hfs1 candida alb
304	7	2.3	195	2	P28170	P28170 ovis aries	377	7	2.3	252	2	09DMG9	09dmg9 rat cytoleg
305	7	2.3	195	2	028561	028561 ovis aries	378	7	2.3	253	2	084G27	084g27 streptomyce
306	7	2.3	195	2	07MZY7	07mzy7 ovis aries	379	7	2.3	253	2	064N05	064n05 bacteroides
307	7	2.3	195	2	06XSY8	06xsy8 oryza sativ	380	7	2.3	254	2	07XFD3	07xf3d oryza sativ
308	7	2.3	195	2	08UH52	08uh52 agrobacteri	381	7	2.3	254	2	09AUNI1	09auni1 oryza sativ
309	7	2.3	196	2	06KZB9	06kzb9 oryza sativ	382	7	2.3	255	2	06FV64	06fv64 candida gla
310	7	2.3	196	2	08VNI9	08vni9 kluvera ci	383	7	2.3	255	2	09N0J3	09n0j3 ovis aries
311	7	2.3	197	1	IE68_HRV2	PI4379 human herpe	384	7	2.3	255	2	08L1Z2	08l1z2 streptomyce
312	7	2.3	197	1	PADI_ECOS57	09x728 escherichia	385	7	2.3	256	2	09P6Y1	09p6y1 neurospora
313	7	2.3	197	2	07XZ04	07x04 griffithsia	386	7	2.3	258	2	06R950	06r950 oryza sativ
314	7	2.3	197	2	09F8R0	09f8r0 escherichia	387	7	2.3	258	2	06R950	06r950 oryza sativ
315	7	2.3	197	2	083Q85	083q85 shigella fl	388	7	2.3	259	2	08XRB1	08xrb1 ralatonia b
316	7	2.3	199	2	07JZ15	07jz15 mycobacteri	389	7	2.3	259	2	06ZGS2	06zgs2 oryza sativ
317	7	2.3	200	1	YN02_SHIFL	P29771 shigella fl	390	7	2.3	259	2	055780	055780 synechocyst
318	7	2.3	200	2	07XN13	07xni3 oryza sativ	391	7	2.3	259	2	0745X8	0745x8 thermus the
319	7	2.3	200	2	08VNT1	08vnt1 enterobacte	392	7	2.3	260	2	094A09	094a09 arabidopsis
320	7	2.3	200	2	0616A9	0616a9 escherichia	393	7	2.3	261	2	07S181	07s181 oryza sativ
321	7	2.3	200	2	06YANI	06yani pigmenticpha	394	7	2.3	262	2	07XIV8	07xiv8 oryza sativ
322	7	2.3	202	2	09V760	09v760 drosophila	395	7	2.3	263	2	08SB70	08sb70 oryza sativ
323	7	2.3	203	2	067VR0	067vr0 oryza sativ	396	7	2.3	263	2	06YVG2	06yv2 oryza sativ

397	2.3	263	2	Q7G6E8	Q7G6E8 oryza sativ	470	7	2.3	314	2	Q6CX46	Q6CX46 kluyveromyc
398	2.3	266	2	Q8S7I0	Q8S7I0 oryza sativ	471	7	2.3	314	2	Q93J09	Q93J09 brassica na
399	2.3	267	2	Q8XMM6	Q8XMM6 clostridium	472	7	2.3	315	2	Q6ASR7	Q6ASR7 oryza sativ
400	2.3	268	1	PGF5	PGF5 homo sapien	473	7	2.3	316	2	Q6ZJ42	Q6ZJ42 oryza sativ
401	2.3	268	2	Q8NF50	Q8NF50 homo sapien	474	7	2.3	318	2	Q75K64	Q75K64 oryza sativ
402	2.3	269	2	Q7Y0A3	Q7Y0A3 oryza sativ	475	7	2.3	318	2	Q06629	Q06629 mycobacteri
403	2.3	269	2	Q6NHR3	Q6NHR3 corynebacte	476	7	2.3	318	2	Q6A9T1	Q6A9T1 propionibac
404	2.3	269	2	Q8Z900	Q8Z900 streptomyce	477	7	2.3	318	2	Q7U185	Q7U185 mycobacteri
405	2.3	270	2	Q7EYMS	Q7EYMS oryza sativ	478	7	2.3	319	2	Q7PVH4	Q7PVH4 anopheles g
406	2.3	270	2	Q84UZ2	Q84UZ2 chlamydomon	479	7	2.3	320	2	Q8B6E9	Q8B6E9 streptomyce
407	2.3	272	1	REFX_HUMAN	REFX_HUMAN homo sapien	480	7	2.3	321	2	Q8NKK6	Q8NKK6 staphylococ
408	2.3	272	2	Q8TCI0	Q8TCI0 homo sapien	481	7	2.3	322	2	Q8KOR4	Q8KOR4 staphylococ
409	2.3	272	2	Q8PAP1	Q8PAP1 xanthomonas	482	7	2.3	322	2	Q6GA81	Q6GA81 staphylococ
410	2.3	273	2	Q99UX0	Q99UX0 staphylococ	483	7	2.3	322	2	Q6GHV2	Q6GHV2 staphylococ
411	2.3	273	2	Q7A6S1	Q7A6S1 staphylococ	484	7	2.3	323	1	VATC_THETH	P74902 thermus the
412	2.3	276	2	Q98IB9	Q98IB9 rhizobium 1	485	7	2.3	323	2	Q8LBF8	Q8LBF8 arabidopsis
413	2.3	277	2	Q7RUC6	Q7RUC6 neurospora	486	7	2.3	323	2	Q9S8G3	Q9S8G3 arabidopsis
414	2.3	277	2	Q82TS3	Q82TS3 nitrosomona	487	7	2.3	323	2	Q9SCU7	Q9SCU7 thermus the
415	2.3	278	1	HT22_ARATH	P46604 arabidopsis	488	7	2.3	324	2	Q8GHB2	Q8GHB2 streptomyce
416	2.3	279	2	Q6CPE1	Q6CPE1 kluyveromyc	489	7	2.3	324	2	Q8GMP5	Q8GMP5 aeromonas s
417	2.3	279	2	Q9Z5A8	Q9Z5A8 streptomyce	490	7	2.3	325	2	Q84PV0	Q84PV0 oryza sativ
418	2.3	281	2	Q8UEM7	Q8UEM7 agrobacteri	491	7	2.3	325	2	Q8NNY3	Q8NNY3 corynebacte
419	2.3	281	2	Q8RZG6	Q8RZG6 oryza sativ	492	7	2.3	325	2	Q8NNY3	Q8NNY3 prochloroco
420	2.3	282	2	Q8Z5B4	Q8Z5B4 streptomyce	493	7	2.3	325	2	Q7V3Z3	Q7V3Z3 halobacteri
421	2.3	283	1	AROE_CORGL	Q9X5C9 corynebacte	494	7	2.3	326	2	Q9HQD4	Q9HQD4 oryza sativ
422	2.3	283	2	Q753B3	Q753B3 ashyba goss	495	7	2.3	326	2	Q94UG3	Q94UG3 oryza sativ
423	2.3	284	2	Q71S18	Q71S18 gallus gall	496	7	2.3	327	2	Q6K7C9	Q6K7C9 oryza sativ
424	2.3	285	2	Q82FB6	Q82FB6 streptomyce	497	7	2.3	327	2	Q6M4I3	Q6M4I3 treponema d
425	2.3	286	2	Q72JZ7	Q72JZ7 thermus the	498	7	2.3	327	2	Q73K65	Q73K65 oryza sativ
426	2.3	287	2	Q6Z8E4	Q6Z8E4 oryza sativ	499	7	2.3	328	2	Q7XR65	Q7XR65 human immun
427	2.3	289	2	Q7EYB7	Q7EYB7 oryza sativ	500	7	2.3	328	2	Q6SEB4	Q6SEB4 anabaena sp
428	2.3	291	2	Q6ZFS8	Q6ZFS8 oryza sativ	501	7	2.3	329	2	Q8YTY3	Q8YTY3 human immun
429	2.3	291	2	Q6ZFT1	Q6ZFT1 oryza sativ	502	7	2.3	330	2	Q8Q174	Q8Q174 human immun
430	2.3	292	2	Q94H41	Q94H41 oryza sativ	503	7	2.3	330	2	Q9L1H6	Q9L1H6 arabidopsis
431	2.3	293	2	Q7U8M8	Q7U8M8 synechococc	504	7	2.3	331	2	Q8BWT4	Q8BWT4 pseudomonas
432	2.3	294	2	Q6WV7	Q6WV7 human immun	505	7	2.3	331	2	Q6D899	Q6D899 erwinia car
433	2.3	294	2	Q93HV7	Q93HV7 arthrobacte	506	7	2.3	331	2	Q91W20	Q91W20 mus musculu
434	2.3	294	2	Q7ZGT7	Q7ZGT7 thermus the	507	7	2.3	332	2	Q6U9Z2	Q6U9Z2 human immun
435	2.3	294	2	Q80VZ5	Q80VZ5 mus musculu	508	7	2.3	332	2	Q6U9A0	Q6U9A0 human immun
436	2.3	294	2	Q91BA3	Q91BA3 xenopus lae	509	7	2.3	332	2	Q7ZLD6	Q7ZLD6 human immun
437	2.3	295	1	U966_HUMAN	Q918A3 xenopus lae	510	7	2.3	332	2	Q7ZLD7	Q7ZLD7 human immun
438	2.3	295	1	U966_MOUSE	Q6UW14 homo sapien	511	7	2.3	332	2	Q7ZLD8	Q7ZLD8 human immun
439	2.3	295	2	Q8XKS7	Q8XKS7 raietonia s	512	7	2.3	332	2	Q7ZLE0	Q7ZLE0 human immun
440	2.3	296	1	MURB_CHLMU	Q9P189 chlamydia m	513	7	2.3	332	2	Q7ZLE1	Q7ZLE1 human immun
441	2.3	296	2	Q8UGF8	Q8UGF8 agrobacteri	514	7	2.3	332	2	Q7ZLE2	Q7ZLE2 human immun
442	2.3	297	2	Q23263	Q23263 caenorhabdi	515	7	2.3	332	2	Q7ZLE3	Q7ZLE3 human immun
443	2.3	298	2	Q9CS83	Q9CS83 mus musculu	516	7	2.3	332	2	Q6P7C4	Q6P7C4 rictus norv
444	2.3	299	1	HEY1_MOUSE	Q9WV93 mus musculu	517	7	2.3	334	2	Q93642	Q93642 caenorhabdi
445	2.3	299	2	Q91NZ8	Q91NZ8 arabidopsis	518	7	2.3	336	2	Q8LFW6	Q8LFW6 gloeobacter
446	2.3	299	2	Q9DOR0	Q9DOR0 mus musculu	519	7	2.3	336	2	Q7NHW0	Q7NHW0 human immun
447	2.3	299	2	Q9QUM5	Q9QUM5 mus musculu	520	7	2.3	336	2	Q90JD5	Q90JD5 human immun
448	2.3	300	2	Q66KX8	Q66KX8 xenopus tro	521	7	2.3	336	2	Q6ZCW6	Q6ZCW6 oryza sativ
449	2.3	301	2	P74823	P74823 sphingomona	522	7	2.3	337	2	Q6ZCW6	Q6ZCW6 oryza sativ
450	2.3	301	2	Q92NX1	Q92NX1 rhizobium m	523	7	2.3	337	2	Q6ZUW2	Q6ZUW2 human immun
451	2.3	301	2	Q88GP9	Q88GP9 pseudomonas	524	7	2.3	338	2	Q67K15	Q67K15 mycobacteri
452	2.3	302	2	Q84O12	Q84O12 pseudomonas	525	7	2.3	338	2	Q741W6	Q741W6 mycobacteri
453	2.3	303	2	Q759J3	Q759J3 ashyba goss	526	7	2.3	340	1	ERF3_HUMAN	Q15768 homo sapien
454	2.3	304	1	HEY1_CANPA	Q9E322 canis famil	527	7	2.3	340	2	Q98ZFP	Q98ZFP human immun
455	2.3	304	1	HEY1_HUMAN	Q9Y5J3 homo sapien	528	7	2.3	340	2	Q7SMX0	Q7SMX0 human immun
456	2.3	304	2	Q66PR6	Q66PR6 homo sapien	529	7	2.3	342	2	Q8RZ07	Q8RZ07 oryza sativ
457	2.3	304	2	Q760I8	Q760I8 bos taurus	530	7	2.3	343	2	Q90J97	Q90J97 human immun
458	2.3	305	2	Q6WI62	Q6WI62 bacterioph	531	7	2.3	343	2	Q88YC7	Q88YC7 human immun
459	2.3	305	2	Q837W0	Q837W0 enterococcu	532	7	2.3	346	1	HM22_CAEEL	P41936 caenorhabdi
460	2.3	306	2	Q7NMG2	Q7NMG2 chryzomabact	533	7	2.3	347	2	Q9RSB8	Q9RSB8 deinococcus
461	2.3	307	2	Q6K1Z4	Q6K1Z4 oryza sativ	534	7	2.3	347	2	Q904G5	Q904G5 human immun
462	2.3	308	2	Q8NMX2	Q8NMX2 homo sapien	535	7	2.3	350	2	Q73MH1	Q73MH1 treponema d
463	2.3	310	2	Q88XK4	Q88XK4 drosophila	536	7	2.3	350	2	Q8R5E6	Q8R5E6 mus musculu
464	2.3	310	2	Q82CNS	Q82CNS streptomyce	537	7	2.3	350	2	Q90HK6	Q90HK6 human immun
465	2.3	310	2	Q81L83	Q81L83 oryza sativ	538	7	2.3	353	2	Q6H521	Q6H521 oryza sativ
466	2.3	311	2	Q62KE6	Q62KE6 burkholderi	539	7	2.3	353	2	Q7NL89	Q7NL89 oryza sativ
467	2.3	312	2	Q63U79	Q63U79 burkholderi	540	7	2.3	353	2	Q90K92	Q90K92 gloeobacter
468	2.3	313	2	Q6SEB3	Q6SEB3 human immun	541	7	2.3	354	2	Q90K81	Q90K81 human immun
469	2.3	313	2	Q6SEB3	Q6SEB3 human immun	542	7	2.3	354	2	Q90K81	Q90K81 human immun

543	7	2.3	355	2	Q9W311	Q9W311 drosophila	616	7	2.3	402	2	Q90F42	Q90F42 human immun
544	7	2.3	355	2	Q8KY55	Q8KY55 neuregia gp	617	7	2.3	402	2	Q90I39	Q90I39 human immun
545	7	2.3	355	2	Q6WNG9	Q6WNG9 bacillus st	618	7	2.3	402	2	Q90I55	Q90I55 human immun
546	7	2.3	355	2	Q90L28	Q90L28 human immun	619	7	2.3	403	2	Q8ZSL7	Q8ZSL7 pyrobaculum
547	7	2.3	356	2	Q8H5D9	Q8H5D9 oryza sativ	620	7	2.3	403	2	Q7W717	Q7W717 bordetella
548	7	2.3	357	2	Q73W61	Q73W61 mycobacteri	621	7	2.3	403	2	Q7W1S4	Q7W1S4 bordetella
549	7	2.3	358	2	Q8GLP0	Q8GLP0 aeromonas h	622	7	2.3	404	2	Q96B18	Q96B18 homo sapien
550	7	2.3	358	2	Q8Z2L6	Q8Z2L6 enterococcu	623	7	2.3	405	2	Q7PYD4	Q7PYD4 anophelis g
551	7	2.3	359	2	Q8JUF4	Q8JUF4 arabidopsis	624	7	2.3	405	2	Q8HY80	Q8HY80 tupia glis
552	7	2.3	359	2	Q8JG42	Q8JG42 streptomyce	625	7	2.3	406	2	Q7NE93	Q7NE93 gloobacter
553	7	2.3	360	2	Q7SB96	Q7SB96 neuropept	626	7	2.3	408	2	Q8JAP2	Q8JAP2 coxiella bu
554	7	2.3	360	2	Q8LMA1	Q8LMA1 oryza sativ	627	7	2.3	410	2	Q8ZCDO	Q8ZCDO streptomyce
555	7	2.3	360	2	Q7NR53	Q7NR53 chromobacte	628	7	2.3	412	2	Q20873	Q20873 caenorhabdi
556	7	2.3	360	2	Q89QF5	Q89QF5 bradyrhizob	629	7	2.3	412	2	Q6APF7	Q6APF7 leifsonia x
557	7	2.3	364	2	Q69Y83	Q69Y83 oryza sativ	630	7	2.3	413	2	Q91IL1	Q91IL1 arabidopsis
558	7	2.3	366	2	Q9JMT1	Q9JMT1 neisseria m	631	7	2.3	413	2	Q6A700	Q6A700 propionibac
559	7	2.3	366	2	Q9JXFB	Q9JXFB neisseria m	632	7	2.3	413	2	P89474	P89474 human hepe
560	7	2.3	367	2	Q90G30	Q90G30 human immun	633	7	2.3	414	1	SPYA_CALTA	P31029 calithrix
561	7	2.3	368	2	Q8KJL2	Q8KJL2 mus musculi	634	7	2.3	414	2	Q44542	Q44542 caenorhabdi
562	7	2.3	369	2	Q8N8M0	Q8N8M0 homo sapien	635	7	2.3	414	2	Q70XK4	Q70XK4 gordonia we
563	7	2.3	371	2	Q39308	Q39308 brassica na	636	7	2.3	416	1	ELT1_CAEEL	P28515 caenorhabdi
564	7	2.3	371	2	Q90IM4	Q90IM4 human immun	637	7	2.3	416	2	Q8CNE9	Q8CNE9 staphylococ
565	7	2.3	372	2	Q982M2	Q982M2 rhizobium l	638	7	2.3	417	2	Q7SV42	Q7SV42 physcomitre
566	7	2.3	373	2	Q6MCM4	Q6MCM4 paracchlamyd	639	7	2.3	418	1	THBG_MOUSE	P61939 mus musculi
567	7	2.3	374	2	Q9SFB3	Q9SFB3 arabidopsis	640	7	2.3	418	1	THBG_RAT	P35577 rattus norv
568	7	2.3	375	2	Q55851	Q55851 synecchocyst	641	7	2.3	418	2	Q8AED6	Q8AED6 human immun
569	7	2.3	375	2	Q72H86	Q72H86 thermus the	642	7	2.3	420	2	Q9QX71	Q9QX71 rattus norv
570	7	2.3	375	2	Q98ZJ4	Q98ZJ4 human immun	643	7	2.3	421	2	Q9RQ37	Q9RQ37 staphylococ
571	7	2.3	378	2	Q7NMY9	Q7NMY9 chromobacte	644	7	2.3	421	2	Q70007	Q70007 streptomyce
572	7	2.3	378	2	Q8D501	Q8D501 vibrio vuln	645	7	2.3	421	2	Q8NVAS	Q8NVAS staphylococ
573	7	2.3	378	2	Q90JV4	Q90JV4 human immun	646	7	2.3	421	2	Q7A2M4	Q7A2M4 staphylococ
574	7	2.3	381	2	Q52563	Q52563 amycolatops	647	7	2.3	421	2	Q7A447	Q7A447 staphylococ
575	7	2.3	381	2	Q90J53	Q90J53 human immun	648	7	2.3	421	2	Q9X4D7	Q9X4D7 staphylococ
576	7	2.3	382	2	Q8S0V8	Q8S0V8 oryza sativ	649	7	2.3	421	2	Q6G760	Q6G760 staphylococ
577	7	2.3	382	2	Q9HXJ9	Q9HXJ9 pseudomonas	650	7	2.3	421	2	Q6GEH2	Q6GEH2 staphylococ
578	7	2.3	383	1	G1C2_YEAST	Q66448 saccharomyc	651	7	2.3	422	2	Q67J17	Q67J17 oryza sativ
579	7	2.3	384	1	R1R2_SPIRO	P07201 splitula sol	652	7	2.3	423	1	PYRX_PSEAB	Q51551 pseudomonas
580	7	2.3	384	1	Y039_MYCPN	P75063 mycoplasma	653	7	2.3	423	2	Q8AH86	Q8AH86 human immun
581	7	2.3	384	2	Q7NBE2	Q7NBE2 photorhabdi	654	7	2.3	423	2	Q8AH83	Q8AH83 human immun
582	7	2.3	385	2	Q8RSC4	Q8RSC4 corynebacte	655	7	2.3	423	2	Q8AHH1	Q8AHH1 human immun
583	7	2.3	385	2	Q90GH4	Q90GH4 human immun	656	7	2.3	423	2	Q8AH17	Q8AH17 human immun
584	7	2.3	385	2	Q90J16	Q90J16 human immun	657	7	2.3	423	2	Q8AH18	Q8AH18 human immun
585	7	2.3	386	2	Q6Z003	Q6Z003 brachyosco	658	7	2.3	423	2	Q8AHM1	Q8AHM1 human immun
586	7	2.3	386	2	Q88G90	Q88G90 pseudomonas	659	7	2.3	423	2	Q8AHM9	Q8AHM9 human immun
587	7	2.3	387	1	YR24_CAEEL	Q09341 caenorhabdi	660	7	2.3	426	2	Q5BX74	Q5BX74 debaryomyce
588	7	2.3	387	2	Q6F8N5	Q6F8N5 acinetobact	661	7	2.3	427	2	Q7JZ69	Q7JZ69 mycobacteri
589	7	2.3	387	2	Q838Y6	Q838Y6 enterococcu	662	7	2.3	428	2	Q6X895	Q6X895 gallus gall
590	7	2.3	388	2	Q8XVY1	Q8XVY1 raietonia s	663	7	2.3	430	2	Q67T20	Q67T20 symbiodacte
591	7	2.3	390	2	Q8AHM4	Q8AHM4 human immun	664	7	2.3	432	2	Q21857	Q21857 caenorhabdi
592	7	2.3	390	2	Q987E4	Q987E4 rhizobium l	665	7	2.3	432	2	Q8UBR5	Q8UBR5 agrobacteri
593	7	2.3	391	2	Q7W043	Q7W043 bordetella	666	7	2.3	432	2	Q7UGK8	Q7UGK8 rhodopirell
594	7	2.3	392	2	Q01479	Q01479 caenorhabdi	667	7	2.3	432	2	Q7W3U8	Q7W3U8 bordetella
595	7	2.3	392	2	Q7R7A1	Q7R7A1 plasmodium	668	7	2.3	433	2	Q7WF78	Q7WF78 bordetella
596	7	2.3	394	2	Q80UMJ7	Q80UMJ7 human immun	669	7	2.3	433	2	Q87A55	Q87A55 xyella fas
597	7	2.3	394	2	Q90K14	Q90K14 human immun	670	7	2.3	433	2	Q9PAB9	Q9PAB9 xyella fas
598	7	2.3	396	2	Q59354	Q59354 pyrococcus	671	7	2.3	433	2	Q8AXK6	Q8AXK6 xenopus lae
599	7	2.3	396	2	Q9SDZ5	Q9SDZ5 oryza sativ	672	7	2.3	434	2	Q6VUAS	Q6VUAS uncultured
600	7	2.3	396	2	Q88P50	Q88P50 pseudomonas	673	7	2.3	434	2	Q648Y7	Q648Y7 uncultured
601	7	2.3	397	2	Q6AM78	Q6AM78 oryza sativ	674	7	2.3	434	2	Q64BJ1	Q64BJ1 uncultured
602	7	2.3	397	2	Q76VJ3	Q76VJ3 oryza sativ	675	7	2.3	434	2	Q6TPS1	Q6TPS1 human immun
603	7	2.3	397	2	Q7VSJ3	Q7VSJ3 bordetella	676	7	2.3	434	2	Q6TPS6	Q6TPS6 human immun
604	7	2.3	397	2	Q7W464	Q7W464 bordetella	677	7	2.3	435	1	Y0D7_CAEEL	Y093267 caenorhabdi
605	7	2.3	397	2	Q7WFM1	Q7WFM1 bordetella	678	7	2.3	437	2	Q7CYG9	Q7CYG9 agrobacteri
606	7	2.3	398	2	Q90JY9	Q90JY9 human immun	679	7	2.3	437	2	Q81Z14	Q81Z14 nitrosomona
607	7	2.3	398	2	Q6AFD2	Q6AFD2 leifsonia x	680	7	2.3	437	2	Q86GT2	Q86GT2 bifidobacte
608	7	2.3	399	2	Q90HC8	Q90HC8 human immun	681	7	2.3	438	2	Q87856	Q87856 streptomyce
609	7	2.3	401	2	Q8NDP0	Q8NDP0 homo sapien	682	7	2.3	438	2	Q7VVB7	Q7VVB7 bordetella
610	7	2.3	401	2	Q95Q88	Q95Q88 caenorhabdi	683	7	2.3	443	2	Q80AT6	Q80AT6 brachydantio
611	7	2.3	401	2	Q9S221	Q9S221 streptomyce	684	7	2.3	444	1	TIG_AZOB	Q966W7 azospirillum
612	7	2.3	401	2	Q90HP5	Q90HP5 human immun	685	7	2.3	445	1	TRX6_HUMAN	Q97412 homo sapien
613	7	2.3	401	2	Q90IB8	Q90IB8 human immun	686	7	2.3	445	1	Q7XHS6	Q7XHS6 oryza sativ
614	7	2.3	402	2	Q7S182	Q7S182 oryza sativ	687	7	2.3	446	2	Q69KW1	Q69KW1 oryza sativ
615	7	2.3	402	2	Q9ZVP2	Q9ZVP2 rhizobium m	688	7	2.3	446	2	Q69885	Q69885 streptomyce

689	7	2.3	447	2	Q72L17	Q72L17	thermus the
690	7	2.3	447	2	Q82EH0	Q82EH0	streptomyce
691	7	2.3	447	2	Q9X7Z6	Q9X7Z6	streptomyce
692	7	2.3	448	2	Q63KQ9	Q63KQ9	burkholderi
693	7	2.3	448	2	Q88XM9	Q88XM9	lactobacilli
694	7	2.3	449	2	Q72G82	Q72G82	thermus the
695	7	2.3	449	2	Q82A36	Q82A36	streptomyce
696	7	2.3	449	2	Q9A3Q1	Q9A3Q1	caulobacter
697	7	2.3	450	2	Q7W6X6	Q7W6X6	bordetella
698	7	2.3	450	2	Q7W1Y3	Q7W1Y3	bordetella
699	7	2.3	450	2	Q9ZL68	Q9ZL68	helicobacte
700	7	2.3	451	2	Q62EH4	Q62EH4	burkholderi
701	7	2.3	451	2	Q63P97	Q63P97	burkholderi
702	7	2.3	455	1	A2AC_CAVPO	A2AC_CAVPO	cavia porce
703	7	2.3	456	1	Q9CL30	Q9CL30	pasteurella
704	7	2.3	458	1	A2AC_MOUSE	A2AC_MOUSE	mus muscicu
705	7	2.3	458	1	A2AC_RAT	A2AC_RAT	rattus norv
706	7	2.3	459	1	Q61OZ2	Q61OZ2	pietrophilus
707	7	2.3	461	2	Q82GP7	Q82GP7	streptomyce
708	7	2.3	461	2	Q9K3U6	Q9K3U6	streptomyce
709	7	2.3	462	1	A2AC_HUMAN	A2AC_HUMAN	homo sapien
710	7	2.3	464	1	IFE_BRALA	IFE_BRALA	branchiost
711	7	2.3	465	2	Q94692	Q94692	schizosacch
712	7	2.3	465	2	Q81VS1	Q81VS1	homo sapien
713	7	2.3	465	2	Q9H7X1	Q9H7X1	homo sapien
714	7	2.3	466	2	Q9H3U5	Q9H3U5	homo sapien
715	7	2.3	466	2	Q84ZB8	Q84ZB8	oryza sativ
716	7	2.3	467	1	CLCA_VIBPA	CLCA_VIBPA	vibri
717	7	2.3	467	1	CLCA_VIBVU	CLCA_VIBVU	vibri
718	7	2.3	467	1	CLCA_VIBVY	CLCA_VIBVY	vibri
719	7	2.3	467	2	Q727H1	Q727H1	desulfovibr
720	7	2.3	468	1	CLCA_VIBCH	CLCA_VIBCH	vibri
721	7	2.3	468	2	Q9NL06	Q9NL06	epitretus
722	7	2.3	469	1	FXGA_HUMAN	FXGA_HUMAN	homo sapien
723	7	2.3	469	2	Q6A613	Q6A613	propionibac
724	7	2.3	469	2	Q7DD55	Q7DD55	neisseria m
725	7	2.3	469	2	Q9JRK0	Q9JRK0	neisseria m
726	7	2.3	470	2	Q8TW17	Q8TW17	methanopyru
727	7	2.3	470	2	Q7W7F2	Q7W7F2	bordetella
728	7	2.3	471	2	Q80TE3	Q80TE3	mus muscicu
729	7	2.3	474	2	Q922J7	Q922J7	rhizobium m
730	7	2.3	475	2	Q9L094	Q9L094	streptomyce
731	7	2.3	477	2	Q9RGW9	Q9RGW9	arabidopsis
732	7	2.3	479	2	Q9GSU8	Q9GSU8	homo sapien
733	7	2.3	479	2	Q8LST7	Q8LST7	chlamydomon
734	7	2.3	482	2	Q7S0U9	Q7S0U9	neutrospora
735	7	2.3	484	2	Q9KYG5	Q9KYG5	streptomyce
736	7	2.3	485	2	Q73VA2	Q73VA2	mycobacteri
737	7	2.3	485	2	Q7ND75	Q7ND75	gloeobacter
738	7	2.3	486	2	Q94815	Q94815	oryza sativ
739	7	2.3	486	2	Q7XEU8	Q7XEU8	oryza sativ
740	7	2.3	488	2	Q9N9Z2	Q9N9Z2	drobophila
741	7	2.3	489	2	Q7SEW1	Q7SEW1	ashbya gos
742	7	2.3	489	2	Q726Q1	Q726Q1	desulfovibr
743	7	2.3	489	2	Q88988	Q88988	muid herpe
744	7	2.3	490	2	Q941W5	Q941W5	oryza sativ
745	7	2.3	490	2	Q95098	Q95098	mycobacteri
746	7	2.3	490	2	Q7TXC5	Q7TXC5	mycobacteri
747	7	2.3	491	2	Q94289	Q94289	bacillus ci
748	7	2.3	492	2	Q6A329	Q6A329	arabidopsis
749	7	2.3	493	2	Q7OZS8	Q7OZS8	anopheles g
750	7	2.3	496	2	Q91TW0	Q91TW0	tupaiid her
751	7	2.3	497	2	Q9PBA2	Q9PBA2	xylella fas
752	7	2.3	497	2	Q9PBA3	Q9PBA3	xylella fas
753	7	2.3	499	2	Q82QV9	Q82QV9	streptomyce
754	7	2.3	499	2	Q88GH8	Q88GH8	pseudomonas
755	7	2.3	499	2	Q67C63	Q67C63	human immun
756	7	2.3	499	2	Q67C83	Q67C83	human immun
757	7	2.3	499	2	Q67C95	Q67C95	human immun
758	7	2.3	499	2	Q67CE7	Q67CE7	human immun
759	7	2.3	499	2	Q67CG3	Q67CG3	human immun
760	7	2.3	499	2	Q67C10	Q67C10	human immun
761	7	2.3	499	2	Q67C14	Q67C14	human immun
762	7	2.3	499	2	Q67CT2	Q67CT2	human immun
763	7	2.3	499	2	Q67CV4	Q67CV4	human immun
764	7	2.3	499	2	Q67DB6	Q67DB6	human immun
765	7	2.3	499	2	Q67DB6	Q67DB6	human immun
766	7	2.3	499	2	Q67DC6	Q67DC6	human immun
767	7	2.3	499	2	Q67D12	Q67D12	human immun
768	7	2.3	499	2	Q67D16	Q67D16	human immun
769	7	2.3	499	2	Q67D35	Q67D35	human immun
770	7	2.3	499	2	Q67DN2	Q67DN2	human immun
771	7	2.3	500	2	Q7URV7	Q7URV7	rhodospirill
772	7	2.3	500	2	Q99KX9	Q99KX9	mus muscicu
773	7	2.3	506	2	Q822R4	Q822R4	chlamydomon
774	7	2.3	507	2	Q69254	Q69254	mus muscicu
775	7	2.3	508	1	CPT7_HORSE	CPT7_HORSE	equus cabal
776	7	2.3	510	2	Q8V178	Q8V178	mycobacteri
777	7	2.3	511	2	Q9V8Z9	Q9V8Z9	drobophila
778	7	2.3	513	2	Q92M58	Q92M58	rhizobium m
779	7	2.3	514	2	Q7XED6	Q7XED6	oryza sativ
780	7	2.3	515	2	Q84HH8	Q84HH8	azarcus ev
781	7	2.3	515	2	Q62FQ6	Q62FQ6	burkholderi
782	7	2.3	515	2	Q63PJ0	Q63PJ0	burkholderi
783	7	2.3	516	2	Q8W080	Q8W080	oryza sativ
784	7	2.3	518	2	Q6PD24	Q6PD24	mus muscicu
785	7	2.3	522	1	GUAA_XYLEFA	GUAA_XYLEFA	xylella fas
786	7	2.3	522	2	GUAA_XYLFT	GUAA_XYLFT	xylella fas
787	7	2.3	522	2	Q6V0L0	Q6V0L0	homo sapien
788	7	2.3	524	2	Q87V45	Q87V45	macaca fasc
789	7	2.3	524	2	Q87V45	Q87V45	pseudomonas
790	7	2.3	524	2	Q8K012	Q8K012	mus muscicu
791	7	2.3	525	2	ALGG_AZOV1	ALGG_AZOV1	azotobacter
792	7	2.3	525	2	Q748H0	Q748H0	geobacter s
793	7	2.3	527	2	Q9SAB5	Q9SAB5	arabidopsis
794	7	2.3	528	2	Q96TW5	Q96TW5	hanseniella a
795	7	2.3	528	2	Q9FMW0	Q9FMW0	arabidopsis
796	7	2.3	529	2	Q7Q299	Q7Q299	anopheles g
797	7	2.3	529	2	Q31001	Q31001	thermus the
798	7	2.3	533	1	RP65_AMBRI	RP65_AMBRI	ambystoma t
799	7	2.3	533	2	Q6EBG1	Q6EBG1	lupinus alb
800	7	2.3	538	2	Q9LSB3	Q9LSB3	arabidopsis
801	7	2.3	538	2	Q6NNU8	Q6NNU8	drobophila
802	7	2.3	542	2	Q93YR0	Q93YR0	arabidopsis
803	7	2.3	543	2	Q6DJU4	Q6DJU4	homo sapien
804	7	2.3	543	2	Q8W3B4	Q8W3B4	oryza sativ
805	7	2.3	543	2	Q75M59	Q75M59	oryza sativ
806	7	2.3	545	2	Q9AJR4	Q9AJR4	streptomyce
807	7	2.3	550	2	Q73YZ0	Q73YZ0	mycobacteri
808	7	2.3	551	2	Q6AUP1	Q6AUP1	oryza sativ
809	7	2.3	551	2	Q87AL4	Q87AL4	xylella fas
810	7	2.3	552	2	Q9NPZ7	Q9NPZ7	homo sapien
811	7	2.3	553	2	Q7VVK5	Q7VVK5	bordetella
812	7	2.3	553	2	Q7W512	Q7W512	bordetella
813	7	2.3	553	2	Q7W512	Q7W512	bordetella
814	7	2.3	554	2	Q7WHY7	Q7WHY7	homo sapien
815	7	2.3	554	2	Q9UHY0	Q9UHY0	homo sapien
816	7	2.3	557	2	Q70Q44	Q70Q44	xenopus lae
817	7	2.3	558	2	Q6NN42	Q6NN42	drobophila
818	7	2.3	558	2	Q8KDW0	Q8KDW0	chlorobium
819	7	2.3	560	2	Q6ZMF6	Q6ZMF6	burkholderi
820	7	2.3	561	1	KCN1_HUMAN	KCN1_HUMAN	homo sapien
821	7	2.3	566	2	Q81XM4	Q81XM4	homo sapien
822	7	2.3	566	2	Q6GC11	Q6GC11	mint vein b
823	7	2.3	567	2	Q6P5X0	Q6P5X0	homo sapien
824	7	2.3	568	2	Q91DD4	Q91DD4	oryza sativ
825	7	2.3	568	2	Q8RC69	Q8RC69	xanthomonas
826	7	2.3	568	2	Q8CMS2	Q8CMS2	streptomyce
827	7	2.3	578	2	Q9XA04	Q9XA04	arabidopsis
828	7	2.3	578	2	Q65KZ4	Q65KZ4	arabidopsis
829	7	2.3	581	2	Q6C8A4	Q6C8A4	yarrowia li
830	7	2.3	581	2	Q6C8A4	Q6C8A4	oryza sativ
831	7	2.3	583	2	Q6C8A4	Q6C8A4	oryza sativ
832	7	2.3	584	2	Q9QAT4	Q9QAT4	muid herpe
833	7	2.3	584	2	Q92YK4	Q92YK4	rhizobium m
834	7	2.3	584	2	Q8VDS0	Q8VDS0	mus muscicu

835	7	2.3	586	2	Q6AW05	Q6AW05 caenorhabdi	908	7	2.3	719	2	Q6CSE9	Q6CSE9 kluyveromyc
836	7	2.3	586	2	Q6Z132	Q6Z132 oryza sativ	909	7	2.3	726	2	Q6RJY1	Q6RJY1 streptomyce
837	7	2.3	587	2	Q7MHB4	Q7MHB4 vibrio vuln	910	7	2.3	727	1	S521_HUMAN	Q96TM7 homo sapien
838	7	2.3	587	2	Q8DCJ4	Q8DCJ4 vibrio vuln	911	7	2.3	727	2	Q8Z0N2	Q8Z0N2 anabaena sp
839	7	2.3	588	2	Q9UYN4	Q9UYN4 pyrococcus	912	7	2.3	730	2	Q8KN10	Q8KN10 streptomyce
840	7	2.3	590	2	Q91VM4	Q91VM4 mus musculu	913	7	2.3	731	2	Q6MXX5	Q6MXX5 mycobacteri
841	7	2.3	591	2	Q942N2	Q942N2 oryza sativ	914	7	2.3	734	1	ZN42_HUMAN	P26698 homo sapien
842	7	2.3	593	2	Q9D114	Q9D114 human immun	915	7	2.3	734	2	Q872N8	Q872N8 neurospora
843	7	2.3	594	2	Q9R1M6	Q9R1M6 arabidopsi	916	7	2.3	734	2	Q96171	Q96171 homo sapien
844	7	2.3	597	2	Q28610	Q28610 oryctolagus	917	7	2.3	738	1	S521_RAT	Q96Y02 rattus norv
845	7	2.3	597	2	Q6R4Q5	Q6R4Q5 bos taurus	918	7	2.3	741	2	Q8BG19	Q8BG19 m mus muscu
846	7	2.3	598	2	Q6X244	Q6X244 bovine herp	919	7	2.3	742	2	Q6P9B2	Q6P9B2 homo sapien
847	7	2.3	599	2	Q6ZVU6	Q6ZVU6 homo sapien	920	7	2.3	742	2	Q23766	Q23766 chironomus
848	7	2.3	605	1	MUTL_RHIME	Q92TP4 rhizobium m	921	7	2.3	743	2	Q9Y1Z2	Q9Y1Z2 ephydratia f
849	7	2.3	605	2	Q97M69	Q97M69 clostridium	922	7	2.3	745	2	Q6Z1Z5	Q6Z1Z5 oryza sativ
850	7	2.3	605	2	Q82MX2	Q82MX2 streptomyce	923	7	2.3	746	1	PPK_STRCO	Q9ZV26 streptomyce
851	7	2.3	607	2	Q25379	Q25379 xenopus lae	924	7	2.3	748	2	O44416	O44416 chironomus
852	7	2.3	609	2	Q70Q63	Q70Q63 xenopus lae	925	7	2.3	748	2	Q72SP6	Q72SP6 leptospira
853	7	2.3	611	2	Q9S767	Q9S767 oryza sativ	926	7	2.3	749	2	Q7TWK6	Q7WK6 mycobacteri
854	7	2.3	612	2	Q88B55	Q88B55 oryza sativ	927	7	2.3	749	2	Q8P2V5	Q8P2V5 leptospira
855	7	2.3	612	2	Q7XR65	Q7XR65 oryza sativ	928	7	2.3	750	1	PRNG_MYCBO	P65729 mycobacteri
856	7	2.3	616	2	Q9PCM5	Q9PCM5 xylella fas	929	7	2.3	750	1	PRNG_MYCTU	P65728 mycobacteri
857	7	2.3	617	2	Q6GQH3	Q6GQH3 xenopus lae	930	7	2.3	754	2	Q873B6	Q873B6 neurospora
858	7	2.3	618	2	Q8B764	Q8B764 xanthomonas	931	7	2.3	761	1	VPA_BPP2	Q06419 bacterioph
859	7	2.3	619	2	Q81VM8	Q81VM8 homo sapien	932	7	2.3	761	2	Q7Y4B8	Q7Y4B8 bacterioph
860	7	2.3	620	2	Q919A7	Q919A7 xenopus lae	933	7	2.3	761	2	Q858M4	Q858M4 bacterioph
861	7	2.3	621	2	Q67RMO	Q67RMO symbiobacte	934	7	2.3	763	2	Q9Z299	Q9Z299 mus musculu
862	7	2.3	621	2	Q8C4D2	Q8C4D2 mus musculu	935	7	2.3	763	2	Q8G618	Q8G618 bitidobacte
863	7	2.3	623	2	Q6Z707	Q6Z707 oryza sativ	936	7	2.3	770	2	Q65Z19	Q65Z19 chlamydomon
864	7	2.3	625	2	Q6CEM7	Q6CEM7 yarrowia li	937	7	2.3	775	2	Q6K393	Q6K393 oryza sativ
865	7	2.3	626	2	Q64N34	Q64N34 bacteroides	938	7	2.3	775	2	Q8VJ15	Q8VJ15 mycobacteri
866	7	2.3	637	2	Q49524	Q49524 arabidopsi	939	7	2.3	780	2	Q70V27	Q70V27 giardia lam
867	7	2.3	642	2	Q817S5	Q817S5 arabidopsi	940	7	2.3	784	2	Q8ZG29	Q8ZG29 streptomyce
868	7	2.3	642	2	Q89MH1	Q89MH1 bradyrhizob	941	7	2.3	786	2	Q6CJ97	Q6CJ97 kluyveromyc
869	7	2.3	643	2	Q28603	Q28603 archaeeoglob	942	7	2.3	790	2	Q6BXG7	Q6BXG7 debaryomyc
870	7	2.3	644	2	Q59116	Q59116 archaeeoglob	943	7	2.3	792	2	Q7WJ82	Q7WJ82 bordetella
871	7	2.3	645	2	Q6FNS2	Q6FNS2 candida gla	944	7	2.3	792	2	Q754U5	Q754U5 ashyba goos
872	7	2.3	648	2	Q31644	Q31644 bacillus su	945	7	2.3	795	2	Q95U02	Q95U02 toxoplasma
873	7	2.3	650	2	Q91ZJ4	Q91ZJ4 arabidopsi	946	7	2.3	795	2	Q6EU01	Q6EU01 oryza sativ
874	7	2.3	651	2	Q6MTX4	Q6MTX4 mycoplasma	947	7	2.3	797	2	Q6CPH3	Q6CPH3 simian aden
875	7	2.3	659	2	Q98R52	Q98R52 mycoplasma	948	7	2.3	800	2	Q7QV15	Q7QV15 anophles g
876	7	2.3	664	2	Q8S5F7	Q8S5F7 oryza sativ	949	7	2.3	800	2	Q6QPA1	Q6QPA1 simian aden
877	7	2.3	664	2	Q7XG58	Q7XG58 oryza sativ	950	7	2.3	801	2	Q8ZJVS	Q8ZJVS salmonella
878	7	2.3	665	2	Q757A0	Q757A0 ashyba goos	951	7	2.3	802	2	Q8ZJVS	Q8ZJVS salmonella
879	7	2.3	668	2	Q8B6N7	Q8B6N7 xanthomonas	952	7	2.3	803	2	Q6FV15	Q6FV15 candida gla
880	7	2.3	671	1	HMOC_DROME	P22810 dirosophila	953	7	2.3	803	2	Q9ULK9	Q9ULK9 homo sapien
881	7	2.3	673	2	Q6E1J3	Q6E1J3 xenopus tro	954	7	2.3	809	2	Q33339	Q33339 cryphonectr
882	7	2.3	674	2	Q91Z86	Q91Z86 arabidopsi	955	7	2.3	810	2	Q8ZK60	Q8ZK60 streptomyce
883	7	2.3	674	2	Q8BH21	Q8BH21 xanthomonas	956	7	2.3	812	2	Q8N0W6	Q8N0W6 homo sapien
884	7	2.3	676	2	Q8BZ20	Q8BZ20 mus musculu	957	7	2.3	813	1	AD33_HUMAN	Q9P211 homo sapien
885	7	2.3	678	2	Q8VDT1	Q8VDT1 mus musculu	958	7	2.3	813	2	Q94LD6	Q94LD6 oryza sativ
886	7	2.3	680	2	Q8QLM5	Q8QLM5 mamestra co	959	7	2.3	813	2	Q8C9X6	Q8C9X6 mus musculu
887	7	2.3	680	2	Q71AK2	Q71AK2 mamestra co	960	7	2.3	818	2	Q93H51	Q93H51 streptomyce
888	7	2.3	681	2	Q8SQX1	Q8SQX1 encephalito	961	7	2.3	821	2	Q6AT74	Q6AT74 oryza sativ
889	7	2.3	683	2	Q7XS06	Q7XS06 oryza sativ	962	7	2.3	823	2	Q67IU6	Q67IU6 oryza sativ
890	7	2.3	685	2	Q8BGU9	Q8BGU9 m mus muscu	963	7	2.3	825	1	AXN1_BRABE	P57094 brachydantio
891	7	2.3	685	2	Q8BZM1	Q8BZM1 mus musculu	964	7	2.3	835	1	NEK4_HUMAN	P51957 homo sapien
892	7	2.3	687	2	Q9KXF3	Q9KXF3 streptomyce	965	7	2.3	842	2	Q9C2C8	Q9C2C8 neurospora
893	7	2.3	690	2	Q9HG51	Q9HG51 aspergillus	966	7	2.3	844	2	Q82RNL	Q82RNL streptomyce
894	7	2.3	691	2	Q9UVX9	Q9UVX9 aspergillus	967	7	2.3	845	2	Q67IW8	Q67IW8 oryza sativ
895	7	2.3	691	2	Q9RZ87	Q9RZ87 deinococcus	968	7	2.3	847	2	Q7R0E9	Q7R0E9 giardia lam
896	7	2.3	693	2	Q21649	Q21649 caenorhabdi	969	7	2.3	851	2	Q9Y4D4	Q9Y4D4 homo sapien
897	7	2.3	694	2	Q7D724	Q7D724 mycobacteri	970	7	2.3	853	1	MUTS_VIBVU	Q84C53 vibrio vuln
898	7	2.3	695	1	Z5M3_MOUSE	Q8C618 mus musculu	971	7	2.3	853	1	MUTS_VIBVY	Q7MHR2 vibrio vuln
899	7	2.3	696	1	Z5W3_HUMAN	Q96MP5 homo sapien	972	7	2.3	855	2	P90549	P90549 leishmania
900	7	2.3	697	2	Q61121	Q61121 citrithidia f	973	7	2.3	856	2	Q7SHJ0	Q7SHJ0 neurospora
901	7	2.3	702	2	Q9ZPN6	Q9ZPN6 zea mays (m	974	7	2.3	857	2	Q9TC08	Q9TC08 arabidopsi
902	7	2.3	702	2	Q97D01	Q97D01 clostridium	975	7	2.3	862	2	Q64C54	Q64C54 uncultured
903	7	2.3	706	2	Q7ZJS2	Q7ZJS2 thermus the	976	7	2.3	869	2	Q8YNN3	Q8YNN3 anabaena sp
904	7	2.3	710	2	Q9XXU6	Q9XXU6 caenorhabdi	977	7	2.3	879	2	Q8KX11	Q8KX11 rhizobium e
905	7	2.3	712	2	Q6CZ84	Q6CZ84 yarrowia.li	978	7	2.3	882	2	Q7SYD6	Q7SYD6 brachydantio
906	7	2.3	713	2	Q81M21	Q81M21 oryza sativ	979	7	2.3	886	2	Q8PCL9	Q8PCL9 xanthomonas
907	7	2.3	716	2	Q81M77	Q81M77 oryza sativ	980	7	2.3	886	2	Q8PPC7	Q8PPC7 xanthomonas

CC -1- TISSUE SPECIFICITY: Expressed in most tissues. High levels were
CC found in liver, kidney, heart, ovary, spleen, testes, skeletal
CC muscle and peripheral blood leukocytes. Expression was absent or
CC low in colon and small intestine. Expression is relatively high in
CC the tumor cell lines chronic myelogenous leukemia K-562 and the
CC colorectal adenocarcinoma SW480. Expression is moderate in the
CC cervical carcinoma HeLa, the Burkitt's lymphoma Raji, the lung
CC carcinoma A549, and the melanoma G361. In contrast, two leukemia
CC cell lines, HL-60 (promyelocytic leukemia) and MOLT-4
CC (lymphoblastic leukemia), show relatively low levels.
CC -1- DOMAIN: Interacts with CASP8 and CASP10 are mediated by the DED
CC domain.
CC -1- SIMILARITY: Contains 1 death effector (DED) domain.
CC -1- CAUTION: Ref.5 (AAH13372) sequence differs from that shown due to
CC a frameshift in position 186.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF443591; AAL48220.1; -
CC EMBL; AF457575; AAM10835.1; -
CC EMBL; AY125448; AAM95240.1; -
CC EMBL; AK075328; BAC11551.1; -
CC EMBL; BC013372; AAH13372.2; ALT_FRAME.
CC EMBL; BC027930; AAH27930.1; -
CC GeneW; HGNC:24450; DEDD2.
CC H-invDB; HIX0015171; -
CC InterPro; IPR011029; DEATH_Like.
CC InterPro; IPR01875; DED.
CC Pfam; PF01335; DED; 1.
CC SMART; SM00031; DED; 1.
CC PROSITE; PS0168; DED; 1.
CC Alternative splicing; Apoptosis; DNA-binding; Nuclear protein;
CC Transcription regulation.
CC DOMAIN 25 104 DED.
CC DOMAIN 104 109 Nuclear localization signal (Potential).
CC DOMAIN 155 173 Bipartite nuclear localization signal
CC (Potential).
CC VARSPLIC 145 149 Missing (in isoform 2).
CC FT CONFLICT 27 27 /FTId=VSP_010312.
CC FT CONFLICT 56 56 H -> N (in Ref. 2).
CC FT CONFLICT 79 79 A -> G (in Ref. 2).
CC FT CONFLICT 207 207 D -> G (in Ref. 2).
CC FT CONFLICT 230 207 C -> R (in Ref. 4).
CC SEQUENCE 326 AA; 36178 MW; 3F7B0B307CC870CD CRC64;
Query Match 73.9%; Score 224; DB 1; Length 326;
Best Local Similarity 100.0%; Pred. No. 7.8e-203;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
ID DED2_MOUSE STANDARD; PRT; 330 AA.
AC Q8QZV0; Q8QZV1;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE DNA-binding death effector domain-containing protein 2 (DED-containing
DE protein FLAME-3).
GN Name=DED2; Synonyms=Flame3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J;
RX MEDLINE=21961615; PubMed=11965497; DOI=10.1038/sj/cdd/4401038;
RA Zhan Y., Hegde R., Srinivasula S.M., Fernandes-Alnemri T.,
RA Alnemri E.S.,
RT "Death effector domain-containing proteins DEDD and FLAME-3 form
RT nuclear complexes with the Ffl1C102 subunit of human transcription
RT factor IIIC".
RL Cell Death Differ. 9:439-447(2002).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX PubMed=12527898; DOI=10.1038/sj.onc.1206099;
RA Alcivar A., Hu S., Tang Y., Yang X.,
RT "DEDD and DEDD2 associate with caspase-8/10 and signal cell death".
RN Oncogene 22:291-297(2003).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Retina;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heltan E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherren A., Schein J.E., Jones S.J.M., Werra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences".
CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: May play a critical role in death receptor-induced
CC apoptosis and may target CASP8 and CASP10 to the nucleus. May
CC regulate degradation of intermediate filaments during apoptosis.
CC May play a role in the general transcription machinery in the
CC nucleus and might be an important regulator of the activity of
CC GTP3C3.
CC -1- SUBUNIT: Interacts with CASP8, CASP10 and GTP3C3. Homodimerizes
CC and heterodimerizes with DEDD (by similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear, accumulated in subnuclear
CC structures resembling nucleoli (by similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q8QZV0-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8QZV0-2; Sequence=VSP_010313, VSP_010314;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Expression is high in liver, heart, kidney,
CC and testis but low in brain, spleen, lung, and skeleton muscle.


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CC -1- DOMAIN: Interactions with CASP8 and CASP10 are mediated by the DED
CC domain (By similarity).
CC -1- SIMILARITY: Contains 1 death effector (DED) domain.
CC -----
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CC -----
DR EMBL: AF457576; AAM0836.1; -
DR EMBL: AF543541; AAN3179.1; -
DR EMBL: BC037043; AAN37043.1; -
DR MGD: MGI:1914629; 2410050E11R1K.
DR InterPro: IPR011029; DEATH_like.
DR InterPro: IPR001875; DED.
DR Pfam: PF01335; DED.
DR SMART: SM00031; DED.
DR PROSITE: PS50166; DED.
DR KW: Alternative splicing; Apoptosis; DNA-binding; Nuclear protein;
DR KW: Transcription regulation.
FT DOMAIN 25 104 DED.
FT DOMAIN 104 109 Nuclear localization signal (Potential).
FT DOMAIN 156 174 Bipartite nuclear localization signal
FT DOMAIN (Potential).
FT VARSPIC 1 171 Missing (in isoform 2).
FT VARSPIC 172 200 /FTid=VSP_010313.
FT VARSPIC 172 200 RRRAGLAASQOHOCHQEGRPSSBQKVC -> MGKAORG
FT VARSPIC 172 200 EVTCPRPRAVAMQSDSLIS (in isoform 2).
FT VARSPIC 172 200 /FTid=VSP_010314.
SQ SEQUENCE 330 AA; 36786 MW; 889BCPF5E01304B0 CRC64;

Query Match 38.6%; Score 117; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.1e-101;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 187 RPSEGGKTCIDIRLRVRAVECEHGPALBEGVARSRRPOLAROLVFGQATVLSRDIGS 246
DB 191 RPSSBGGKTCIDIRLRVRAVECEHGPALBEGVARSRRPOLAROLVFGQATVLSRDIGS 250
OY 247 VVCIIKFESELYLDAFMGDYLSGALLQALRGVFTLEALREAVGEAVLTVSVDAD 303
DB 251 VVCIIKFESELYLDAFMGDYLSGALLQALRGVFTLEALREAVGEAVLTVSVDAD 307

RESULT 3
O8BRM9 PRELIMINARY; PRT; 168 AA.
ID O8BRM9 PRELIMINARY; PRT; 168 AA.
AC O8BRM9 PRELIMINARY; PRT; 168 AA.
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched
DE library, clone: A830049M19 product: similar to death effector domain-
DE containing and DNA-binding protein 2, full insert sequence.
DE Name=Ded2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RT Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

```

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RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kanno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subcloning of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Kanno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Niehine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kaishiki M.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsubiki M.,
RA Yoneda Y., Ishiura T., Ozawa K., Tanaka T., Matsubara S., Kawai U.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hoti F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kawai H., Kawai U., Kojima Y., Kondo S., Kono H., Koda M., Koya S.,
RA Kuyihara C., Matsuyama T., Miyazaki A., Murata N., Nakamura M.,
RA Nishihara K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Yamamoto M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK043908; BAC31699.1; -
DR MGD: MGI:1914629; Ded2.
DR GO: GO:0042981; P:regulation of apoptosis; TAS.
KW DNA-binding.
SQ SEQUENCE 168 AA; 17442 MW; F75D71DC48992425 CRC64;

Query Match 7.6%; Score 23; DB 2; Length 168;
Best Local Similarity 100.0%; Pred. No. 4.1e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 195 TCDIRLRVRAVECEHGPALBEGV 217
DB 83 TCDIRLRVRAVECEHGPALBEGV 105

RESULT 4
O919M3 PRELIMINARY; PRT; 369 AA.
ID O919M3 PRELIMINARY; PRT; 369 AA.
AC O919M3 PRELIMINARY; PRT; 369 AA.
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ded1.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

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CC -1- TISSUE SPECIFICITY: widely expressed with highest levels in
CC testis.
CC -1- PTM: Exists predominantly in a mono- or dibiquitinated form.
CC -1- SIMILARITY: Contains 1 death effector (DED) domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF083236; AAC33105.1; -
CC EMBL; AF100341; AAD16414.1; -
CC EMBL; AF043733; AAC80280.1; -
CC EMBL; AJ010973; CA09445.1; -
CC EMBL; AF064605; AAC17110.3; -
CC EMBL; BC016724; AAH16724.1; -
CC EMBL; BC013910; AAH13910.1; -
CC Genew; HGNC:2755; DEDD.
CC H-invdb; HIX0001231; -.
CC MIM; 606841; -.
CC DR GO; GO:0005737; C:cytoplasm; ISS.
CC DR GO; GO:0005730; C:nucleolus; ISS.
CC DR GO; GO:0003677; F:DNA binding; ISS.
CC DR GO; GO:0006917; P:induction of apoptosis; ISS.
CC DR GO; GO:0006825; P:induction of apoptosis via death domain rec. .; TMS.
CC DR GO; GO:0016481; P:negative regulation of transcription; ISS.
CC DR GO; GO:0007283; P:spermatogenesis; TMS.
CC DR InterPro; IPR011029; DEATH_like.
CC DR InterPro; IPR001875; DED.
CC DR Pfam; PF01335; DED; 1.
CC DR SMART; SM00031; DED; 1.
CC DR PROSITE; PS00168; DED; 1.
CC KW Alternative splicing; Apoptosis; DNA-binding; Nuclear protein;
CC Repressor; Transcription regulation.
CC FT DOMAIN 25 103 DED. GEEIQGFRMSRLGEYKELGHMVAVIAIQ (in
CC FT VARSPLIC 194 194 isoform 2).
CC FT CONFLICT 13 13 /Pfam:VSP_003846.
CC FT SEQUENCE 318 AA; 36794 MW; FFD5F9B61FEBB6 CRC64;
CC SQ
CC Query Match 4.3%; Score 13; DB 1; Length 318;
CC Best Local Similarity 100.0%; Pred. No. 0.0021;
CC Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 195 TCDIRLRVAEYC 207
CC Db 192 TCDIRLRVAEYC 204
CC
CC RESULT 6
CC DEDD_MOUSE STANDARD; PRT; 318 AA.
CC ID DEDD_MOUSE STANDARD; PRT; 318 AA.
CC AC Q9ZIL3; Q7TQH8; Q9R227;
CC DT 28-FEB-2003 (rel. 41, Created)
CC DT 28-FEB-2003 (rel. 41, Last sequence update)
CC DT 05-JUL-2004 (rel. 44, Last annotation update)
CC DE Death effector domain-containing protein (DEDDPro1).
CC GN Name=dedd;
CC OS Mus musculus (Mouse).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC OC NCBI_Taxid=10090;
CC RN [1]
CC RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
CC SPECIFICITY.
CC RX MEDLINE=98447599; PubMed=9774341; DOI=10.1093/emboj/17.20.5974;
CC RX Stegh A.H., Schickling O., Ehret A., Scafield C., Peterhaensel C.,
CC RX Hofmann T.G., Grummt I., Kramer P.H., Peter M.E.;
CC RT "DEDD, a novel death effector domain containing protein, targeted to

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RT the nucleolus."
RL EMBO J. 17:5974-5986 (1998).
RN [2]
RN SEQUENCE FROM N.A.
RA Thome M., Tschopp J.;
RT "DEDDPro1, a novel DED-containing protein."
RN submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N-3; TISSUE=Colon, and Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feinberg E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.B.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman W., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Snechenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallie D.E.,
RA Scherch A., Schein J.R., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- FUNCTION: A scaffold protein that directs CASP3 to certain
CC substrates and facilitates their ordered degradation during
CC apoptosis. May also play a role in mediating CASP3 cleavage of
CC KRT18. Regulates degradation of intermediate filaments during
CC apoptosis. May play a role in the general transcription machinery
CC in the nucleus and might be an important regulator of the activity
CC of GTF3C3 (By similarity). Inhibits DNA transcription in vitro.
CC -1- SUBUNIT: Interacts with CASP8, CASP10, KRT8, KRT18, CASP3 and
CC FADD. Homodimerizes and heterodimerizes with DEDD2 (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Translocated to the nucleus
CC during CP95-mediated apoptosis where it is localized in the
CC nucleoli. Following apoptosis induction, the mono and/or
CC dibiquitination form increases and forms filamentous structures
CC that colocalize with KRT8 and KRT18 intermediate filament network
CC in simple epithelial cells (By similarity).
CC -1- TISSUE SPECIFICITY: Ubiquitously expressed.
CC -1- PTM: Exists predominantly in a mono- or dibiquitinated form.
CC -1- SIMILARITY: Contains 1 death effector (DED) domain.
CC -----
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CC -----
CC EMBL; AJ011386; CA09604.1; -
CC DR EMBL; AF100342; AAD16415.1; -
CC DR EMBL; BC023668; AAH23668.1; -
CC DR EMBL; BC054445; AAH54445.1; -
CC DR MGD; MGI:133874; Dedd.
CC DR GO; GO:0005737; C:cytoplasm; IDA.
CC DR GO; GO:0005730; C:nucleolus; IDA.
CC DR GO; GO:0003677; F:DNA binding; IDA.
CC DR GO; GO:0006917; P:induction of apoptosis; IDA.
CC DR GO; GO:0016481; P:negative regulation of transcription; IDA.
CC DR InterPro; IPR011029; DEATH_like.
CC DR InterPro; IPR001875; DED.
CC DR Pfam; PF01335; DED; 1.
CC DR SMART; SM00031; DED; 1.

```


DR PROSITE; PSS0168; DED; 1.
 KM Apoptosis; DNA-binding; Nuclear protein; Repressor;
 KW Transcription regulation.
 FT DOMAIN 25 103 DED.
 FT CONFLICT 237 237 K -> N (in Ref. 2).
 FT CONFLICT 316 316 A -> V (in Ref. 3; AAHS4445).
 SQ SEQUENCE 318 AA; 36805 MW; C9A3IDPC4C0E57CA CRC64;

Query Match 4.3%; Score 13; DB 1; Length 318;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 195 TCDIRLRVRAEYC 207
 Db 192 TCDIRLRVRAEYC 204

RESULT 7

ID DEDD_RAT STANDARD; PRT; 318 AA.

AC 0922X0;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Death effector domain-containing protein (Death effector domain-
 DE containing testicular molecule).
 OS Name=Ded; Synonyms=Defc;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
 RC TISSUE-Testis;
 RX MEDLINE=99049260; PubMed=9832420; DOI=10.1210/en.139.12.4839;
 RA Leo C.P., Hsu S.Y., McGea E.A., Salanova M., Hsueh A.U.W.;
 RT "DEFT, a novel death effector domain-containing molecule predominantly
 RT expressed in testicular germ cells.";
 RL Endocrinology 139:4839-4848(1998).

CC -1- FUNCTION: A scaffold protein that directs CASP3 to certain
 CC substrates and facilitates their ordered degradation during
 CC apoptosis. May also play a role in mediating CASP3 cleavage of
 CC KR18. Regulates degradation of intermediate filaments during
 CC apoptosis. May play a role in the general transcription machinery
 CC in the nucleus and might be an important regulator of the activity
 CC of GTF3C3. Inhibits DNA transcription in vitro (By similarity).
 CC -1- SUBUNIT: Interacts with CASP8, CASP10, KR18, KR19, CASP3 and
 CC FADD. Homodimerizes and heterodimerizes with DEDD2 (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Translocated to the nucleus
 CC during CD95-mediated apoptosis where it is localized in the
 CC nucleoli. Following apoptosis induction, the mono and/or
 CC dimerization form increases and forms filamentous structures
 CC that colocalize with KR18 and KR19 intermediate filament network
 CC in simple epithelial cells (By similarity).
 CC -1- TISSUE SPECIFICITY: Widely expressed with highest levels in
 CC testis. Within the testis, highly expressed in germ cells but not
 CC expressed in Sertoli cells.
 CC -1- DEVELOPMENTAL STAGE: First detected in 20-day-old animals. Reaches
 CC a peak at 30 days.
 CC -1- PTM: Exists predominantly in a mono- or dimerized form.
 CC -1- SIMILARITY: Contains 1 death effector (DED) domain.

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 CC
 CC EMBL, AF053362; AAC80287.1; -;
 DR GO; GO:0005737; C:cytoplasm; ISS.

DR GO; GO:0005730; C:nucleus; ISS.
 DR GO; GO:0003677; F:DNA binding; ISS.
 DR GO; GO:0006917; P:induction of apoptosis; ISS.
 DR GO; GO:0016481; P:negative regulation of transcription; ISS.
 DR InterPro; IPR011029; DEATH-like.
 DR InterPro; IPR001875; DED.
 DR Pfam; PF01335; DED; 1.
 DR SMART; SM00031; DED; 1.
 DR PROSITE; PSS0168; DED; 1.
 KW Apoptosis; DNA-binding; Nuclear protein; Repressor;
 KW Transcription regulation.

Query Match 4.3%; Score 13; DB 1; Length 318;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 195 TCDIRLRVRAEYC 207
 Db 192 TCDIRLRVRAEYC 204

RESULT 8

ID 06DHN2 PRELIMINARY; PRT; 404 AA.

AC 06DHN2;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Zgc:92202.
 OS Name=zgc:92202;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NC NCBI_TaxId=7955;
 RN [1]
 RP SEQUENCE FROM N.A.

CC TISSUE-whole;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marinova K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stachleiron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
 RA Krzywinski M.I., Skliska U., Smalios D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [12]
 RP SEQUENCE FROM N.A.

RC TISSUE-whole;
 RA Strusberg R.;
 RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC075935; AAH75935.1; -;
 DR GO; GO:0005515; F:protein binding; IEA.
 DR GO; GO:0042981; P:regulation of apoptosis; IEA.
 DR InterPro; IPR011029; DEATH-like.
 DR InterPro; IPR001875; DED.
 DR Pfam; PF01335; DED; 1.
 DR SMART; SM00031; DED; 1.

DR PROSITE; PS50168; DED; 1.
SQ SEQUENCE 404 AA; 44888 MW; 3C949DB3B07B81A CRC64;

Query Match 4.3%; Score 13; DB 2; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCDIRLRVRAEYC 207
Db 267 TCDIRLRVRAEYC 279

RESULT 9
ID Q6GNZ8 PRELIMINARY; PRT; 243 AA.
AC Q6GNZ8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE MGC80767 protein.
GN Name=MGC80767;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=SpLeen;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko I., Matusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stepelman M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein W.J., Ueda T.B., Toshiyuki S., Carinci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gitwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=SpLeen;
RA MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391(2002).
[3]
RN SEQUENCE FROM N.A.
RP TISSUE=SpLeen;
RA Klein S., Gerhard D.S.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073351; AAH73351.1; -;
DR GO; GO:000515; F:protein binding; IEA.
DR GO; GO:0042881; F:regulation of apoptosis; IEA.
DR InterPro; IPR011029; DEATH_Like.
DR InterPro; IPR011875; DEATH_Like.
DR Pfam; PF01335; DED; 1.
DR PROSITE; PS50168; DED; 1.
SQ SEQUENCE 243 AA; 27767 MW; 57A2B89CFBD3DB0BC CRC64;

Query Match 3.6%; Score 11; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 YYGMLSLHRMF 30
Db 21 YYGMLSLHRMF 31

RESULT 10
ID Q91W13 PRELIMINARY; PRT; 218 AA.
AC Q91W13;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Interleukin 18 binding protein.
GN Name=054L;
OS Molluscum contagiosum virus subtype 1 (MCV1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Molluscipoxvirus.
OX NCBI_TaxID=10280;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=20231932; PubMed=10769064;
RA Smith V.P., Bryant N.A., Alcamí A.;
RT "Ectromelia, vaccinia and cowpox viruses encode secreted interleukin
RT 18 binding proteins";
RL J. Gen. Virol. 81:1223-1230(2000).
DR EMBL; AJ271163; CAB89814.1; -;
SQ SEQUENCE 218 AA; 23853 MW; 3FFA9C240DD24E75 CRC64;

Query Match 3.3%; Score 10; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GARRRRRGAP 176
Db 160 GARRRRRGAP 169

RESULT 11
ID Q98222 PRELIMINARY; PRT; 235 AA.
AC Q98222;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE MCO54L.
GN Name=MCO54L;
OS Molluscum contagiosum virus subtype 1 (MCV1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Molluscipoxvirus.
OX NCBI_TaxID=10280;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=96325459; PubMed=8670425;
RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,
RA Moss B.;
RT "Genome sequence of a human tumorigenic poxvirus: prediction of
RT specific host response-evasion genes";
RL Science 273:813-816(1996).
DR EMBL; U60315; AAC55182.1; -;
DR FIR; T30656; T30656.
SQ SEQUENCE 235 AA; 25209 MW; BA47745C68608889 CRC64;

Query Match 3.3%; Score 10; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GARRRRRGAP 176
Db 156 GARRRRRGAP 165

RESULT 12

```

O6DHV2
ID O6DHV2 PRELIMINARY; PRT; 244 AA.
AC O6DHV2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Dedd protein.
GN Name=Dedd;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguellano N.A., Peters G.D., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Strausberg R.;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC075865; AAH75865.1; -.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001875; DED.
DR Pfam; PF01335; DED.1.
DR PROSITE; PS50168; DED.1.
SQ SEQUENCE 244 AA; 28051 MW; 043225AEASD79527 CRC64;

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Query Match 3.3%; Score 10; DB 2; Length 244;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 67 ELLLEERRG 76
 |||||
 Db 113 ELLLEERRG 122

RESULT 13

```

O9Y9Y9
ID O9Y9Y9 PRELIMINARY; PRT; 127 AA.
AC O9Y9Y9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE Hypothetical protein APE2150.
DE OrderedLocustNames=APE2150;
GN Aeropyrum pernix.
OS

```

OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;
 OC Desulfurococcaceae; Aeropyrum.
 OX NCBI_TaxID=56636;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=KL;
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Halkawa Y.,
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Anrui A., Kowugi H.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudo Y.,
 RA Yamazaki J., Kushiida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix KL.1";
 RL DNA Res. 6:83-101(1999).
 DR EMBL; AP000063; BAA81161.1; -.
 DR PIR; A72522; A72522.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 127 AA; 13517 MW; 1C28D0E67B34434C CRC64;

Query Match 3.0%; Score 9; DB 2; Length 127;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 116 SYGTSSSSK 124
 |||||
 Db 95 SYGTSSSSK 103

RESULT 14

```

O67IV3
ID O67IV3 PRELIMINARY; PRT; 222 AA.
AC O67IV3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein OSUNBA0048L03.36.
GN Name=OSUNBA0048L03.36;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  

OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN (1)  

RP SEQUENCE FROM N.A.  

RA Sasaki T., Matsumoto T., Fujisawa M.;  

RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, BAC  

RT clone:OSUNBA0048L03.36";  

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  

DR EMBL; AP007205; BAD38588.1; -.  

KW Hypothetical protein.  

SQ SEQUENCE 222 AA; 24596 MW; 95C5B33F65534936 CRC64;

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Query Match 3.0%; Score 9; DB 2; Length 222;
 Best Local Similarity 100.0%; Pred. No. 9.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 166 GGARRRRRG 174
 |||||
 Db 85 GGARRRRRG 93

RESULT 15

```

O7O6G3
ID O7O6G3 PRELIMINARY; PRT; 227 AA.
AC O7O6G3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AgCP6626 (Fragment).
GN Name=agCG48835; ORFNames=ENSANG00000015017;
OS Anopheles gambiae str. PE8T.

```


OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
 CC -! CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAB01008960; EA11634.1; -
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR InterPro; IPR008958; Transglut_C.
 DR InterPro; IPR008856; TRAP_beta.
 DR Pfam; PF05753; TRAP_beta; 1.
 FT NON_TER 1
 SQ SEQUENCE 227 AA; 24921 MW; 2ADF4D013495ED59 CRC64;
 Query Match 3.0%; Score 9; DB 2; Length 227;
 Best Local Similarity 100.0%; Pred.No. 9.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 FEVVGQOLT 38

DB 109 FEVVGQOLT 117

Search completed: February 12, 2005, 16:39:14
 Job time : 126 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2005, 16:34:11 ; Search time 20 Seconds
(without alignments)
1457.684 Million cell updates/sec

Title: US-10-030-271-2

Perfect score: 303

Sequence: 1 MALSGSTPAPCWEDECLDY.....LREAVGREAVRLVSVDEAD 303

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 1000 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	3.3	235	2 T30656	hypothetical prote
2	9	3.0	127	2 A72522	hypothetical prote
3	8	2.6	75	2 AE2664	ATP synthase C cha
4	8	2.6	75	2 D97446	hypothetical prote
5	8	2.6	170	2 C84492	hypothetical prote
6	8	2.6	197	2 C70601	hypothetical prote
7	8	2.6	224	2 B87197	hypothetical prote
8	8	2.6	224	2 E70790	probable transcrip
9	8	2.6	279	2 B70328	hypothetical prote
10	8	2.6	282	2 S46793	vacuolar protein s
11	8	2.6	339	2 S20880	homeotic protein H
12	8	2.6	342	2 S18649	homeotic protein H
13	8	2.6	363	2 T34931	cell division prote
14	8	2.6	417	2 E86858	66k glycoprotein p
15	8	2.6	475	2 A83340	hypothetical prote
16	8	2.6	528	2 AC3236	pgqr protein - Kle
17	8	2.6	761	2 S20458	oncogene 1 (tre-2
18	8	2.6	786	2 S22155	hypothetical prote
19	8	2.6	828	2 T33481	probable ubiquitin
20	8	2.6	914	2 T00757	hypothetical prote
21	8	2.6	928	2 T04192	hypothetical prote
22	8	2.6	937	2 T04194	hypothetical prote
23	8	2.6	963	2 T09478	ubiquitin thioleat
24	8	2.6	1089	2 S22158	transforming prote
25	8	2.6	1095	2 B83471	probable nuclear a
26	8	2.6	1733	1 B45344	hypothetical prote
27	8	2.6	1958	2 B40505	hypothetical prote
28	7	2.3	47	2 T2970	hypothetical prote
29	7	2.3	66	2 T15539	hypothetical prote

30	7	2.3	92	2 T37077	hypothetical prote
31	7	2.3	115	2 S28937	proctamine 2 precu
32	7	2.3	116	2 AH3150	hypothetical prote
33	7	2.3	118	2 G02438	D-dopachrome tauro
34	7	2.3	118	2 JE0162	dopachrome isomera
35	7	2.3	118	2 T16216	hypothetical prote
36	7	2.3	152	2 A43627	hypothetical 17.1K
37	7	2.3	152	2 AB2011	two-component resp
38	7	2.3	153	2 G72476	hypothetical prote
39	7	2.3	155	2 G72580	hypothetical prote
40	7	2.3	157	2 T27697	VPS29-like phospho
41	7	2.3	184	2 G70321	GTP cyclohydrolyase
42	7	2.3	186	2 T06911	H+-transporting tw
43	7	2.3	187	2 E71464	interferon RNA meth
44	7	2.3	195	1 IYB011	interferon alpha-I
45	7	2.3	195	2 A61403	interferon alpha-I
46	7	2.3	195	2 I47070	interferon omega -
47	7	2.3	195	2 I46397	interferon alpha -
48	7	2.3	195	2 A12678	hypothetical prote
49	7	2.3	197	2 B85923	probable decarboxy
50	7	2.3	197	2 A91078	probable phenylact
51	7	2.3	197	2 T44998	phenylacrylic acid
52	7	2.3	200	2 S23148	hypothetical prote
53	7	2.3	206	2 G75396	hypothetical prote
54	7	2.3	212	2 E69522	hypothetical prote
55	7	2.3	213	2 JC4928	histone H1x - huma
56	7	2.3	215	2 A71541	hypothetical prote
57	7	2.3	225	2 D95183	conserved hypotet
58	7	2.3	225	2 H98050	conserved hypotet
59	7	2.3	242	2 A43904	homeotic protein G
60	7	2.3	246	2 G75570	conserved hypotet
61	7	2.3	255	2 JC7264	CCAAT-enhancer bin
62	7	2.3	256	2 T48787	hypothetical prote
63	7	2.3	259	2 S76585	hypothetical prote
64	7	2.3	267	1 TVHUF5	fibroblast growth
65	7	2.3	273	2 B89884	hypothetical prote
66	7	2.3	277	2 T49543	hypothetical prote
67	7	2.3	278	2 T06026	homeobox protein H
68	7	2.3	279	2 T14848	probable transcrip
69	7	2.3	281	2 AC2789	conserved hypotet
70	7	2.3	281	2 D97568	hypothetical prote
71	7	2.3	291	2 T43139	hypothetical prote
72	7	2.3	296	2 H81726	UDP-N-acetylglucos
73	7	2.3	296	2 AC2698	DNA polymerase IIm
74	7	2.3	297	2 C97480	hypothetical prote
75	7	2.3	297	2 T27525	hypothetical prote
76	7	2.3	299	1 RDSS2R	ribonucleoside-dip
77	7	2.3	314	1 T07898	myrosinase-associat
78	7	2.3	318	1 F70536	3',5'-cyclic-nucle
79	7	2.3	323	2 T51621	myb-like protein (
80	7	2.3	323	2 T51645	myb-related trans
81	7	2.3	326	2 A84277	hypothetical prote
82	7	2.3	329	2 AE2128	transcription regu
83	7	2.3	336	2 T21565	hypothetical prote
84	7	2.3	337	2 E95871	probable oxidoredu
85	7	2.3	346	2 T26097	hypothetical prote
86	7	2.3	346	2 T21552	hypothetical prote
87	7	2.3	347	2 F75319	conserved hypotet
88	7	2.3	366	2 H81010	D-amino acid oxida
89	7	2.3	366	2 F82032	myrosinase-associat
90	7	2.3	371	2 T07896	hypothetical prote
91	7	2.3	375	2 S76663	hypothetical prote
92	7	2.3	382	2 A83171	probable aminotran
93	7	2.3	383	2 S61195	hypothetical prote
94	7	2.3	384	2 S24585	ribonucleoside-dip
95	7	2.3	384	2 S73429	glycerol-3-phosphat
96	7	2.3	396	2 G71044	probable molybdopt
97	7	2.3	401	2 T36882	hypothetical prote
98	7	2.3	402	2 A95924	probable glycosylt
99	7	2.3	412	2 T16480	hypothetical prote
100	7	2.3	414	2 S24154	alanine-glyoxylate
101	7	2.3	414	2 T15086	hypothetical prote
102	7	2.3	416	1 A41267	transcription fact

103	2.3	418	2	A39567	thyroxine-binding
104	2.3	421	2	T35205	citrate synthase-1
105	2.3	A99924	7		Fmb protein limpo
106	2.3	423	2	G83595	noncatalytic dihyd
107	2.3	432	2	T24072	hypothetical prote
108	2.3	432	2	AE2799	HyD family secret
109	2.3	433	2	B82537	probable phosphodi
110	2.3	435	2	T15737	hypothetical prote
111	2.3	437	2	G97578	probable periplasm
112	2.3	438	2	T35789	probable secreted
113	2.3	446	2	T34782	probable signal pe
114	2.3	447	2	T35519	hypothetical prote
115	2.3	449	2	B87639	hypothetical prote
116	2.3	450	2	B71909	hypothetical prote
117	2.3	454	2	T26296	hypothetical prote
118	2.3	458	2	T49480	alpha-2-adrenergic
119	2.3	458	2	A37869	alpha-2B-adrenergic
120	2.3	458	2	A40392	alpha-2-adrenergic
121	2.3	464	2	A56600	intermediate filam
122	2.3	465	2	T40697	probable tata bind
123	2.3	468	2	C82449	conserved hypotet
124	2.3	469	2	D81017	chloride channel p
125	2.3	469	2	I37451	HBF-G2 (HPK-2) pro
126	2.3	474	2	H95322	hypothetical prote
127	2.3	485	2	A40751	finger protein MZF
128	2.3	490	2	B70649	probable regulator
129	2.3	497	2	B82721	ribonuclease G XPI
130	2.3	514	2	T41648	C2 domain family p
131	2.3	517	2	T18636	hypothetical prote
132	2.3	522	2	A82558	glutamine amidotra
133	2.3	527	2	B86432	T518.15 protein -
134	2.3	527	2	T36729	probable serine/th
135	2.3	576	2	H95370	probable transpor
136	2.3	584	2	E75060	hydrogenase-4 comp
137	2.3	603	2	T16655	hypothetical prote
138	2.3	605	2	C96940	sporulation specif
139	2.3	607	2	D64603	hypothetical prote
140	2.3	616	2	C82641	hypothetical prote
141	2.3	637	2	T04552	hypothetical prote
142	2.3	643	2	B69458	adenylyl-sulfate r
143	2.3	648	2	F69848	transcription anti
144	2.3	650	2	T48060	beta-D-glucan exch
145	2.3	659	2	F90531	lipoprotein limpor
146	2.3	671	2	A35912	homeotic protein o
147	2.3	674	2	T48261	hypothetical prote
148	2.3	691	2	B75622	hypothetical prote
149	2.3	694	2	F70868	hypothetical glyci
150	2.3	702	2	F97352	membrane-associate
151	2.3	727	2	AC1814	hypothetical prote
152	2.3	731	2	C70974	hypothetical glyci
153	2.3	750	1	H70628	probable pknC prot
154	2.3	776	2	T51911	related to protein
155	2.3	823	1	A58788	procollagen C-endo
156	2.3	826	2	B81706	conserved hypotet
157	2.3	841	1	I78885	serine/threonine-s
158	2.3	851	2	T00374	hypothetical prote
159	2.3	857	2	T04208	probable anthranil
160	2.3	869	2	AD2418	SM/ SNF family hel
161	2.3	904	2	G64840	protein-histidine
162	2.3	904	2	D90772	sensor protein tor
163	2.3	904	2	H85634	probable DNA damag
164	2.3	935	2	T39389	probable tetrahydr
165	2.3	969	2	T40147	probable RND efflu
166	2.3	1029	2	D83120	probable efflux syst
167	2.3	1054	2	S77008	cation efflux syst
168	2.3	1065	2	T49827	hypothetical prote
169	2.3	1069	2	T43280	nonsense-mediated
170	2.3	1077	2	A44067	serine-rich protei
171	2.3	1083	2	T00790	ubiquitin-specific
172	2.3	1083	2	E70726	probable polyketid
173	2.3	1168	2	T43218	proline dehydrogen
174	2.3	1224	2	T09908	hypothetical prote
175	2.3	1288	2		
176	2.3	1293	2	S42402	xeroderma pigmento
177	2.3	1378	1	T48751	protein-tyrosine k
178	2.3	1400	1	T38185	protein-tyrosine k
179	2.3	1404	1	A48186	protein-tyrosine k
180	2.3	1429	2	T41699	C2-domain family p
181	2.3	2108	2	H70819	probable polyketid
182	2.3	2424	2	T46480	calcium channel Bi
183	2.3	2559	2	T09144	probable guanine n
184	2.3	7576	2	T17428	PF506 polyketide s
185	2.0	11	2	PC2372	58k heat shock pro
186	2.0	20	2	PC4387	GroEL protein homo
187	2.0	21	2	PT0089	4-hydroxybenzoate
188	2.0	27	1	SRAPAS	proteinase A - steel
189	2.0	27	1	SRAPC	proteinase B - Russ
190	2.0	30	1	IRTR78	proteinase CIII, mi
191	2.0	30	1	IRTRC2	proteinase Ia - rai
192	2.0	30	1	IRTRC3	proteinase CIII, ma
193	2.0	31	2	I51349	proteinase - rainbo
194	2.0	31	2	B20883	variant surface gl
195	2.0	32	1	IRTR2	proteinase II - rai
196	2.0	32	1	SIOMN1	proteinase Ai - chu
197	2.0	32	1	VZPK1	proteinase I - nort
198	2.0	32	2	B02669	proteinase (bealme
199	2.0	32	2	F24970	proteinase 3a - rai
200	2.0	32	2	I51089	proteinase - Japane
201	2.0	33	1	IRTR1A	proteinase IA - rai
202	2.0	33	1	IRTR1B	proteinase IB - rai
203	2.0	33	1	IRTR42	proteinase 2c - rai
204	2.0	33	1	IRTR59	proteinase CII - ra
205	2.0	33	1	D21211	proteinase TP17 - r
206	2.0	33	2	S00710	proteinase CII - ch
207	2.0	33	2	A21211	proteinase TP14 - r
208	2.0	33	2	E21211	proteinase TP21 - r
209	2.0	33	2	C21211	proteinase TP16 - r
210	2.0	33	2	T01070	proteinase - rainbo
211	2.0	34	1	TYTUZ2	proteinase Z2 - blu
212	2.0	34	1	TYTUZ2	proteinase Y2 - blu
213	2.0	34	1	TYTUZ1	proteinase Z1 - blu
214	2.0	34	2	JX0204	proteinase Z2 - str
215	2.0	34	2	JX0203	proteinase Z1 - str
216	2.0	34	2	A44806	variant surface gl
217	2.0	37	2	S29829	proteinase Z3 - sma
218	2.0	41	2	A58213	proteinase I - green
219	2.0	41	2	G58208	proteinase I - blac
220	2.0	43	2	D58213	proteinase III - Am
221	2.0	45	2	C58208	proteinase II-2 - p
222	2.0	45	2	D58208	proteinase II-3 - p
223	2.0	45	2	B58208	proteinase II-1 - p
224	2.0	47	2	F58208	proteinase II-5 - p
225	2.0	48	2	E58208	proteinase II-4 - p
226	2.0	48	2	C60505	hemoglobin A1-3 be
227	2.0	53	2	H84319	hypothetical prote
228	2.0	55	1	VRBO	vasoactive intesti
229	2.0	55	1	VRBR	vasoactive intesti
230	2.0	55	1	VRGP	vasoactive intesti
231	2.0	55	1	VRSH	vasoactive intesti
232	2.0	56	2	C58213	proteinase II - Ame
233	2.0	57	2	H95296	hypothetical prote
234	2.0	58	1	VRPG	vasoactive intesti
235	2.0	58	2	S34045	proteinase I - North
236	2.0	58	2	A58208	proteinase I-1 - pa
237	2.0	60	2	D82277	hypothetical prote
238	2.0	60	2	B37290	homeotic protein G
239	2.0	61	1	DNVPRF	DNA-binding protei
240	2.0	61	2	H82779	hypothetical prote
241	2.0	65	2	AE2370	hypothetical prote
242	2.0	66	2	DNVBP	DNA-binding protei
243	2.0	66	2	I37232	calcitonin gene-re
244	2.0	72	2	B89853	hypothetical prote
245	2.0	72	2	AC9722	hypothetical prote
246	2.0	74	1	DNVPR	DNA-binding protei
247	2.0	75	2	AC3445	H+-transporting tw
248	2.0	77	2	C82988	hypothetical prote

249	6	2.0	78	2	T29828	hypotheical prote	322	6	2.0	129	2	S37670	trab protein - Bsc
250	6	2.0	80	2	AH1057	Relb protein (impo	323	6	2.0	130	2	T47751	ribosomal protein
251	6	2.0	81	2	B91000	hypotheical prote	324	6	2.0	130	2	C70971	hypotheical prote
252	6	2.0	83	2	E71267	hypotheical prote	325	6	2.0	130	2	S34493	cellulase (Ec 3.2.
253	6	2.0	85	2	I39718	hypotheical prote	326	6	2.0	130	2	T29498	hypotheical prote
254	6	2.0	85	2	H87164	hypotheical prote	327	6	2.0	131	2	D72855	AcOlf-44 protein -
255	6	2.0	85	2	G84527	hypotheical prote	328	6	2.0	131	2	T41790	AcMPV orf44 - Bom
256	6	2.0	86	2	F86294	hypotheical prote	329	6	2.0	132	2	H83048	hypotheical transcrip
257	6	2.0	87	2	AD3436	hypotheical prote	330	6	2.0	132	2	B69889	hypotheical prote
258	6	2.0	88	2	T36458	hypotheical prote	331	6	2.0	132	2	S10305	protamine - boll w
259	6	2.0	91	2	A59493	protamine p2 - Sty	332	6	2.0	132	2	I39004	cyclin-dependent k
260	6	2.0	92	2	S13132	protamine 2 precu	333	6	2.0	133	2	E72603	trans-regulatory s
261	6	2.0	94	2	E84502	probable MYB fami1	334	6	2.0	133	1	VKLJCE	hypotheical prote
262	6	2.0	95	2	AH0905	probable sigma(54)	335	6	2.0	133	2	T26755	hypotheical prote
263	6	2.0	95	2	B85984	probable sigma-54	336	6	2.0	133	2	D87593	hypotheical prote
264	6	2.0	95	2	B91139	probable sigma-54	337	6	2.0	133	2	D86697	hypotheical prote
265	6	2.0	95	2	I76719	hypotheical prote	338	6	2.0	134	1	WMVA16	B2IR 16K protein -
266	6	2.0	95	2	B41026	hypotheical prote	339	6	2.0	134	1	B64664	hypotheical prote
267	6	2.0	96	2	T26651	phosphoglyceromuta	340	6	2.0	135	2	F71852	hypotheical prote
268	6	2.0	97	2	AC2927	hypotheical prote	341	6	2.0	135	2	F87264	MABPG family prote
269	6	2.0	97	2	D98355	hypotheical prote	342	6	2.0	136	2	D75009	hypotheical prote
270	6	2.0	97	2	C70828	hypotheical prote	343	6	2.0	136	2	B90440	hypotheical prote
271	6	2.0	99	2	T30451	probable DNA-bind1	344	6	2.0	136	2	C95291	hypotheical prote
272	6	2.0	99	2	B83335	hypotheical prote	345	6	2.0	137	2	AF2435	ATP synthase eps11
273	6	2.0	101	2	F71059	hypotheical prote	346	6	2.0	137	2	G69461	small multidrug ex
274	6	2.0	101	2	F90470	hypotheical prote	347	6	2.0	138	2	AG2914	hypotheical prote
275	6	2.0	102	2	S33336	protamine p2 - rbe	348	6	2.0	138	2	B97689	hypotheical prote
276	6	2.0	103	2	S33337	protamine p2 - pig	349	6	2.0	138	2	TI0309	hypotheical prote
277	6	2.0	103	2	T28354	hypotheical prote	350	6	2.0	138	2	S30092	hypotheical prote
278	6	2.0	104	2	S53118	hypotheical prote	351	6	2.0	138	2	A84482	hypotheical prote
279	6	2.0	104	2	S57666	protamine 2 - com	352	6	2.0	139	2	B85845	unknown prote1n en
280	6	2.0	104	2	AG0706	probable membrane	353	6	2.0	140	2	D72680	hypotheical prote
281	6	2.0	105	2	E87149	conserved hypotcet	354	6	2.0	141	2	AE1255	transcription regu
282	6	2.0	106	1	L4HUKN	Ig lambda chain V-	355	6	2.0	141	2	T46654	transcription regu
283	6	2.0	106	1	G1BEP	tegment protein -	356	6	2.0	141	2	AB1618	transcription regu
284	6	2.0	107	2	A29995	protamine p2 precu	357	6	2.0	141	2	H85217	hypotheical prote
285	6	2.0	107	2	B72716	hypotheical prote	358	6	2.0	141	2	AE4725	hypotheical prote
286	6	2.0	108	2	A85844	unknown prote1n en	359	6	2.0	141	2	B84522	hypotheical prote
287	6	2.0	108	2	H90875	hypotheical prote	360	6	2.0	141	2	C83768	hypotheical prote
288	6	2.0	108	2	F85691	unknown prote1n en	361	6	2.0	142	2	D90269	conserved hypotcet
289	6	2.0	108	2	A99822	hypotheical prote	362	6	2.0	142	2	S34257	hypotheical prote
290	6	2.0	108	2	G90909	hypotheical prote	363	6	2.0	143	2	D75617	response regulator
291	6	2.0	108	2	G85629	hypotheical prote	364	6	2.0	143	2	E72504	hypotheical prote
292	6	2.0	108	2	D90853	hypotheical prote	365	6	2.0	143	2	B86857	conserved hypotcet
293	6	2.0	108	2	C83528	hypotheical prote	366	6	2.0	143	2	AC1730	hypotheical prote
294	6	2.0	108	2	F72653	hypotheical prote	367	6	2.0	144	2	G83342	hypotheical prote
295	6	2.0	109	2	D81996	hypotheical prote	368	6	2.0	145	2	S60456	cysteine proteins
296	6	2.0	110	2	D84378	hypotheical prote	369	6	2.0	146	2	D82315	probable ribonucle
297	6	2.0	112	2	JQ1063	glycine-rich prote	370	6	2.0	146	2	T14667	hypotheical prote
298	6	2.0	113	2	A99915	hypotheical prote	371	6	2.0	146	2	T49867	hemoglobin beta ch
299	6	2.0	113	2	F85763	hypotheical prote	372	6	2.0	147	1	H8CY	hemoglobin beta ch
300	6	2.0	113	2	G75581	hypotheical prote	373	6	2.0	147	1	H8TR4	hemoglobin IV beta
301	6	2.0	113	2	B71088	hypotheical prote	374	6	2.0	147	2	S03400	hemoglobin beta ch
302	6	2.0	113	4	A31199	beta-galactosidase	375	6	2.0	148	2	A70077	conserved hypotcet
303	6	2.0	114	2	AB3583	hislone H2A relate	376	6	2.0	148	2	JC7261	receptor activity-
304	6	2.0	115	2	I37901	hypotheical prote	377	6	2.0	148	2	JC7235	hemoglobin beta ch
305	6	2.0	115	2	B90742	hypotheical prote	378	6	2.0	148	2	S41625	hemoglobin beta ch
306	6	2.0	115	2	B85592	hypotheical prote	379	6	2.0	149	1	G70400	phosphohistidine p
307	6	2.0	118	2	A75108	hypotheical prote	380	6	2.0	149	2	C75598	response regulator
308	6	2.0	118	2	B71026	hypotheical prote	381	6	2.0	149	2	S02164	regulatory protein
309	6	2.0	119	2	G69106	transcription regu	382	6	2.0	149	2	F75327	hypotheical prote
310	6	2.0	121	2	A71344	conserved hypotcet	383	6	2.0	150	2	B70519	probable furu prot
311	6	2.0	121	2	S42590	hypotheical 14.1K	384	6	2.0	150	2	S09872	hypotheical prote
312	6	2.0	123	2	A71312	probable anti-sigm	385	6	2.0	151	2	T14948	hypotheical prote
313	6	2.0	123	2	E72680	hypotheical prote	386	6	2.0	152	2	D75367	hypotheical prote
314	6	2.0	125	2	S76216	hypotheical prote	387	6	2.0	152	2	S46272	hypotheical prote
315	6	2.0	125	2	AH4235	hypotheical prote	388	6	2.0	152	2	F72667	hypotheical prote
316	6	2.0	126	2	AD3508	transcription regu	389	6	2.0	153	2	AC2653	hypotheical prote
317	6	2.0	127	2	A86155	hypotheical prote	390	6	2.0	153	2	A70855	hypotheical prote
318	6	2.0	127	2	F95976	hypotheical expor	391	6	2.0	153	2	AC1710	hypotheical prote
319	6	2.0	127	2	AH2680	conserved hypotcet	392	6	2.0	153	2	F97462	hypotheical prote
320	6	2.0	128	2	C84515	hypotheical prote	393	6	2.0	154	2	AE0445	biotin carboxyl ca
321	6	2.0	129	2	T08527	trab protein - Ent	394	6	2.0	154	2	B75358	hypotheical prote

395	6	2.0	155	1	IGRO2	insulin-like growt
396	6	2.0	155	2	T28945	hypothetical prote
397	6	2.0	155	2	C95002	hypothetical prote
398	6	2.0	155	2	P97874	conserved hypotet
399	6	2.0	155	2	P90740	probable toxin [im
400	6	2.0	155	2	P87696	hypothetical prote
401	6	2.0	155	2	A85591	probable toxin Z10
402	6	2.0	155	2	A64819	hypothetical prote
403	6	2.0	156	2	H82496	ribose ABC transpo
404	6	2.0	157	2	G64459	hypothetical prote
405	6	2.0	157	2	G82214	hypothetical prote
406	6	2.0	157	2	A10601	transcription regu
407	6	2.0	157	2	E75530	hypothetical prote
408	6	2.0	158	2	G83847	hypothetical prote
409	6	2.0	159	2	F86541	Ct102 hypothetical
410	6	2.0	159	2	G72082	conserved hypotet
411	6	2.0	160	2	E72631	hypothetical prote
412	6	2.0	161	2	JC4275	pleiotrophic facto
413	6	2.0	161	2	J00141	hypothetical 17.6K
414	6	2.0	162	2	T10928	3C3.19c protein -
415	6	2.0	162	2	A84217	hypothetical prote
416	6	2.0	162	2	E87685	hypothetical prote
417	6	2.0	163	1	MMW8M	18k protein - Aba1
418	6	2.0	163	2	B39662	18k protein - mous
419	6	2.0	163	2	D87293	Fur family protein
420	6	2.0	164	2	S31480	hypothetical prote
421	6	2.0	165	2	S43302	single-stranded DN
422	6	2.0	165	2	B83417	hypothetical prote
423	6	2.0	165	2	A59492	proctamine P1 - Sty
424	6	2.0	166	1	S35973	regulatory protein
425	6	2.0	166	2	T08208	nonstructural prot
426	6	2.0	166	2	C72641	hypothetical prote
427	6	2.0	168	1	P68P6	Pe protein - phase
428	6	2.0	168	2	B72635	hypothetical prote
429	6	2.0	168	2	T35737	probable integral
430	6	2.0	169	2	C95394	protein [imported
431	6	2.0	170	2	B69587	adenine phosphorib
432	6	2.0	170	2	A83135	4-hydroxyphenylac
433	6	2.0	170	2	S74997	hypothetical prote
434	6	2.0	171	2	D75174	hypothetical prote
435	6	2.0	171	2	B38162	hypothetical prote
436	6	2.0	172	2	H83634	conserved hypotet
437	6	2.0	173	2	H75553	hypothetical prote
438	6	2.0	173	2	G96549	hypothetical prote
439	6	2.0	174	2	F87632	conserved hypotet
440	6	2.0	175	1	Q14D22	early R1B 21k prot
441	6	2.0	176	2	T45308	hypothetical prote
442	6	2.0	177	2	D69062	imidazoleglycerol-
443	6	2.0	177	2	T12717	hypothetical prote
444	6	2.0	177	2	T49802	hypothetical prote
445	6	2.0	177	2	B83271	hypothetical prote
446	6	2.0	179	2	S04858	insulin-like growt
447	6	2.0	179	2	C86853	hypothetical prote
448	6	2.0	180	2	E84260	hypothetical prote
449	6	2.0	180	2	A75579	ankyrin-related pr
450	6	2.0	180	2	AD3499	ribosomal-protein-
451	6	2.0	181	2	AF2468	50S ribosomal prot
452	6	2.0	181	2	AT1222	Salmonella enteric
453	6	2.0	181	2	AD1576	Salmonella enteric
454	6	2.0	182	2	AG0040	single-strand bind
455	6	2.0	183	2	B75152	adenyllyl cyclase r
456	6	2.0	183	2	B81089	hypothetical prote
457	6	2.0	183	2	H81853	hypothetical prote
458	6	2.0	183	2	B86374	protein T23E23.20
459	6	2.0	183	2	AB3181	hypothetical prote
460	6	2.0	184	2	C71193	hypothetical prote
461	6	2.0	184	2	JC2429	activin-A protein
462	6	2.0	184	2	AG0115	probable membrane
463	6	2.0	184	2	S63441	hypothetical prote
464	6	2.0	184	2	T29373	hypothetical prote
465	6	2.0	185	2	F91020	acid phosphatase r
466	6	2.0	185	2	C75169	molYdennum cofacto
467	6	2.0	186	2	F87250	
468	6	2.0	186	2	G82110	Tip repressor-bind
469	6	2.0	187	2	A82746	conserved hypotet
470	6	2.0	187	2	S09806	hypothetical prote
471	6	2.0	188	2	AB2761	thymidilate kinase
472	6	2.0	188	2	DB1149	deoxycytidine triph
473	6	2.0	190	2	G82624	glutathione peroxi
474	6	2.0	191	2	G82765	deoxycytidine triph
475	6	2.0	191	2	S57642	interferon precurs
476	6	2.0	191	2	S75503	hypothetical prote
477	6	2.0	192	1	G64746	phosphopheptose 180
478	6	2.0	192	2	AD0542	phosphopheptose 180
479	6	2.0	192	2	A90660	phosphopheptose 180
480	6	2.0	192	2	G85510	phosphopheptose 180
481	6	2.0	192	2	S56309	probable membrane
482	6	2.0	192	2	AH3220	transcription regu
483	6	2.0	195	2	D96817	hypothetical prote
484	6	2.0	196	1	BYRCAL	transcription regu
485	6	2.0	196	2	AH0963	Two-component sys
486	6	2.0	196	2	H86050	hypothetical prote
487	6	2.0	196	2	T06261	transcription regu
488	6	2.0	196	2	F91204	hexose phosphate t
489	6	2.0	196	2	A41853	conserved hypotet
490	6	2.0	196	2	F83625	probable decarboxy
491	6	2.0	197	2	AD0855	probable imidazole
492	6	2.0	198	2	T06261	acp-22 protein - y
493	6	2.0	199	2	S16063	acp-22 protein - y
494	6	2.0	199	2	S32224	transcription regu
495	6	2.0	200	2	E72303	hypothetical prote
496	6	2.0	200	2	AD3633	hypothetical prote
497	6	2.0	200	2	S61025	amylin-like prote
498	6	2.0	201	1	VCVQGB	coat protein - bee
499	6	2.0	201	2	DB3288	acyl-CoA thioester
500	6	2.0	201	2	P95270	hypothetical prote
501	6	2.0	201	2	AD1191	conserved hypotet
502	6	2.0	202	1	VCVQFL	coat protein - bee
503	6	2.0	202	2	B81371	hypothetical prote
504	6	2.0	203	2	T39877	spindle assembly c
505	6	2.0	204	2	B83279	hypothetical prote
506	6	2.0	205	2	AH3407	hypothetical cytos
507	6	2.0	205	2	F87660	hydrolyase, haloaci
508	6	2.0	205	2	T35707	hypothetical prote
509	6	2.0	206	2	B71821	hypothetical prote
510	6	2.0	207	2	AC3381	hypothetical prote
511	6	2.0	207	1	VCVQL2	coat protein - pot
512	6	2.0	208	1	S24593	coat protein - pot
513	6	2.0	208	2	S24593	coat protein - pot
514	6	2.0	208	2	S41878	coat protein - pot
515	6	2.0	208	2	S41874	hypothetical prote
516	6	2.0	208	2	AE2378	hypothetical prote
517	6	2.0	208	2	D71313	response regulator
518	6	2.0	209	2	T28656	response regulator
519	6	2.0	209	2	T30899	ribosomal protein
520	6	2.0	210	2	S34135	hypothetical phage
521	6	2.0	210	2	AC0259	collagen - nematod
522	6	2.0	210	2	B44984	hypothetical prote
523	6	2.0	210	2	T41982	amidoxanferase I
524	6	2.0	211	2	AB1977	fixd protein - Azo
525	6	2.0	211	2	S15167	hypothetical prote
526	6	2.0	211	2	AO5123	hypothetical prote
527	6	2.0	211	2	T08764	thymidylate kinase
528	6	2.0	212	2	S66058	thymidylate kinase
529	6	2.0	212	2	AH0195	dTMP kinase (EC 2.
530	6	2.0	212	2	F82581	ribonuclease III X
531	6	2.0	212	2	T10883	probable response
532	6	2.0	212	2	A84359	hypothetical prote
533	6	2.0	213	2	T36076	tmsr-like protein
534	6	2.0	213	2	C83243	acyl carrier prote
535	6	2.0	213	2	C49918	hypothetical prote
536	6	2.0	213	2	F70080	hypothetical prote
537	6	2.0	214	2	F75521	DNA-binding respon
538	6	2.0	214	2	E75613	hypothetical prote
539	6	2.0	214	2	A70846	hypothetical prote
540	6	2.0	215	1	WMBE21	UL14 protein - hum

541	6	2.0	215	2	A41681	S-crystallin 1 - g	614	6	2.0	235	2	F86598	pseudouridine synt
542	6	2.0	215	2	JC5114	glutathione transf	615	6	2.0	235	2	G81515	ribosomal large ch
543	6	2.0	215	2	E72736	probable DNA polym	616	6	2.0	235	2	G64915	detribiotin synth
544	6	2.0	215	2	H87602	flagellin modifica	617	6	2.0	235	2	H85764	detribiotin synth
545	6	2.0	216	2	C83879	transcription regu	618	6	2.0	235	2	C90916	detribiotin synth
546	6	2.0	216	2	AF2905	esterase [imported	619	6	2.0	235	2	A75413	hypothetical prote
547	6	2.0	216	2	T46688	hypothetical prote	620	6	2.0	236	2	T07260	sulfate transport
548	6	2.0	217	2	T47175	hypothetical prote	621	6	2.0	236	2	A84319	DNA repair protei
549	6	2.0	218	2	E85021	hypothetical prote	622	6	2.0	236	2	D97128	probable pseudouri
550	6	2.0	218	2	B72116	hypothetical prote	623	6	2.0	236	2	S51332	ubiquitin thiole
551	6	2.0	218	2	H82758	hypothetical prote	624	6	2.0	236	2	AG0589	probable polyacch
552	6	2.0	219	2	S62804	cytoskeletal prote	625	6	2.0	237	2	AG4153	dtmp kinase (BC 2.
553	6	2.0	219	2	I52911	ABC-type transport	626	6	2.0	237	2	C64637	amino acid ABC tra
554	6	2.0	219	2	C84280	multidrug efflux p	627	6	2.0	237	2	D71877	probable amino aci
555	6	2.0	220	2	A97953	hypothetical prote	628	6	2.0	237	2	A88640	protein C3H4.4 [l
556	6	2.0	220	2	AC1109	conserved hypotet	629	6	2.0	237	2	A64352	hypothetical prote
557	6	2.0	221	2	G83604	hypothetical prote	630	6	2.0	237	2	T13649	hypothetical prote
558	6	2.0	221	2	E71477	hypothetical prote	631	6	2.0	237	2	JC7217	paternally imprint
559	6	2.0	221	2	F84148	hypothetical prote	632	6	2.0	238	1	S72623	ribulose-5-phospha
560	6	2.0	222	2	AE0276	detribiotin synth	633	6	2.0	238	1	WZBR2	gene 2 protein - h
561	6	2.0	222	2	S07280	para protein - Agr	634	6	2.0	238	2	T05962	1,3-beta-glucanase
562	6	2.0	222	2	B49599	polymerase-associa	635	6	2.0	238	2	T05959	1,3-beta-glucanase
563	6	2.0	222	2	F86758	DNA replication pr	636	6	2.0	238	2	T05957	probable membrane
564	6	2.0	222	2	A36730	hutc protein - Kle	637	6	2.0	238	2	T35088	hypothetical prote
565	6	2.0	222	2	S19931	glycine-rich prote	638	6	2.0	238	2	H72646	conserved hypotet
566	6	2.0	223	2	E87654	hypothetical prote	639	6	2.0	239	2	AB3143	gntr family regula
567	6	2.0	223	2	T08672	hypothetical prote	640	6	2.0	239	2	AC0987	conserved hypotet
568	6	2.0	224	2	H97541	thymidylate kinase	641	6	2.0	239	2	AB3193	coat protein - nar
569	6	2.0	224	2	T43331	clathrin light cha	642	6	2.0	240	1	VCWGN4	hypothetical prote
570	6	2.0	224	2	G97680	arylesterase VCA07	643	6	2.0	240	2	A95219	hypothetical prote
571	6	2.0	224	2	S61386	lcmy protein - Leg	644	6	2.0	240	2	G98082	ribosomal large ch
572	6	2.0	224	2	D95335	hypothetical prote	645	6	2.0	241	2	E81741	probable pseudouri
573	6	2.0	225	2	G83244	probable two-compo	646	6	2.0	241	2	F71478	croptomycin - hydr
574	6	2.0	225	2	G84310	cobalamin adenosyl	647	6	2.0	242	2	S35060	uridylylate kinases
575	6	2.0	225	2	T08780	hypothetical prote	648	6	2.0	242	2	A11238	uridylylate kinases
576	6	2.0	226	2	G83336	probable two-compo	649	6	2.0	242	2	AB1601	ABC transporter, A
577	6	2.0	226	2	F83406	hypothetical prote	650	6	2.0	242	2	F95256	hypothetical prote
578	6	2.0	226	2	G95247	hypothetical prote	651	6	2.0	242	2	G98121	probable sodium-tr
579	6	2.0	226	2	PC6047	probable ABC-type	652	6	2.0	244	2	B81690	hypothetical prote
580	6	2.0	227	2	D75522	oxidoreductase, sh	653	6	2.0	244	2	H75107	hypothetical prote
581	6	2.0	227	2	A35514	[D-Ala(2)] deltorp	654	6	2.0	244	2	E70905	hypothetical prote
582	6	2.0	227	2	G83110	hypothetical prote	655	6	2.0	244	2	T02511	DREB-like AP2 doma
583	6	2.0	227	2	T37134	hypothetical prote	656	6	2.0	245	2	C95314	TRM33b IS ATP-bind
584	6	2.0	228	2	S46965	microfilariar shea	657	6	2.0	245	2	D95334	conserved hypotet
585	6	2.0	228	2	S19132	rab25 protein - ri	658	6	2.0	245	2	F81223	hypothetical prote
586	6	2.0	228	2	C70884	probable transcrip	659	6	2.0	245	2	E84169	hypothetical prote
587	6	2.0	228	2	T49891	glycine-rich prote	660	6	2.0	245	2	E32057	hypothetical prote
588	6	2.0	229	2	S66342	ribonuclease II (E	661	6	2.0	246	1	S71283	myb-related protei
589	6	2.0	229	2	T40789	clathrin light cha	662	6	2.0	246	2	C81679	dihydrodipicolinat
590	6	2.0	229	2	D82426	conserved hypotet	663	6	2.0	246	2	A33692	cytotoxic T-lympho
591	6	2.0	229	2	H83980	ABC transporter (A	664	6	2.0	246	2	D86197	hypothetical prote
592	6	2.0	230	2	AC2281	cob(I)alamin adeno	665	6	2.0	246	2	B48350	infected-cell prote
593	6	2.0	231	2	B81215	thiol-disulfide in	666	6	2.0	246	2	E95085	transcription regu
594	6	2.0	231	2	AG0681	detribiotin synth	667	6	2.0	246	2	F72766	hypothetical prote
595	6	2.0	231	2	C97552	hypothetical prote	668	6	2.0	246	2	D83476	probable sigma-70
596	6	2.0	231	2	AD2772	hypothetical prote	669	6	2.0	246	2	S74408	lipopeptide antibi
597	6	2.0	231	2	F83032	hypothetical prote	670	6	2.0	246	2	D98112	hypothetical prote
598	6	2.0	231	2	AH2872	hypothetical prote	671	6	2.0	246	2	AH3072	transcription regu
599	6	2.0	231	2	B97649	probable ATP-bindi	672	6	2.0	246	2	AD2084	transcription regu
600	6	2.0	232	2	G69080	conserved hypotet	673	6	2.0	247	2	S06035	type II site-speci
601	6	2.0	232	2	T04354	hypothetical prote	674	6	2.0	247	2	A55717	myelin/oligodendro
602	6	2.0	232	2	H75422	probable polyacch	675	6	2.0	248	2	T35870	hypothetical prote
603	6	2.0	232	2	B46665	phocovsystem 1-like	676	6	2.0	248	2	G98224	serine dehydrogena
604	6	2.0	233	2	T33946	hexon-associated p	677	6	2.0	249	2	AH3061	conserved hypotet
605	6	2.0	233	2	T35594	hypothetical prote	678	6	2.0	249	2	B70427	hypothetical prote
606	6	2.0	233	2	C64412	hypothetical prote	679	6	2.0	249	2	B64404	hypothetical prote
607	6	2.0	233	2	A83862	initiation of chro	680	6	2.0	249	2	E72646	probable molybdopt
608	6	2.0	233	2	G70776	hypothetical prote	681	6	2.0	249	2	JC7857	NADP+-dependent se
609	6	2.0	234	2	T26560	hypothetical prote	682	6	2.0	250	2	D69470	conserved hypotet
610	6	2.0	234	2	A87337	conserved hypotet	683	6	2.0	251	2	D96010	hypothetical expor
611	6	2.0	235	2	T42096	ATP-dependent Clp	684	6	2.0	251	2	G95361	probable ABC trans
612	6	2.0	235	2	H75539	branched-chain ami	685	6	2.0	252	2	H82956	probable short-cha
613	6	2.0	235	2	H72025	probable pseudouri	686	6	2.0	252	2	AB1030	probable membrane

687	6	2.0	252	2	B83570	hypotheical prote	760	6	2.0	268	2	A49303	homeotic protein C
688	6	2.0	253	2	T04642	hypotheical prote	761	6	2.0	269	2	H82616	hypotheical prote
689	6	2.0	253	2	D11975	hypotheical prote	762	6	2.0	269	2	G98144	hypotheical prote
690	6	2.0	253	2	B64532	hypotheical prote	763	6	2.0	269	2	AH0838	probable exported
691	6	2.0	253	2	T31021	hypotheical prote	764	6	2.0	269	2	T16910	hypotheical prote
692	6	2.0	254	2	A82625	endoonlease V (de	765	6	2.0	270	2	G75412	spermdine/putresc
693	6	2.0	254	2	T26793	hypotheical prote	766	6	2.0	270	2	T11759	LeF-1 orl14 - Bomb
694	6	2.0	254	2	T35366	probable membrane	767	6	2.0	270	2	T35721	hypotheical prote
695	6	2.0	255	2	C75594	phosphoadenosine p	768	6	2.0	271	2	F81381	2-dehydro-3-deoxy-
696	6	2.0	255	2	A27122	cachepin G (EC 3.	769	6	2.0	272	2	T48567	ABA-responsive pro
697	6	2.0	255	2	B95931	probable amino aci	770	6	2.0	272	2	A11098	PuRr, transcriptio
698	6	2.0	255	2	T35217	hypotheical prote	771	6	2.0	272	2	AH1461	PuRr, transcriptio
699	6	2.0	255	2	A39195	DAL82 protein - ye	772	6	2.0	272	2	H83269	hypotheical prote
700	6	2.0	255	2	B84179	hypotheical prote	773	6	2.0	272	2	H83004	hypotheical prote
701	6	2.0	255	2	T46350	hypotheical prote	774	6	2.0	272	2	S52977	hypotheical prote
702	6	2.0	256	2	A11119	transcription regu	775	6	2.0	272	2	C75548	hypotheical prote
703	6	2.0	256	2	AD1480	transcription regu	776	6	2.0	272	2	AC0140	probable membrane
704	6	2.0	256	2	T47020	hypotheical prote	777	6	2.0	273	1	X1ECRO	rRNA (adenine-N6,N
705	6	2.0	256	2	AEO236	probable deor-fam1	778	6	2.0	273	2	C75562	probable shikimate
706	6	2.0	256	2	H72078	probable sodium-tr	779	6	2.0	273	2	AF0513	dimethyladenosine
707	6	2.0	256	2	D66544	NADH (ubiquinone)	780	6	2.0	273	2	H06635	dimethyladenosine
708	6	2.0	256	2	A96027	probable ABC trans	781	6	2.0	273	2	H06635	chlorophyll a/b-pi
709	6	2.0	257	2	AF0396	probable amino aci	782	6	2.0	273	2	J50172	transposase - Esch
710	6	2.0	257	2	C86784	pseudouridine synt	783	6	2.0	273	2	S12637	hypotheical prote
711	6	2.0	257	2	G72648	hypotheical prote	784	6	2.0	273	2	B83318	hypotheical prote
712	6	2.0	257	2	A81412	SMF family protein	785	6	2.0	273	2	T33619	probable formate d
713	6	2.0	257	2	B97726	hypotheical prote	786	6	2.0	274	2	AF0493	probable oxidoredu
714	6	2.0	258	2	T32939	hypotheical prote	787	6	2.0	274	2	T36680	myelin regulatory
715	6	2.0	259	2	A83294	probable permease	788	6	2.0	274	2	A55335	conserved hypotnet
716	6	2.0	259	2	T34536	hypotheical prote	789	6	2.0	274	2	H83525	hypotheical prote
717	6	2.0	259	2	T29459	hypotheical prote	790	6	2.0	274	2	F83601	homeotic protein H
718	6	2.0	259	2	S32898	hypotheical prote	791	6	2.0	275	1	WJ2FX2	hypotheical prote
719	6	2.0	259	2	A86409	hypotheical prote	792	6	2.0	275	2	H83325	probable partition
720	6	2.0	259	2	G81714	ABC transporter, A	793	6	2.0	275	2	T36573	hypotheical prote
721	6	2.0	259	2	F71561	probable RNA meth	794	6	2.0	275	2	T16312	hypotheical prote
722	6	2.0	260	2	G75169	abc transporter AT	795	6	2.0	275	2	B55224	ABC transporter, p
723	6	2.0	260	2	E71045	probable ABC trans	796	6	2.0	276	2	DV5302	probable ABC trans
724	6	2.0	261	2	A95930	probable enoyl-CoA	797	6	2.0	276	2	H86922	hypotheical prote
725	6	2.0	261	2	JC4110	triacylglycerol 1i	798	6	2.0	276	2	G75358	endopeptidase Clp
726	6	2.0	261	2	A99965	flagellar biosynth	799	6	2.0	277	1	S68421	short chain alcoh
727	6	2.0	261	2	A85813	flagellar biosynth	800	6	2.0	277	2	G84473	probable short-cha
728	6	2.0	261	2	C64959	probable export pr	801	6	2.0	277	2	T51975	proteasome endopep
729	6	2.0	261	2	E72735	hypotheical prote	802	6	2.0	277	2	AB3185	conserved hypotnet
730	6	2.0	261	2	AC0332	probable Ompa fam1	803	6	2.0	278	2	A81185	alpha-tocopherol t
731	6	2.0	261	2	G72470	probable ABC trans	804	6	2.0	278	1	A47404	probable short-cha
732	6	2.0	261	2	S63604	homeobox protein G	805	6	2.0	278	2	B83152	epoxide hydrolase-
733	6	2.0	263	2	D90231	conserved hypotet	806	6	2.0	278	2	H75259	alpha-tocopherol t
734	6	2.0	264	2	B95231	pyruvate formate-I	807	6	2.0	278	2	S54352	integral membrane
735	6	2.0	264	2	E98095	formate acetyltran	808	6	2.0	278	2	C43670	probable ATP-bind
736	6	2.0	264	2	T09449	allergen V - velve	809	6	2.0	278	2	S44796	quonolinate phosph
737	6	2.0	264	2	AF0753	flagellar biosynth	810	6	2.0	278	2	B83354	thioesterase - Str
738	6	2.0	264	2	B86432	protein T518.12 1i	811	6	2.0	279	2	A69112	probable pseudour
739	6	2.0	265	2	T36396	probable short cha	812	6	2.0	280	2	T34920	allergen Phl p Vp
740	6	2.0	265	2	AH0775	hydroxyethylthiaz	813	6	2.0	280	2	H71276	probable pseudour
741	6	2.0	265	2	B98322	phosphomethylpyrim	814	6	2.0	280	2	S36584	allergen Phl p Vp
742	6	2.0	265	2	AD2961	phosphomethylpyrim	815	6	2.0	280	2	F81827	Tomb protein NMA19
743	6	2.0	265	2	A33513	hypotheical prote	816	6	2.0	280	2	A81049	granzyme B (EC 3.4
744	6	2.0	265	2	T17386	vr1g protein - Dic	817	6	2.0	281	1	A61021	aldo/keto reductas
745	6	2.0	265	2	T48410	hypotheical prote	818	6	2.0	281	2	A97604	probable oxidoredu
746	6	2.0	265	2	B61188	SCI protein - mous	819	6	2.0	281	2	AB2826	probable imidazole
747	6	2.0	265	2	H72574	hypotheical prote	820	6	2.0	281	2	T06530	hypotheical prote
748	6	2.0	266	2	F70595	hypotheical prote	821	6	2.0	281	2	T34282	hypotheical prote
749	6	2.0	266	2	F72851	late expression fa	822	6	2.0	281	2	T26795	T16B15.10 protein
750	6	2.0	266	2	T20142	hypotheical prote	823	6	2.0	281	2	F86355	probable RNA meth
751	6	2.0	266	2	T02807	arsenate reductase	824	6	2.0	282	2	T36832	hypotheical prote
752	6	2.0	266	2	S54440	hemim-specific ATP	825	6	2.0	282	2	A12081	phosphoprotein pho
753	6	2.0	267	2	T08283	hypotheical prote	826	6	2.0	282	2	H75537	hypotheical prote
754	6	2.0	267	2	E83232	probable ATP-bind	827	6	2.0	283	2	H95194	hypotheical prote
755	6	2.0	267	2	AB2933	hypotheical prote	828	6	2.0	283	2	E82979	conserved hypotet
756	6	2.0	267	2	E98349	hypotheical prote	829	6	2.0	283	2	E98061	transcription regu
757	6	2.0	268	2	E75607	2-oxo-hepta-3-ene-	830	6	2.0	283	2	A13027	lyser-type tranact
758	6	2.0	268	2	T51066	hypotheical prote	831	6	2.0	284	2	B98257	deoxyribonuclease
759	6	2.0	268	2	B30819	interferon-regulat	832	6	2.0	284	1	S13676	

833	6	2.0	284	2	T28018	hypothetical prote
834	6	2.0	284	2	T13621	hypothetical prote
835	6	2.0	284	2	E69113	hypothetical prote
836	6	2.0	284	2	S18957	fix3-5 protein -
837	6	2.0	284	2	S04278	hypoxanthine phosph
838	6	2.0	284	2	B41224	homeotic protein p
839	6	2.0	285	1	NDBCA	deoxyribonuclease
840	6	2.0	285	1	E85854	endonuclease IV (l
841	6	2.0	285	2	AC0783	endonuclease IV (l
842	6	2.0	285	2	C91010	endonuclease IV (l
843	6	2.0	285	2	S66076	transcription repr
844	6	2.0	285	2	A82609	hypothetical prote
845	6	2.0	285	2	C84170	ribosomal protein
846	6	2.0	285	2	A40657	hypoxanthine phosph
847	6	2.0	285	2	S09614	hypoxanthine phosph
848	6	2.0	286	2	B70833	carbon-monoxide de
849	6	2.0	286	2	B64536	hypothetical prote
850	6	2.0	286	2	B84537	hypothetical prote
851	6	2.0	288	2	S62175	transport vesicle
852	6	2.0	288	2	D82781	conserved hypotet
853	6	2.0	289	2	H95929	probable hydroxyme
854	6	2.0	289	2	G95963	probable transcrip
855	6	2.0	289	2	H85434	hypothetical prote
856	6	2.0	289	2	F87110	probable signal pep
857	6	2.0	289	2	C69349	conserved hypotet
858	6	2.0	290	2	I39522	3-dehydroquinase d
859	6	2.0	290	2	T03552	malose transport
860	6	2.0	290	2	H98336	malose transport
861	6	2.0	290	2	A82946	hypothetical prote
862	6	2.0	290	2	A11014	4-hydroxybenzoate
863	6	2.0	291	2	S64825	hypothetical prote
864	6	2.0	291	2	AC3299	glutamate-cRNA lig
865	6	2.0	292	2	H82113	dihydrodipicolinat
866	6	2.0	292	2	G75288	hypothetical prote
867	6	2.0	292	2	C95147	11c protein (limp
868	6	2.0	293	2	D90978	hypothetical prote
869	6	2.0	293	2	D95381	probable LysR-fam
870	6	2.0	294	2	H84023	phosphate ABC tran
871	6	2.0	295	2	AE0993	glycerol-3-phospha
872	6	2.0	295	2	H98222	hypothetical prote
873	6	2.0	295	2	AH3063	hypothetical prote
874	6	2.0	295	2	AD3552	high-affinity bran
875	6	2.0	295	2	B83433	translocator prote
876	6	2.0	295	2	E82659	peptidyl-prolyl ci
877	6	2.0	295	2	T22833	hypothetical prote
878	6	2.0	296	2	F87411	hypothetical prote
879	6	2.0	296	2	A98015	hypothetical prote
880	6	2.0	297	2	A83049	hypothetical prote
881	6	2.0	297	2	B89473	hypothetical prote
882	6	2.0	297	2	T13317	protein F52D2.3 (l
883	6	2.0	297	2	H95323	hypothetical prote
884	6	2.0	298	2	AG3165	hypothetical prote
885	6	2.0	298	2	H82953	conserved hypotet
886	6	2.0	299	2	A95878	hypothetical prote
887	6	2.0	299	2	S12874	probable N-acetyl
888	6	2.0	299	2	T35765	hyb protein - Rhl
889	6	2.0	299	2	S55472	hypothetical prote
890	6	2.0	300	2	T06569	pectin lyase (EC 4
891	6	2.0	300	2	F63793	farneesyltransfera
892	6	2.0	300	2	H86358	site-specific reco
893	6	2.0	300	2	G82975	zinc finger protei
894	6	2.0	301	1	RCEGCT	probable two-compo
895	6	2.0	301	2	E85902	GTP-binding protei
896	6	2.0	301	2	A80829	GTP-binding protei
897	6	2.0	301	2	H91057	GTP-binding protei
898	6	2.0	301	2	E97972	conserved hypotet
899	6	2.0	301	2	T36520	hypothetical prote
900	6	2.0	301	2	B84533	hypothetical prote
901	6	2.0	301	2	A98214	hypothetical prote
902	6	2.0	303	2	T36826	probable 3-hydroxy
903	6	2.0	303	2	S73051	triopinssterase hom
904	6	2.0	303	2	F83791	hydroxymethylgluta
905	6	2.0	303	2	S23440	hypothetical prote
906	6	2.0	303	2	A43708	gamma-interferon-1
907	6	2.0	303	2	H83108	hypothetical prote
908	6	2.0	303	2	T02588	hypothetical prote
909	6	2.0	304	2	T22602	hypothetical prote
910	6	2.0	305	2	F83548	GTP-binding protei
911	6	2.0	305	2	UN0647	hydrogenase expres
912	6	2.0	305	2	T20470	hypothetical prote
913	6	2.0	305	2	T36261	hypothetical prote
914	6	2.0	305	2	I57039	genomic screen hom
915	6	2.0	306	2	F98183	malose transport
916	6	2.0	306	2	A90966	probable transmem
917	6	2.0	306	2	US0266	membrane protein y
918	6	2.0	306	2	G70481	thiamin monophosph
919	6	2.0	306	2	T21220	hypothetical prote
920	6	2.0	306	2	A85814	probable transmem
921	6	2.0	306	2	E72598	probable ABC-trans
922	6	2.0	307	2	D86194	hypothetical prote
923	6	2.0	307	2	T27609	hypothetical prote
924	6	2.0	307	2	G69505	hypothetical prote
925	6	2.0	307	2	B96745	unknown protein T9
926	6	2.0	307	2	A45581	Distal-less homeob
927	6	2.0	308	2	S77938	E8NA-LP protein -
928	6	2.0	308	2	F72704	probable iron (III
929	6	2.0	308	2	A70761	hypothetical prote
930	6	2.0	308	2	H87095	conserved hypotet
931	6	2.0	308	2	A12993	hypothetical prote
932	6	2.0	309	2	F70394	3-coxacyl-lacyl-ca
933	6	2.0	309	2	A24849	ADP-ATP carrier pr
934	6	2.0	309	2	AE1904	hypothetical prote
935	6	2.0	309	2	B96032	probable two-compo
936	6	2.0	310	2	A83353	probable binding-P
937	6	2.0	310	2	G95395	probable LysR-fam
938	6	2.0	310	2	G87624	integral membrane
939	6	2.0	310	2	AC2035	phytoene synthase
940	6	2.0	310	2	D70745	hypothetical prote
941	6	2.0	310	2	A70620	probable PB protei
942	6	2.0	311	2	F75366	hypothetical prote
943	6	2.0	311	2	T23438	hypothetical prote
944	6	2.0	311	2	A24400	nodulation protein
945	6	2.0	312	2	E63045	8-oxoguanine DNA g
946	6	2.0	312	2	D95891	probable glycine-b
947	6	2.0	312	2	AP2772	lipid A biosynthes
948	6	2.0	312	2	D97552	lipid A biosynthes
949	6	2.0	313	1	XYNHCL	site-specific DNA-
950	6	2.0	313	2	AC0603	asparaginase (EC 3
951	6	2.0	313	2	F72575	hypothetical prote
952	6	2.0	313	2	AH0966	conserved hypotet
953	6	2.0	313	2	C75288	conserved hypotet
954	6	2.0	313	2	G71550	probable phospholi
955	6	2.0	313	2	AB0596	formimidoylglutama
956	6	2.0	313	2	F64069	survival protein 8
957	6	2.0	314	2	F96574	hypothetical prote
958	6	2.0	314	2	B83559	probable peptidyl-
959	6	2.0	314	2	S70101	hypothetical prote
960	6	2.0	314	2	JC5273	paired type homeob
961	6	2.0	314	2	T03775	DNA-binding homeob
962	6	2.0	315	2	B84403	dipeptide ABC tran
963	6	2.0	316	2	G64762	acetaldehyde dehyd
964	6	2.0	316	2	B85530	acetaldehyde dehyd
965	6	2.0	316	2	F90679	acetaldehyde dehyd
966	6	2.0	316	2	T44749	hypothetical prote
967	6	2.0	316	2	G81045	pllin gene inverti
968	6	2.0	316	2	B70571	hypothetical prote
969	6	2.0	316	2	T10436	probable transposa
970	6	2.0	317	1	E87185	3',5'-cyclic-nucle
971	6	2.0	317	2	T35981	retinol dehydrogen
972	6	2.0	317	2	A55884	probable peptide t
973	6	2.0	317	2	I55462	hypothetical prote
974	6	2.0	317	2	F66901	hypothetical prote
975	6	2.0	318	2	A82319	hypothetical prote
976	6	2.0	318	2	AG0829	glutathione synth
977	6	2.0	318	2	I83298	sigma-B factor reg
978	6	2.0	318	2	C85903	sigma-B factor reg
						regulates activity


```

979 6 2.0 318 2 B91058 sigma-E factor reg
980 6 2.0 318 2 T02998 sigma-E factor reg
981 6 2.0 318 2 C83209 probable oxidoredu
982 6 2.0 319 2 T35538 cytochrome-c oxida
983 6 2.0 319 2 G83888 transmembrane lip
984 6 2.0 319 2 G82694 ABC transporter su
985 6 2.0 319 2 P75420 hypothetical prote
986 6 2.0 320 2 E88176 hypothetical prote
987 6 2.0 320 2 AG3110 dehydrogenase Atu4
988 6 2.0 320 2 AD0563 ferrochelatase (im
989 6 2.0 320 2 A12305 hypothetical prote
990 6 2.0 321 2 D64820 probable asparagin
991 6 2.0 322 2 T27308 hypothetical prote
992 6 2.0 322 2 T04595 hypothetical prote
993 6 2.0 322 2 E70306 conserved hypotnet
994 6 2.0 322 2 C86165 P15K9.4 protein -
995 6 2.0 323 2 D90413 chlorodioxin reduct
996 6 2.0 323 2 H70765 hypothetical prote
997 6 2.0 324 1 C42728 porphobilinogen sy
998 6 2.0 324 2 E75522 probable class II
999 6 2.0 324 2 AB1269 delta-aminolevulin
1000 6 2.0 324 2 AD1631 delta-aminolevulin

```

ALIGNMENTS

```

RESULT 1
T30656
hypothetical protein 54L - Moluscum contagiosum virus 1
N:Alternate names: MC054L
C:Species: Moluscum contagiosum virus 1
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T30656
R:Senkevich, T.G.; Buger, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Mose, B.
Science 273, 813-816, 1996
A:Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re
A:Reference number: Z20876; MUID:9625459; PMID:8670425
A:Accession: T30656
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-235 <SEN>
A:Cross-references: UNIPROT:Q98222; EMBL:U60315; PIDN:AAC55182.1
C:Genetics:
A:Note: MC054L

Query Match 3.3%; Score 10; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GARRRRGAP 176
DB 156 GARRRRGAP 165

RESULT 2
A72522
hypothetical protein APE2150 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: A72522
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
dna Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: A72522
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-127 <KAW>
A:Cross-references: UNIPROT:Q9Y9Y9; DDBJ:AP000063; NID:G5105654; PIDN:BAAB1161.1; PID:dl
A:Experimental source: strain K1
C:Genetics:

```

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A:Gene: APE2150
C:Superfamily: Aeropyrum pernix hypothetical protein APE2150

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Query Match 3.0%; Score 9; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 116 SYGRSSSSK 124
DB 95 SYGRSSSSK 103

```

```

RESULT 3
AE2664
ATP synthase C chain atpC [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AE2664
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutlyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AE2664
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-75 <KUR>
A:Cross-references: UNIPROT:Q8UH67; GB:AE008688; PIDN:AAL41731.1; PID:gl7739081; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: atpC
A:Map position: circular chromosome
C:Superfamily: H+-transporting ATP synthase lipid-binding protein

```

```

Query Match 2.6%; Score 8; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 264 GDYLSGAL 271
DB 30 GDYLSGAL 37

```

```

RESULT 4
D97446
ATP synthase chain C (AF054609) [imported] - Agrobacterium tumefaciens (strain C58, Cere
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: D97446
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Gurollo, B.; Goldman,
A.; Liu, F.; Woliam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.,
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: D97446
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-75 <KUR>
A:Cross-references: UNIPROT:Q8UH67; GB:AE007869; PIDN:AAK86525.1; PID:g15155683; GSPDB:G
C:Genetics:
A:Gene: AGR_C 1297
A:Map position: circular chromosome
C:Superfamily: H+-transporting ATP synthase lipid-binding protein

```

```

Query Match 2.6%; Score 8; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 264 GDYLSGAL 271

```


Db 30 GDYLSGAL 37

RESULT 5

C84492 hypothetical protein At2g10550 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: C84492

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Motilal, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L.

eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:1061197

A:Accession: C84492

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-170 <STO>

A:Cross-references: UNIPROT:Q9S187; GB:AE002093; NID:g4733994; PIDN:AAD28673.1; GSPDB:GN

C:Genetics:

A:Gene: At2g10550

A:Map position: 2

Query Match 2.6%; Score 8; DB 2; Length 170;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 240 RSRDLGVS 247

Db 37 RSRDLGVS 44

RESULT 6

C70601 hypothetical protein RV0992c - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C:Accession: C70601

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Feldwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: C70601

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-197 <COL>

A:Cross-references: UNIPROT:O05575; GB:Z94752; GB:AL123456; NID:g3261731; PIDN:CAB08152.

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: RV0992c

C:Superfamily: human 5-formyltetrahydrofolate cyclo-ligase

Query Match 2.6%; Score 8; DB 2; Length 197;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 56 AGGLARAR 63

Db 95 AGGLARAR 102

RESULT 7

B87197 hypothetical protein ML2302 [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C:Accession: B87197

R:Coile, S.T.; Eigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho

R.; Davies, R.M.; Devlin, K.; Dutchoy, S.; Feldwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sc

A:Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: B87197

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-224 <STO>

A:Cross-references: UNIPROT:Q9CB91; GB:AL450380; NID:g13093927; PIDN:CAC31818.1; GSPDB:C

C:Genetics:

A:Gene: ML2302

C:Superfamily: regulatory protein fnr; cAMP receptor protein cyclic nucleotide-binding c

Query Match 2.6%; Score 8; DB 2; Length 224;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 88 QLLRVTLAR 95

Db 122 QLLRVTLAR 129

RESULT 8

E70790 probable transcription regulator RV3676 - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C:Accession: E70790

R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Feldwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: E70790

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-224 <COL>

A:Cross-references: UNIPROT:O69644; GB:AL022121; GB:AL123456; NID:g3261559; PIDN:CAA1799

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: RV3676

C:Superfamily: regulatory protein fnr; cAMP receptor protein cyclic nucleotide-binding d

Query Match 2.6%; Score 8; DB 2; Length 224;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 88 QLLRVTLAR 95

Db 122 QLLRVTLAR 129

RESULT 9

B70328 hypothetical protein ag_313 - Aquifex aeolicus

C:Species: Aquifex aeolicus

C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C:Accession: B70328

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-279 <AGP>

A:Cross-references: UNIPROT:O66554; GB:AE000683; NID:g2982996; PIDN:AAC06617.1; PID:g298

A:Experimental source: strain VPS

C:Genetics:

A:Gene: ag_313


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A:Gene: eq_313
C:Superfamily: hypothetical protein HP0152

Query Match          2.6%; Score 8; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      289 GREAVRL 236
      |||||
DB      248 GREAVRL 255

RESULT 10
S46793
N:Alternate names: protein PEP1; protein VPS29; protein YHR012w
C:Species: Saccharomyces cerevisiae
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C:Accession: S46793
R:Du. 2.
Submitted to the EMBL Data Library, June 1994
A:Description: The sequence of S. cerevisiae cosmid L2825.
A:Reference number: S46774
A:Accession: S46793
A:Molecule type: DNA
A:Residues: 1-282 <DUB>
A:Cross-references: UNIPROT:P38759; EMBL:U10400; NID:G500701; PID:G500712; GSPDB:GN00008
C:Genetics:
A:Gene: VPS29; MIPS:YHR012w
A:Cross-references: MIPS:YHR012w; SGD:S0001054
A:Map position: 8R
A:Introns: 16/3
C:Superfamily: VPS29-like phosphoesterase-related protein

Query Match          2.6%; Score 8; DB 2; Length 282;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      224 ALAROLDV 231
      |||||
DB      120 ALAROLDV 127

RESULT 11
S20880
N:Alternate names: Mus musculus (house mouse)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-2004
C:Accession: S20880; S09569; S09398
R:Renucci, A.; Zappavigna, V.; Zakany, J.; Izpisua-Belmonte, J.C.; Buerki, K.; Duboule,
EMBO J. 11, 1459-1468, 1992
A:Title: Comparison of mouse and human HOX-4 complexes defines conserved sequences invol
A:Reference number: S20879; MUID:92224884; PMID:1348690
A:Accession: S20880
A:Molecule type: DNA
A:Residues: 1-339 <RNA>
A:Cross-references: UNIPROT:P28357; EMBL:X62669; NID:G51414; PIDN:CAA44542.1; PID:G51416
R:Duboule, D.; Dolle, P.
EMBO J. 8, 1497-1505, 1989
A:Title: The structural and functional organization of the murine HOX gene family resemb
A:Reference number: S09569; MUID:89356621; PMID:2569969
A:Accession: S09569
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 272-331 <DUB>
A:Cross-references: EMBL:X14714; NID:G51427; PIDN:CAB57813.1; PID:G6015583
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1989
R:Dolle, P.; Duboule, D.
EMBO J. 8, 1507-1515, 1989
A:Title: Two gene members of the murine HOX-5 complex show regional and cell-type specific
A:Reference number: S09398; MUID:89356622; PMID:2569970
A:Accession: S09398
A:Molecule type: DNA

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A:Residues: 272-331 <DOL>
A:Cross-references: GB:X14714; GB:W21040; NID:G51427; PIDN:CAB57813.1; PID:G6015583
C:Genetics:
A:Gene: Hox-4.5
A:Introns: 260/1
C:Superfamily: homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:273-329/Domain: homeobox homology <HOX>

Query Match          2.6%; Score 8; DB 2; Length 339;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      120 SSSSKRTE 127
      |||||
DB      173 SSSSKRTE 180

RESULT 12
S18649
N:Alternate names: homeotic protein Hox D9 - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Aug-2004
C:Accession: S18649; S05958; S14935; A32830
R:Zappavigna, V.; Renucci, A.; Izpisua-Belmonte, J.C.; Uribe, G.; Peschle, C.; Duboule,
EMBO J. 10, 4177-4187, 1991
A:Title: HOX4 gene encodes transcription factors with potential auto- and cross-regulatory
A:Reference number: S18649; MUID:92097538; PMID:1756725
A:Accession: S18649
A:Molecule type: mRNA
A:Residues: 1-342 <ZAP>
A:Cross-references: UNIPROT:P28356; EMBL:X59372; NID:G32390; PIDN:CAA42016.1; PID:G32391
A>Note: intron position was determined by sequencing of genomic DNA
R:Oliver, G.; Sidel, N.; Fliske, W.; Heinemann, C.; Mohandes, T.; Sparkes, R.S.; De Robe
Genes Dev. 3, 641-650, 1989
A:Title: Complementary homeo protein gradients in developing limb buds.
A:Reference number: A32830; MUID:89306602; PMID:2568311
A:Accession: S05958
A:Molecule type: DNA
A:Residues: 264-265, 'A', 267-342 <OLI>
A:Cross-references: EMBL:X15506; NID:G32397; PIDN:CAA33528.1; PID:G32398
R:Acampora, D.; d'Esposito, M.; Falletta, A.; Pannese, W.; Migliaccio, E.; Morelli, F.; S
Nucleic Acids Res. 17, 10385-10402, 1989
A:Title: The human HOX gene family.
A:Reference number: S07541; MUID:90098876; PMID:2574852
A:Accession: S14935
A:Molecule type: DNA
A:Residues: 275-340 <ACA>
C:Genetics:
A:Gene: GDB:HOXD9
A:Cross-references: GDB:120678; OMIM:142982
A:Map position: 2q31-2q31
A:Introns: 263/1
C:Superfamily: homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:276-332/Domain: homeobox homology <HOX>

Query Match          2.6%; Score 8; DB 2; Length 342;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      120 SSSSKRTE 127
      |||||
DB      175 SSSSKRTE 182

RESULT 13
T34931
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C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T34931

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R:Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1998
A:Reference number: Z21562
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A>Status: preliminary; translated from GB/EMBL/DBJ
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A:Experimental source: strain A312
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RESULT 14
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C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #ext_change 09-Jul-2004
C:Accession: E86858
R:Boletín, A.; Wincker, P.; Manger, S.; Jallón, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A>Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; WUID:21235186; PMID:11337471
A:Accession: E86858
A>Status: preliminary
A:Molecule type: DNA
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C:Genetics:
A:Gene: ftsZ
C:Superfamily: cell division protein ftsZ

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Db 180 LREALREA 187

RESULT 15
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C:Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #ext_change 09-Jul-2004
C:Accession: A38340
R:Sato, R.; Komine, Y.; Imanaka, T.; Takano, T.
J. Biol. Chem. 265, 21232-21236, 1990
A>Title: Monoclonal antibody EMRIA/212D recognizing site of deposition of extracellular
A:Reference number: A38340; WUID:91065939; PMID:1701177
A:Accession: A38340
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C:Keywords: glycoprotein
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626	7	2.3	323	15	US-10-374-780A-2048	Sequence 2048, App
627	7	2.3	323	15	US-10-412-609B-1802	Sequence 1802, App
628	7	2.3	325	9	US-09-738-626-5740	Sequence 5740, App
629	7	2.3	325	16	US-10-408-765A-5559	Sequence 5559, App
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643	7	2.3	332	16	US-10-437-963-184955	Sequence 184955, A
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649	7	2.3	340	13	US-10-021-111-4	Sequence 4, App1
650	7	2.3	340	13	US-10-138-787-3	Sequence 3, App1
651	7	2.3	340	15	US-10-417-924A-5750	Sequence 2, App1
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663	7	2.3	344	15	US-10-425-114-60418	Sequence 60418, A
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672	7	2.3	350	15	US-10-425-114-6358	Sequence 46358, A	745	7	2.3	379	16	US-10-741-204-50	Sequence 50, App1
673	7	2.3	350	15	US-10-425-114-62053	Sequence 62053, A	746	7	2.3	379	16	US-10-741-204-51	Sequence 51, App1
674	7	2.3	351	15	US-10-425-114-59492	Sequence 59492, A	747	7	2.3	379	16	US-10-741-204-52	Sequence 52, App1
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690	7	2.3	359	15	US-10-413-6998-924	Sequence 924, App	763	7	2.3	384	16	US-10-437-963-158069	Sequence 158069, A
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699	7	2.3	365	15	US-10-243-552-443	Sequence 443, App	772	7	2.3	396	15	US-10-374-780A-1781	Sequence 1781, App
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710	7	2.3	372	15	US-10-412-699B-1257	Sequence 1257, App	783	7	2.3	413	14	US-10-237-551-196	Sequence 196, App
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725	7	2.3	376	15	US-10-671-134-107	Sequence 107, App	798	7	2.3	422	16	US-10-437-963-112684	Sequence 112684, A
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733	7	2.3	376	15	US-10-670-817-107	Sequence 107, App	806	7	2.3	432	15	US-10-425-114-65445	Sequence 65445, A
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735	7	2.3	376	16	US-10-673-119-107	Sequence 107, App	808	7	2.3	434	15	US-10-437-963-125350	Sequence 125350, A
736	7	2.3	376	16	US-10-673-119-107	Sequence 107, App	809	7	2.3	434	15	US-10-369-493-14100	Sequence 14100, A
737	7	2.3	376	16	US-10-671-207-107	Sequence 108, App	810	7	2.3	437	10	US-08-374-064A-66	Sequence 66, App1
738	7	2.3	377	16	US-10-671-207-108	Sequence 107, App	811	7	2.3	437	15	US-10-616-263-66	Sequence 66, App1
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818	7	2.3	454	15	US-10-671-403-5	Sequence 5, Appli	891	7	2.3	529	16	US-10-671-207-2	Sequence 2, Appli
819	7	2.3	454	15	US-10-671-419-5	Sequence 5, Appli	892	7	2.3	533	15	US-10-230-818-13	Sequence 13, Appli
820	7	2.3	454	15	US-10-670-844-5	Sequence 5, Appli	893	7	2.3	542	16	US-10-437-963-192411	Sequence 192411, Appli
821	7	2.3	454	15	US-10-671-134-5	Sequence 5, Appli	894	7	2.3	550	10	US-09-882-227-62	Sequence 62, Appli
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823	7	2.3	454	15	US-10-672-638-5	Sequence 5, Appli	896	7	2.3	552	15	US-10-072-012-439	Sequence 439, App
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825	7	2.3	454	16	US-10-670-817-5	Sequence 5, Appli	898	7	2.3	554	15	US-10-425-114-47532	Sequence 47532, A
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831	7	2.3	460	9	US-09-925-297-584	Sequence 584, App	904	7	2.3	561	14	US-10-115-415-1	Sequence 1, Appli
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836	7	2.3	464	15	US-10-670-844-4	Sequence 4, Appli	909	7	2.3	568	15	US-10-287-122A-71031	Sequence 71031, A
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843	7	2.3	464	16	US-10-671-119-4	Sequence 4, Appli	916	7	2.3	582	15	US-10-295-027-853	Sequence 853, App
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855	7	2.3	485	14	US-10-029-386-33023	Sequence 33023, A	928	7	2.3	596	15	US-10-332-447-16	Sequence 16, App
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882	7	2.3	529	15	US-10-671-403-2	Sequence 2, Appli	955	7	2.3	674	15	US-10-451-822-1	Sequence 1, Appli
883	7	2.3	529	15	US-10-671-419-2	Sequence 2, Appli	956	7	2.3	674	15	US-10-451-822-11	Sequence 41, Appli
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885	7	2.3	529	15	US-10-671-134-2	Sequence 2, Appli	958	7	2.3	678	15	US-10-072-012-438	Sequence 438, App
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663 7 2.3 681 15 US-10-451-822-26 Sequence 26, Appl
664 7 2.3 684 15 US-10-425-114-56849 Sequence 56849, A
965 7 2.3 687 15 US-10-144-194A-101 Sequence 101, App
966 7 2.3 688 15 US-10-282-122A-49414 Sequence 49414, A
967 7 2.3 690 14 US-10-262-083-2 Sequence 2, Appl1
968 7 2.3 690 14 US-10-262-083-18 Sequence 18, Appl1
969 7 2.3 690 15 US-10-424-599-283913 Sequence 283913, A
970 7 2.3 691 15 US-10-369-493-23473 Sequence 64726, A
971 7 2.3 694 15 US-10-282-122A-64726 Sequence 26877, A
972 7 2.3 696 15 US-10-094-749-2687 Sequence 96, Appl
973 7 2.3 700 16 US-10-772-656-96 Sequence 125013,
974 7 2.3 710 16 US-10-437-963-125013 Sequence 8477, Ap
975 7 2.3 721 14 US-10-138-714-8477 Sequence 187018,
976 7 2.3 724 16 US-10-437-963-187018 Sequence 94, Appl
977 7 2.3 726 16 US-10-772-656-94 Sequence 63691, A
978 7 2.3 728 15 US-10-425-114-63691 Sequence 7056, Ap
979 7 2.3 731 17 US-10-741-849-7056 Sequence 13, Appl
980 7 2.3 738 14 US-10-173-123-13 Sequence 19, Appl
981 7 2.3 741 15 US-10-181-108-19 Sequence 11, Appl
982 7 2.3 745 14 US-10-173-123-11 Sequence 3664, Ap
983 7 2.3 746 15 US-10-369-493-3664 Sequence 4, Appl1
984 7 2.3 746 15 US-10-670-184-4 Sequence 20, Appl1
985 7 2.3 752 15 US-10-297-022-20 Sequence 134895,
986 7 2.3 754 16 US-10-437-963-134895 Sequence 130, App
987 7 2.3 760 10 US-09-948-783-130 Sequence 19, Appl
988 7 2.3 760 14 US-10-288-252-19 Sequence 2269, Ap
989 7 2.3 760 16 US-10-398-038-19 Sequence 169426,
990 7 2.3 768 15 US-10-264-049-2269 Sequence 1603, A
991 7 2.3 777 16 US-10-437-963-189426 Sequence 16, Appl
992 7 2.3 784 14 US-10-156-761-11603 Sequence 5, Appl
993 7 2.3 787 15 US-10-363-937-16 Sequence 16, Appl
994 7 2.3 787 15 US-10-670-184-5 Sequence 169427,
995 7 2.3 797 16 US-10-437-963-189427 Sequence 2, Appl1
996 7 2.3 802 14 US-10-177-308-2 Sequence 81, Appl
997 7 2.3 802 15 US-10-028-248A-81 Sequence 81, Appl
998 7 2.3 802 15 US-10-107-782-81 Sequence 154500,
999 7 2.3 806 16 US-10-437-963-154500 Sequence 10081, A
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ALIGNMENTS

RESULT 1

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US-10-013-477-11
; Sequence 11, Application US/10013477
; Publication No. US20030049732A1
; GENERAL INFORMATION:
; APPLICANT: N1 et al.
; TITLE OF INVENTION: Apoptosis Related Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PTO002P1
; CURRENT APPLICATION NUMBER: US/10/013,477
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: 09/669,445
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: PCT/US00/06642
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/126,018
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/139,638
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/149,449
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-013-477-11
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| 140 ANSQOGWETGSPPTKQRGRSGRPSGGARRRRGAPAPQOSEPARPSSEGVTCDIR 199
| 118 ANSQOGWETGSPPTKQRGRSGRPSGGARRRRGAPAPQOSEPARPSSEGVTCDIR 177
| 200 LRVRAEYCEHGPALIEQVASRRPQALARQDLVFGQATVLRSLDGSVVCIDIKFSELSTL 259
| 178 LRVRAEYCEHGPALIEQVASRRPQALARQDLVFGQATVLRSLDGSVVCIDIKFSELSTL 237
| 260 DAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 303
| 238 DAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 281
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RESULT 2

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US-10-001-254-18
; Sequence 18, Application US/10001254
; Publication No. US20030049702A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Pawlowski, Krzysztof
; APPLICANT: Fiorentino, Loredana
; APPLICANT: Lee, Sung Hyung
; APPLICANT: Roth, Wilfred
; APPLICANT: Stenmer-Liwen, Frank
; TITLE OF INVENTION: No. US20030049702A1e1 Death Domain Proteins
; FILE REFERENCE: P-LJ 5037
; CURRENT APPLICATION NUMBER: US/10/001,254
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/301,889
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/715,893
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-254-18
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| 200 LRVRAEYCEHGPALIEQVASRRPQALARQDLVFGQATVLRSLDGSVVCIDIKFSELSTL 259
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RESULT 3

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US-10-296-539-1
; Sequence 1, Application US/10296539
; Publication No. US20030165933A1
; GENERAL INFORMATION:
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/ APPLICANT: INCYTE GENOMICS, INC.
/ APPLICANT: TANG, Y. Tom
/ APPLICANT: AZIMZAI, Yalda
/ APPLICANT: YUE, Henry
/ APPLICANT: BURFORD, Neil
/ APPLICANT: DING, Li
/ APPLICANT: ELIOTT, Vicki S.
/ APPLICANT: PATTERSON, Chandra
/ APPLICANT: BAUGHN, Mariah R.
/ TITLE OF INVENTION: REGULATORS OF APOPTOSIS
/ FILE REFERENCE: PI-0307 PCT
/ CURRENT APPLICATION NUMBER: US/10/296,539
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: 60/209,407; 60/250,326
/ PRIOR FILING DATE: 2000-06-01; 2000-11-30
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PERL Program
/ SEQ ID NO 1
/ LENGTH: 326
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ NAME/KEY: misc_feature
/ OTHER INFORMATION: incyte ID No. US20030165933A1 3102521CD1
US-10-296-539-1
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DB      140 ANSOGQWETGSPPTKRQRRSRGRPSGARRRRRGAAPAPQOQSEPARSSSEKVTCDIR 199
QY      200 LRVRAEYCEHGPALBEGVARRRPOALARDVFGATAVLRSDIGSVVCDIKFSELSTYL 259
DB      200 LRVRAEYCEHGPALBEGVARRRPOALARDVFGATAVLRSDIGSVVCDIKFSELSTYL 259
QY      260 DAFWGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVDEAD 303
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US-10-106-698-4626
/ Sequence 4626, Application US/10106698
/ Publication No. US20030109690A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruden et al.
/ TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
/ FILE REFERENCE: PA005P1
/ CURRENT APPLICATION NUMBER: US/10/106,698
/ CURRENT FILING DATE: 2002-03-27
/ PRIOR APPLICATION NUMBER: PCT/US00/26524
/ PRIOR FILING DATE: 2000-09-28
/ PRIOR APPLICATION NUMBER: US 60/157,137
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: US 60/163,280
/ PRIOR FILING DATE: 1999-11-03
/ NUMBER OF SEQ ID NOS: 8564
/ SOFTWARE: PatentIn Ver. 3.0
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/ LENGTH: 366
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-106-698-4626
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Best Local Similarity 100.0%; Pred. No. 6.3e-189;
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DB      180 ANSOGQWETGSPPTKRQRRSRGRPSGARRRRRGAAPAPQOQSEPARSSSEKVTCDIR 239
QY      200 LRVRAEYCEHGPALBEGVARRRPOALARDVFGATAVLRSDIGSVVCDIKFSELSTYL 259
DB      240 LRVRAEYCEHGPALBEGVARRRPOALARDVFGATAVLRSDIGSVVCDIKFSELSTYL 299
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RESULT 5
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/ Sequence 758, Application US/09925302
/ Patent No. US20020044941A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
/ FILE REFERENCE: PA104
/ CURRENT APPLICATION NUMBER: US/09/925,302
/ PRIOR FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: PCT/US00/05918
/ PRIOR FILING DATE: 2000-03-08
/ PRIOR APPLICATION NUMBER: 60/124,270
/ PRIOR FILING DATE: 1998-03-12
/ NUMBER OF SEQ ID NOS: 896
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 758
/ LENGTH: 319
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-925-302-758
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DB      180 ANSOGQWETGSPPTKRQRRSRGRPSGARRRRRGAAPAPQOQSEPARSSSEKVTCDIR 239
QY      200 LRVRAEYCEHGPALBEGVARRRPOALARDVFGATAVLRSDIGSVVCDIKFSELSTYL 259
DB      240 LRVRAEYCEHGPALBEGVARRRPOALARDVFGATAVLRSDIGSVVCDIKFSELSTYL 299
QY      260 DAFWGDYLSGALLQ 273
DB      300 DAFWGDYLSGALLQ 313
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RESULT 6
US-09-925-302-758
/ Sequence 758, Application US/09925302
/ Publication No. US20030064072A9
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
/ FILE REFERENCE: PA104
/ CURRENT APPLICATION NUMBER: US/09/925,302
/ PRIOR FILING DATE: 2001-08-10
/ PRIOR APPLICATION NUMBER: PCT/US00/05918
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;; PRIOR FILING DATE: 2000-03-08
;; PRIOR APPLICATION NUMBER: 60/124,270
;; PRIOR FILING DATE: 1999-03-12
;; NUMBER OF SEQ ID NOS: 896
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 758
;; LENGTH: 319
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-925-302-758

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DB 180 ANSOGQWETSSPTKRRRRSGRRSGARRRRRGAPAPQOQSEPARPSRGKTCIDR 239
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DB 240 LRVRAEYCEHGPALGQVARRRRPOLARQDVFGQATVLRSRDLGSVVCIDIKFSELSTL 299
QY 260 DAFMGDYLSGALLQ 273
DB 300 DAFMGDYLSGALLQ 313

RESULT 7
US-10-296-115-1220
;; Sequence 1220; Application US/10296115
;; Publication No. US20040053248A1
;; GENERAL INFORMATION:
;; APPLICANT: Hyseq Inc
;; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
;; FILE REFERENCE: 784PCT
;; CURRENT APPLICATION NUMBER: US/10/296,115
;; CURRENT FILING DATE: 2002-11-18
;; PRIOR APPLICATION NUMBER: US09/488,725
;; PRIOR FILING DATE: 2000-01-21
;; PRIOR APPLICATION NUMBER: US09/552,317
;; PRIOR FILING DATE: 2000-04-25
;; NUMBER OF SEQ ID NOS: 1478
;; SEQ ID NO: 1220
;; LENGTH: 242
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-296-115-1220

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Best Local Similarity 100.0%; Pred. No. 1e-109;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 86 RRRRGAPAPQOQSEPARPSRGKTCIDRLRVRAEYCEHGPALGQVARRRRPOLARQ 145
QY 230 DVFQATVLRSRDLGSVVCIDIKFSELSTYLDAFMGDYLSGALLQALRGVFLTEALREAVG 289
DB 146 DVFQATVLRSRDLGSVVCIDIKFSELSTYLDAFMGDYLSGALLQALRGVFLTEALREAVG 205
QY 290 REAVRLVSVDEAD 303
DB 206 REAVRLVSVDEAD 219

RESULT 8
US-09-799-777-26
;; Sequence 26; Application US/09799777

;; Patent No. US20020091244A1
;; GENERAL INFORMATION:
;; APPLICANT: IAL, Preeti
;; Hillman, Jennifer L.
;; Corley, Neil C.
;; Guebler, Karl J.
;; Baugh, Mariah
;; Sather, Susan
;; Shah, Purvi
;; TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
;; NUMBER OF SEQUENCES: 154
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;; STREET: 3174 PORTER DRIVE
;; CITY: PALO ALTO
;; STATE: CALIFORNIA
;; COUNTRY: USA
;; ZIP: 94304
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/799,777
;; FILING DATE: 06-Mar-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/002,485
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BILLINGS, LUCY J.
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0459 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650) 855-0555
;; TELEFAX: (650) 845-4166
;; INFORMATION FOR SEQ ID NO: 26:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 217 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: UTRSN0T06
;; CLONE: 1638407
;; SEQUENCE DESCRIPTION: SEQ ID NO: 26 :
US-09-799-777-26

Query Match 35.3%; Score 107; DB 9; Length 217;
Best Local Similarity 100.0%; Pred. No. 5.8e-86;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 88 DIRLRVRAEYCEHGPALGQVARRRRPOLARQDVFGQATVLRSRDLGSVVCIDIKFSEL 147
QY 257 SYLDAFMGDYLSGALLQALRGVFLTEALREAVGRVRLVSVDEAD 303
DB 148 SYLDAFMGDYLSGALLQALRGVFLTEALREAVGRVRLVSVDEAD 194

RESULT 9
US-10-001-254-8
;; Sequence 8; Application US/10001254
;; Publication No. US20030049702A1
;; GENERAL INFORMATION:
;; APPLICANT: Reed, John C.
;; APPLICANT: Godzik, Adam
;; APPLICANT: Pawloweki, Krzysztof
;; APPLICANT: Fiorentino, Loredana
;; APPLICANT: Lee, Sung Hyung
;; APPLICANT: Roth, Wilfred


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/ APPLICANT: Stenner-Liewen, Frank
/ TITLE OF INVENTION: No. US20030049702A1el Death Domain Proteins
/ FILE REFERENCE: P-LJ 5037
/ CURRENT APPLICATION NUMBER: US10/001,254
/ PRIOR FILING DATE: 2001-11-15
/ PRIOR APPLICATION NUMBER: 60/301,889
/ PRIOR FILING DATE: 2001-06-29
/ PRIOR APPLICATION NUMBER: 09/715,893
/ PRIOR FILING DATE: 2000-11-17
/ NUMBER OF SEQ ID NOS: 62
/ SOFTWARE: PaeSeq for Windows Version 4.0
/ SEQ ID NO 8
/ LENGTH: 101
/ TYPE: PRT
/ ORGANISM: Homo sapien
US-10-001-254-8

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Best Local Similarity 100.0%; Pred. No. 5,6e-51;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 WEDECLDYGMISLRMEVVGSGUTCELELAFILDEAPAGGLARASGLLELL 60
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QY 72 LRRGQC 78
    |||||
Db 61 LRRGQC 67

RESULT 10
US-09-733-167-6
/ Sequence 6, Application US/09733167
/ Patent No. US20020099009A1
/ GENERAL INFORMATION:
/ APPLICANT: Peter, Marcus
/ APPLICANT: Kramer, Peter
/ TITLE OF INVENTION: Protein for Regulation of Apoptosis
/ FILE REFERENCE: 4121-120
/ CURRENT APPLICATION NUMBER: US/09/733,167
/ PRIOR FILING DATE: 2000-12-08
/ PRIOR APPLICATION NUMBER: PCT/DE99/01712
/ PRIOR FILING DATE: 1999-06-08
/ PRIOR APPLICATION NUMBER: German Patent Application No. US20020099009A1 198 25 621.3
/ PRIOR FILING DATE: 1998-06-08
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 6
/ LENGTH: 210
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: C-DEDD, which is a deletion mutant of human DEDD comprising amino
/ OTHER INFORMATION: acids 109-318 of the naturally occurring human DEDD.
US-09-733-167-6

Query Match          4.3%; Score 13; DB 9; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCDIRLRVRAEYC 207
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Db 84 TCDIRLRVRAEYC 96

RESULT 11
US-09-935-223-4
/ Sequence 4, Application US/09935223
/ Patent No. US20020086983A1
/ GENERAL INFORMATION:
/ APPLICANT: Alnemri, Emad S.
/ APPLICANT: Kramer, Peter
/ TITLE OF INVENTION: Fadd-Like Anti-Apoptotic Molecules, Methods Of Using The Same, An
/ TITLE OF INVENTION: Compositions For And Methods Of Making The Same
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/ FILE REFERENCE: TJU2499
/ CURRENT APPLICATION NUMBER: US/09/935,223
/ PRIOR FILING DATE: 2001-08-22
/ CURRENT APPLICATION NUMBER: 09/723,450
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: 09/276,993
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: 08/859,167
/ PRIOR FILING DATE: 1997-05-20
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 4
/ LENGTH: 318
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Novel Sequence
US-09-935-223-4

Query Match          4.3%; Score 13; DB 9; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCDIRLRVRAEYC 207
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Db 192 TCDIRLRVRAEYC 204

RESULT 12
US-09-935-223-6
/ Sequence 6, Application US/09935223
/ Patent No. US20020086983A1
/ GENERAL INFORMATION:
/ APPLICANT: Alnemri, Emad S.
/ APPLICANT: Kramer, Peter
/ TITLE OF INVENTION: Fadd-Like Anti-Apoptotic Molecules, Methods Of Using The Same, An
/ TITLE OF INVENTION: Compositions For And Methods Of Making The Same
/ FILE REFERENCE: TJU2499
/ CURRENT APPLICATION NUMBER: US/09/935,223
/ PRIOR FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: 09/723,450
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: 09/276,993
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: 08/859,167
/ PRIOR FILING DATE: 1997-05-20
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 6
/ LENGTH: 318
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Novel Sequence
US-09-935-223-6

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Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCDIRLRVRAEYC 207
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Db 192 TCDIRLRVRAEYC 204

RESULT 13
US-09-733-167-1
/ Sequence 1, Application US/09733167
/ Patent No. US20020099009A1
/ GENERAL INFORMATION:
/ APPLICANT: Peter, Marcus
/ APPLICANT: Kramer, Peter
/ TITLE OF INVENTION: Protein for Regulation of Apoptosis
/ FILE REFERENCE: 4121-120
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; CURRENT APPLICATION NUMBER: US/09/733,167
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/DE99/01712
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: German Patent Application No. US20020099009A1 198 25 621.3
; PRIOR FILING DATE: 1998-06-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-733-167-1

Query Match          4.3%; Score 13; DB 9; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      195 TCDIRLRVRAEYC 207
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Db      192 TCDIRLRVRAEYC 204

RESULT 14
US-09-733-167-3
; Sequence 3, Application US/09733167
; Patent No. US20020099009A1
; GENERAL INFORMATION:
; APPLICANT: Peter, Marcus
; TITLE OF INVENTION: Protein for Regulation of Apoptosis
; FILE REFERENCE: 4121-120
; CURRENT APPLICATION NUMBER: US/09/733,167
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: PCT/DE99/01712
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: German Patent Application No. US20020099009A1 198 25 621.3
; PRIOR FILING DATE: 1998-06-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-733-167-3

Query Match          4.3%; Score 13; DB 9; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      195 TCDIRLRVRAEYC 207
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Db      192 TCDIRLRVRAEYC 204

RESULT 15
US-10-437-963-166242
; Sequence 166242, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bardazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
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; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 166242
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_64970C.1.pep
US-10-437-963-166242

Query Match          3.6%; Score 11; DB 16; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      169 RRRRGAPAP 179
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Db      51 RRRRGAPAP 61

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OM protein - protein search, using sw model

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(without alignments)
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Title: US-10-030-271-2

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Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	13	4.3	318	3 US-09-109-373-4	Sequence 4, Appl1
5	13	4.3	318	3 US-09-109-373-6	Sequence 6, Appl1
6	13	4.3	318	3 US-09-276-593-4	Sequence 4, Appl1
7	13	4.3	318	3 US-09-276-593-6	Sequence 6, Appl1
8	13	4.3	318	4 US-09-723-450-4	Sequence 4, Appl1
9	13	4.3	318	4 US-09-723-450-6	Sequence 6, Appl1
10	13	4.3	318	4 US-09-723-167A-1	Sequence 1, Appl1
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13	9	3.0	316	4 US-09-602-777A-230	Sequence 230, App
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15	9	3.0	356	4 US-09-252-991A-25124	Sequence 25124, A
16	9	3.0	504	4 US-09-252-991A-23374	Sequence 23374, A
17	9	3.0	657	4 US-09-252-991A-28601	Sequence 28601, A
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19	8	2.6	67	1 US-08-159-340A-6	Sequence 6, Appl1
20	8	2.6	133	4 US-09-252-991A-17914	Sequence 17914, A
21	8	2.6	179	4 US-09-252-991A-24966	Sequence 24966, A
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24	8	2.6	266	4 US-09-252-991A-17835	Sequence 17835, A
25	8	2.6	300	3 US-09-261-599B-6	Sequence 6, Appl1
26	8	2.6	300	3 US-09-261-599B-7	Sequence 7, Appl1
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28	8	2.6	354	4 US-09-949-016-11550	Sequence 11550, A
29	8	2.6	361	3 US-09-261-599B-1	Sequence 1, Appl1
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33	8	2.6	452	4 US-09-252-991A-24195	Sequence 24195, A
34	8	2.6	462	4 US-09-166-350-18	Sequence 18, Appl1
35	8	2.6	493	4 US-09-252-991A-32463	Sequence 32463, A
36	8	2.6	679	4 US-09-252-991A-25400	Sequence 25400, A
37	8	2.6	679	4 US-09-252-991A-28950	Sequence 28950, A
38	8	2.6	690	4 US-09-252-991A-32350	Sequence 32350, A
39	8	2.6	810	4 US-09-489-039A-9748	Sequence 9748, Ap
40	8	2.6	989	4 US-09-252-991A-17435	Sequence 17435, A
41	8	2.6	1116	4 US-09-252-991A-24374	Sequence 24374, A
42	8	2.6	1958	1 US-07-945-283-2	Sequence 2, Appl1
43	7	2.3	31	3 US-09-327-357-653	Sequence 653, App
44	7	2.3	37	1 US-08-438-753B-35	Sequence 35, Appl1
45	7	2.3	37	1 US-08-443-883A-35	Sequence 35, Appl1
46	7	2.3	37	2 US-08-631-328-35	Sequence 35, Appl1
47	7	2.3	37	2 US-08-455-524B-35	Sequence 35, Appl1
48	7	2.3	37	2 US-08-455-021B-35	Sequence 35, Appl1
49	7	2.3	37	3 US-09-045-467-35	Sequence 35, Appl1
50	7	2.3	87	4 US-09-270-767-38674	Sequence 38674, A
51	7	2.3	87	4 US-09-270-767-53891	Sequence 53891, A
52	7	2.3	91	4 US-09-270-767-62183	Sequence 62183, A
53	7	2.3	103	4 US-09-513-999C-4915	Sequence 4915, Ap
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59	7	2.3	127	4 US-09-949-016-10809	Sequence 10809, A
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77	7	2.3	172	3 US-08-616-904A-6	Sequence 6, Appl1
78	7	2.3	173	4 US-09-252-991A-24327	Sequence 24327, A
79	7	2.3	173	4 US-09-543-681A-5934	Sequence 5934, Ap
80	7	2.3	177	4 US-09-252-991A-27363	Sequence 27363, A
81	7	2.3	194	4 US-09-252-991A-30404	Sequence 30404, A
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92	7	2.3	210	4 US-09-489-039A-9923	Sequence 9923, Ap
93	7	2.3	212	4 US-09-489-039A-10046	Sequence 10046, A
94	7	2.3	214	4 US-09-252-991A-27795	Sequence 27795, A
95	7	2.3	214	4 US-09-252-991A-17700	Sequence 17700, A
96	7	2.3	224	4 US-09-107-433-4706	Sequence 4706, Ap
97	7	2.3	225	4 US-09-583-110-3301	Sequence 3301, Ap
98	7	2.3	240	4 US-09-252-991A-17701	Sequence 17701, A
99	7	2.3	247	3 US-09-240-952-5	Sequence 5, Appl1
100	7	2.3	248	3 US-09-240-952-3	Sequence 3, Appl1

101	7	2.3	249	4	US-09-252-991A-28972	Sequence 28972, A	174	7	2.3	376	4	US-09-072-596-197	Sequence 197, App
102	7	2.3	251	4	US-09-248-796A-23216	Sequence 23216, A	175	7	2.3	376	4	US-09-072-967-202	Sequence 202, App
103	7	2.3	255	4	US-09-489-039A-9075	Sequence 9075, Ap	176	7	2.3	385	4	US-09-252-991A-22010	Sequence 22010, A
104	7	2.3	255	4	US-09-710-279-1304	Sequence 1304, Ap	177	7	2.3	393	4	US-09-543-681A-5865	Sequence 5865, Ap
105	7	2.3	264	4	US-09-252-991A-21057	Sequence 21057, A	178	7	2.3	397	4	US-09-949-016-10967	Sequence 10967, A
106	7	2.3	265	4	US-09-252-991A-29150	Sequence 29150, A	179	7	2.3	399	4	US-09-252-991A-25039	Sequence 25039, A
107	7	2.3	266	4	US-09-417-721-9	Sequence 9, App11	180	7	2.3	402	4	US-09-252-991A-18195	Sequence 18195, A
108	7	2.3	266	4	US-09-417-721-15	Sequence 15, App11	181	7	2.3	402	4	US-09-252-991A-20147	Sequence 20147, A
109	7	2.3	266	6	5175383-5	Patent No. 5175383	182	7	2.3	403	4	US-09-902-540-11445	Sequence 11445, A
110	7	2.3	266	6	5175383-5	Patent No. 5175383	183	7	2.3	413	4	US-10-237-551-196	Sequence 196, App
111	7	2.3	267	1	US-08-462-169B-13	Sequence 13, App1	184	7	2.3	416	4	US-09-710-279-2402	Sequence 2402, Ap
112	7	2.3	267	3	US-09-103-079-13	Sequence 13, App1	185	7	2.3	417	3	US-09-134-001C-5006	Sequence 5006, Ap
113	7	2.3	267	3	US-09-425-021-13	Sequence 13, App1	186	7	2.3	422	4	US-09-252-991A-19452	Sequence 19452, A
114	7	2.3	267	4	US-09-564-829-7	Sequence 7, App11	187	7	2.3	422	4	US-09-252-991A-30625	Sequence 30625, A
115	7	2.3	268	1	US-08-439-725A-12	Sequence 12, App1	188	7	2.3	429	4	US-09-252-991A-23556	Sequence 23556, A
116	7	2.3	268	1	US-08-464-590A-17	Sequence 17, App1	189	7	2.3	432	4	US-09-328-353-4955	Sequence 4955, Ap
117	7	2.3	268	2	US-08-307-412B-12	Sequence 12, App1	190	7	2.3	440	4	US-09-252-991A-17112	Sequence 17112, A
118	7	2.3	268	2	US-08-867-471-12	Sequence 12, App1	191	7	2.3	440	4	US-09-252-991A-30167	Sequence 30167, A
119	7	2.3	268	2	US-08-438-439C-8	Sequence 8, App11	192	7	2.3	444	4	US-09-107-532A-3952	Sequence 3952, Ap
120	7	2.3	268	2	US-08-951-822-33	Sequence 33, App1	193	7	2.3	448	4	US-09-252-991A-30230	Sequence 30230, A
121	7	2.3	268	3	US-08-705-245-14	Sequence 14, App1	194	7	2.3	450	4	US-09-252-991A-32284	Sequence 32284, A
122	7	2.3	268	3	US-08-718-904-14	Sequence 14, App1	195	7	2.3	455	4	US-08-635-130A-2	Sequence 2, App11
123	7	2.3	268	3	US-09-023-082A-15	Sequence 15, App1	196	7	2.3	456	4	US-09-252-991A-19417	Sequence 19417, A
124	7	2.3	268	3	US-09-093-585-17	Sequence 17, App1	197	7	2.3	459	4	US-09-252-991A-29528	Sequence 29528, A
125	7	2.3	268	3	US-09-240-952-2	Sequence 2, App11	198	7	2.3	461	4	US-09-252-991A-23456	Sequence 23456, A
126	7	2.3	268	3	US-09-368-951-33	Sequence 33, App1	199	7	2.3	468	4	US-09-252-991A-21575	Sequence 21575, A
127	7	2.3	268	4	US-09-449-249-14	Sequence 14, App1	200	7	2.3	472	4	US-09-252-991A-32068	Sequence 32068, A
128	7	2.3	268	4	US-09-390-207-20	Sequence 20, App1	201	7	2.3	477	4	US-09-252-991A-27516	Sequence 27516, A
129	7	2.3	268	4	US-09-329-947-33	Sequence 33, App1	202	7	2.3	482	4	US-09-252-991A-31492	Sequence 31492, A
130	7	2.3	268	4	US-09-248-998-15	Sequence 15, App1	203	7	2.3	484	4	US-09-252-991A-24249	Sequence 24249, A
131	7	2.3	268	4	US-09-572-406B-11	Sequence 11, App1	204	7	2.3	486	4	US-09-252-991A-31404	Sequence 31404, A
132	7	2.3	268	4	US-09-490-714-14	Sequence 14, App1	205	7	2.3	490	4	US-09-252-991A-22715	Sequence 22715, A
133	7	2.3	268	4	US-09-610-651-15	Sequence 15, App1	206	7	2.3	493	4	US-09-270-767-44663	Sequence 44663, A
134	7	2.3	268	4	US-09-949-016-7942	Sequence 18, App1	207	7	2.3	496	4	US-09-252-991A-26668	Sequence 26668, A
135	7	2.3	269	2	US-08-438-439C-18	Sequence 18, App1	208	7	2.3	499	4	US-09-252-991A-19691	Sequence 19691, A
136	7	2.3	269	3	US-09-252-991A-28651	Sequence 28651, A	209	7	2.3	501	4	US-09-252-991A-16795	Sequence 16795, A
137	7	2.3	273	3	US-08-928-213B-9	Sequence 9, App11	210	7	2.3	501	4	US-09-252-991A-17730	Sequence 17730, A
138	7	2.3	273	4	US-09-252-991A-16693	Sequence 16693, A	211	7	2.3	501	4	US-09-252-991A-17730	Sequence 17730, A
139	7	2.3	273	4	US-09-252-991A-31733	Sequence 31733, A	212	7	2.3	506	4	US-09-252-991A-31885	Sequence 31885, A
140	7	2.3	279	4	US-09-252-991A-30528	Sequence 30528, A	213	7	2.3	507	4	US-09-252-991A-18390	Sequence 18390, A
141	7	2.3	281	4	US-09-252-991A-17748	Sequence 17748, A	214	7	2.3	528	3	US-09-252-991A-17468	Sequence 17468, A
142	7	2.3	281	4	US-09-252-991A-24898	Sequence 24898, A	215	7	2.3	533	4	US-09-252-991A-17429	Sequence 17429, A
143	7	2.3	284	4	US-09-352-991A-27572	Sequence 27572, A	216	7	2.3	530	4	US-09-252-991A-26107	Sequence 26107, A
144	7	2.3	285	4	US-09-270-767-46359	Sequence 46359, A	217	7	2.3	561	4	US-09-922-36A-1	Sequence 1, App11
145	7	2.3	297	4	US-09-252-991A-18932	Sequence 18932, A	218	7	2.3	561	4	US-09-254-599-1	Sequence 1, App11
146	7	2.3	300	4	US-09-902-540-14290	Sequence 14290, A	219	7	2.3	561	4	US-09-949-016-6197	Sequence 6197, Ap
147	7	2.3	304	4	US-09-949-016-6824	Sequence 6824, Ap	220	7	2.3	561	4	US-10-115-415-1	Sequence 1, App11
148	7	2.3	312	4	US-09-949-016-7149	Sequence 7149, Ap	221	7	2.3	561	4	US-10-116-263-1	Sequence 1, App11
149	7	2.3	313	4	US-09-352-991A-21867	Sequence 21867, A	222	7	2.3	561	4	US-10-116-671-1	Sequence 1, App11
150	7	2.3	314	4	US-09-252-991A-18836	Sequence 18836, A	223	7	2.3	568	4	US-09-252-991A-32461	Sequence 32461, A
151	7	2.3	318	4	US-09-252-991A-23557	Sequence 23557, A	224	7	2.3	571	4	US-09-248-796A-22498	Sequence 22498, A
152	7	2.3	321	4	US-09-134-000C-3807	Sequence 3807, Ap	225	7	2.3	572	4	US-09-252-991A-33956	Sequence 33956, A
153	7	2.3	325	4	US-09-252-991A-28166	Sequence 28166, A	226	7	2.3	576	3	US-09-134-001C-3955	Sequence 3955, Ap
154	7	2.3	330	4	US-09-252-991A-18573	Sequence 18573, A	227	7	2.3	587	4	US-09-252-991A-18280	Sequence 18280, A
155	7	2.3	331	4	US-09-949-016-9220	Sequence 9220, Ap	228	7	2.3	587	4	US-09-949-016-10091	Sequence 10091, A
156	7	2.3	340	4	US-09-214-631-3	Sequence 3, App11	229	7	2.3	590	4	US-09-252-991A-19127	Sequence 19127, A
157	7	2.3	340	4	US-09-051-994-2	Sequence 2, App11	230	7	2.3	590	4	US-09-443-067-22	Sequence 22, App1
158	7	2.3	340	4	US-08-635-130A-4	Sequence 4, App11	231	7	2.3	593	4	US-09-252-991A-33340	Sequence 33340, A
159	7	2.3	340	4	US-09-949-016-6076	Sequence 6076, Ap	232	7	2.3	599	4	US-09-252-991A-30462	Sequence 30462, A
160	7	2.3	342	4	US-09-270-767-46587	Sequence 46587, Ap	233	7	2.3	602	4	US-09-252-991A-30458	Sequence 30458, A
161	7	2.3	346	4	US-09-252-991A-22101	Sequence 22101, A	234	7	2.3	619	4	US-09-902-540-14059	Sequence 14059, A
162	7	2.3	348	4	US-09-252-991A-25605	Sequence 25605, A	235	7	2.3	632	4	US-09-252-991A-31646	Sequence 31646, A
163	7	2.3	348	4	US-09-710-279-1702	Sequence 1702, Ap	236	7	2.3	635	4	US-09-252-991A-17495	Sequence 17495, A
164	7	2.3	351	4	US-09-710-279-338	Sequence 338, App	237	7	2.3	655	4	US-09-252-991A-30167	Sequence 30167, A
165	7	2.3	355	4	US-09-902-540-15046	Sequence 15046, A	238	7	2.3	658	4	US-09-252-991A-17112	Sequence 17112, A
166	7	2.3	357	4	US-09-107-433-5014	Sequence 5014, Ap	239	7	2.3	659	4	US-09-252-991A-30353	Sequence 30353, A
167	7	2.3	368	4	US-09-489-039A-17553	Sequence 17553, A	240	7	2.3	659	4	US-09-270-767-43969	Sequence 43969, A
168	7	2.3	368	4	US-09-668-097A-10	Sequence 10, App1	241	7	2.3	672	4	US-09-252-991A-22407	Sequence 22407, A
169	7	2.3	372	4	US-09-252-991A-27359	Sequence 27359, A	242	7	2.3	684	4	US-09-252-991A-32342	Sequence 32342, A
170	7	2.3	374	4	US-09-252-991A-22425	Sequence 22425, A	243	7	2.3	690	4	US-10-262-083-2	Sequence 2, App11
171	7	2.3	375	4	US-09-134-000C-5852	Sequence 5852, Ap	244	7	2.3	702	4	US-09-252-991A-31609	Sequence 31609, A
172	7	2.3	375	4	US-09-818-780-23	Sequence 23, App1	245	7	2.3	702	4	US-09-252-991A-32740	Sequence 32740, A
173	7	2.3	376	3	US-09-056-556-202	Sequence 202, App	246	7	2.3	715	4	US-09-252-991A-32740	Sequence 32740, A

247	7	2.3	722	4	US-09-252-991A-18481	Sequence 18481, A	320	6	2.0	12	5	PCT-US91-08328-28	Sequence 28, Appl
248	7	2.3	724	4	US-09-252-991A-31715	Sequence 31715, A	321	6	2.0	13	1	US-08-469-582-2	Sequence 2, Appl
249	7	2.3	731	4	US-09-902-540-13763	Sequence 13763, A	322	6	2.0	13	2	US-08-753-781-24	Sequence 24, Appl
250	7	2.3	746	4	US-09-548-7978-4	Sequence 4, Appl	323	6	2.0	13	5	PCT-US91-08328-27	Sequence 27, Appl
251	7	2.3	767	4	US-09-548-7978-5	Sequence 5, Appl	324	6	2.0	13	5	US-08-469-582-13	Sequence 13, Appl
252	7	2.3	802	4	US-09-632-098-2	Sequence 2, Appl	325	6	2.0	14	1	US-08-469-582-12	Sequence 12, Appl
253	7	2.3	802	4	US-10-177-308-4	Sequence 4, Appl	326	6	2.0	14	1	US-08-473-025-8	Sequence 8, Appl
254	7	2.3	812	4	US-09-632-098-2	Sequence 2, Appl	327	6	2.0	14	2	US-08-473-025-8	Sequence 8, Appl
255	7	2.3	812	4	US-10-177-308-4	Sequence 4, Appl	328	6	2.0	14	5	PCT-US91-08328-36	Sequence 36, Appl
256	7	2.3	830	4	US-09-252-991A-28961	Sequence 28961, A	329	6	2.0	15	1	US-08-439-905-5	Sequence 5, Appl
257	7	2.3	841	4	US-09-538-092-1183	Sequence 1183, A	330	6	2.0	15	1	US-08-469-582-13	Sequence 13, Appl
258	7	2.3	849	4	US-09-548-7978-6	Sequence 6, Appl	331	6	2.0	15	2	US-08-335-832-13	Sequence 13, Appl
259	7	2.3	855	4	US-09-949-016-7263	Sequence 7263, Ap	332	6	2.0	15	2	US-08-902-367-6	Sequence 6, Appl
260	7	2.3	863	4	US-09-252-991A-20821	Sequence 20821, A	333	6	2.0	15	3	US-09-100-536-5	Sequence 5, Appl
261	7	2.3	869	4	US-09-252-991A-22748	Sequence 22748, A	334	6	2.0	15	3	US-09-100-536-5	Sequence 5, Appl
262	7	2.3	883	4	US-09-489-039A-13542	Sequence 13542, A	335	6	2.0	15	3	US-08-535-170-14	Sequence 14, Appl
263	7	2.3	885	4	US-09-252-991A-26129	Sequence 26129, A	336	6	2.0	15	3	US-08-141-127-7	Sequence 7, Appl
264	7	2.3	889	4	US-09-949-016-6036	Sequence 6036, Ap	337	6	2.0	16	2	US-08-753-781-6	Sequence 6, Appl
265	7	2.3	892	4	US-09-949-016-7055	Sequence 7055, Ap	338	6	2.0	16	2	US-08-440-861-13	Sequence 13, Appl
266	7	2.3	910	4	US-09-252-991A-31682	Sequence 31682, A	339	6	2.0	20	1	US-08-440-861-13	Sequence 13, Appl
267	7	2.3	922	4	US-09-252-991A-16655	Sequence 16655, A	340	6	2.0	23	2	US-08-847-176-2	Sequence 2, Appl
268	7	2.3	951	4	US-09-252-991A-26766	Sequence 26766, A	341	6	2.0	23	2	US-08-847-176-16	Sequence 16, Appl
269	7	2.3	977	4	US-09-252-991A-20611	Sequence 20611, A	342	6	2.0	23	2	US-08-847-176-19	Sequence 19, Appl
270	7	2.3	1033	4	US-09-252-991A-20611	Sequence 20611, A	343	6	2.0	26	2	US-08-847-176-6	Sequence 6, Appl
271	7	2.3	1037	4	US-09-902-540-9845	Sequence 9845, Ap	344	6	2.0	26	2	US-08-847-176-7	Sequence 7, Appl
272	7	2.3	1046	4	US-09-252-991A-27508	Sequence 27508, A	345	6	2.0	26	2	US-08-847-176-8	Sequence 8, Appl
273	7	2.3	1186	2	US-08-861-464-8	Sequence 8, Appl	346	6	2.0	26	2	US-08-847-176-21	Sequence 21, Appl
274	7	2.3	1186	2	US-08-396-001-8	Sequence 8, Appl	347	6	2.0	26	2	US-08-847-176-22	Sequence 22, Appl
275	7	2.3	1186	3	US-09-323-433A-8	Sequence 8, Appl	348	6	2.0	26	2	US-08-847-176-125	Sequence 125, Appl
276	7	2.3	1186	4	US-09-826-752-8	Sequence 8, Appl	349	6	2.0	27	1	US-07-776-272-27	Sequence 27, Appl
277	7	2.3	1195	4	US-09-540-236-3165	Sequence 3165, Ap	350	6	2.0	27	3	US-09-260-846-17	Sequence 17, Appl
278	7	2.3	1364	4	US-09-252-991A-26680	Sequence 26680, A	351	6	2.0	27	4	US-08-469-260A-481	Sequence 481, App
279	7	2.3	1404	4	US-09-345-473E-24	Sequence 24, Appl	352	6	2.0	27	4	US-08-488-446-481	Sequence 481, App
280	7	2.3	1466	4	US-09-252-991A-30085	Sequence 30085, A	353	6	2.0	27	4	US-08-467-344A-481	Sequence 481, App
281	7	2.3	2353	2	US-08-984-709A-50	Sequence 50, Appl	354	6	2.0	27	4	US-08-424-508A-481	Sequence 481, App
282	7	2.3	3724	2	US-08-804-227C-10	Sequence 10, Appl	355	6	2.0	27	4	US-10-014-269-51	Sequence 51, Appl
283	7	2.3	3724	2	US-08-804-198-4	Sequence 4, Appl	356	6	2.0	28	4	US-10-014-269-17	Sequence 17, Appl
284	6	2.0	8	2	US-08-473-025-11	Sequence 11, Appl	357	6	2.0	31	4	US-09-358-321C-15	Sequence 15, Appl
285	6	2.0	9	1	US-08-178-570-36	Sequence 36, Appl	358	6	2.0	32	1	US-08-152-488-9	Sequence 9, Appl
286	6	2.0	9	3	US-08-369-643-36	Sequence 36, Appl	359	6	2.0	32	1	US-08-303-025-9	Sequence 9, Appl
287	6	2.0	9	5	PCT-US91-08328-31	Sequence 31, Appl	360	6	2.0	32	2	US-08-677-304-9	Sequence 9, Appl
288	6	2.0	9	5	PCT-US91-00147-36	Sequence 36, Appl	361	6	2.0	32	2	US-08-436-703B-14	Sequence 14, Appl
289	6	2.0	10	4	US-09-648-400A-7	Sequence 7, Appl	362	6	2.0	33	3	US-09-122-144-4	Sequence 4, Appl
290	6	2.0	10	4	US-09-792-480-7	Sequence 7, Appl	363	6	2.0	33	3	US-09-172-841-37	Sequence 37, Appl
291	6	2.0	10	4	US-10-209-421-7	Sequence 7, Appl	364	6	2.0	38	3	US-09-172-841-39	Sequence 39, Appl
292	6	2.0	10	5	PCT-US91-08328-30	Sequence 30, Appl	365	6	2.0	38	4	US-08-951-621-37	Sequence 37, Appl
293	6	2.0	11	1	US-08-462-880-13	Sequence 13, Appl	366	6	2.0	38	4	US-08-951-621-39	Sequence 39, Appl
294	6	2.0	11	2	US-08-273-474-13	Sequence 13, Appl	367	6	2.0	40	4	US-09-270-767-37180	Sequence 37180, A
295	6	2.0	11	2	US-08-475-041-13	Sequence 13, Appl	368	6	2.0	40	4	US-09-270-767-52397	Sequence 52397, A
296	6	2.0	11	2	US-08-484-773-13	Sequence 13, Appl	369	6	2.0	40	4	US-09-385-219A-67	Sequence 67, Appl
297	6	2.0	11	2	US-08-361-864-17	Sequence 17, Appl	370	6	2.0	42	3	US-09-172-841-1	Sequence 1, Appl
298	6	2.0	11	3	US-09-208-966-7	Sequence 7, Appl	371	6	2.0	42	4	US-08-951-621-1	Sequence 1, Appl
299	6	2.0	11	3	US-09-208-966-8	Sequence 8, Appl	372	6	2.0	43	3	US-09-007-905-57	Sequence 57, Appl
300	6	2.0	11	3	US-09-083-259-20	Sequence 20, Appl	373	6	2.0	43	4	US-09-232-074-57	Sequence 57, Appl
301	6	2.0	11	4	US-09-396-195-20	Sequence 20, Appl	374	6	2.0	44	4	US-09-385-219A-15	Sequence 15, Appl
302	6	2.0	11	4	US-09-775-052A-7	Sequence 7, Appl	375	6	2.0	44	4	US-09-823-266-17	Sequence 17, Appl
303	6	2.0	11	5	US-09-775-052A-8	Sequence 8, Appl	376	6	2.0	46	3	US-08-483-533-30	Sequence 30, Appl
304	6	2.0	11	5	PCT-US91-08328-29	Sequence 29, Appl	377	6	2.0	46	3	US-09-283-471A-30	Sequence 30, Appl
305	6	2.0	12	1	US-08-177-551-52	Sequence 52, Appl	378	6	2.0	46	3	US-08-861-476C-7	Sequence 7, Appl
306	6	2.0	12	1	US-08-480-367B-52	Sequence 52, Appl	379	6	2.0	46	4	US-09-732-210-258	Sequence 258, App
307	6	2.0	12	1	US-08-487-221A-52	Sequence 52, Appl	380	6	2.0	48	3	US-09-314-268-16	Sequence 16, App
308	6	2.0	12	1	US-08-480-370-52	Sequence 52, Appl	381	6	2.0	48	4	US-09-369-247-117	Sequence 117, App
309	6	2.0	12	1	US-08-299-636-32	Sequence 32, Appl	382	6	2.0	50	4	US-09-902-540-10534	Sequence 10534, A
310	6	2.0	12	1	US-08-279-155-32	Sequence 32, Appl	383	6	2.0	53	4	US-09-513-999C-7165	Sequence 7165, Ap
311	6	2.0	12	1	US-08-445-745-124	Sequence 124, App	384	6	2.0	55	2	US-08-459-568-80	Sequence 80, Appl
312	6	2.0	12	1	US-08-464-456-30	Sequence 30, Appl	385	6	2.0	55	2	US-08-399-411-80	Sequence 80, Appl
313	6	2.0	12	1	US-08-703-988A-32	Sequence 32, Appl	386	6	2.0	55	3	US-08-516-859A-80	Sequence 80, Appl
314	6	2.0	12	1	US-08-463-052-30	Sequence 30, Appl	387	6	2.0	55	3	US-09-586-472-80	Sequence 80, Appl
315	6	2.0	12	2	US-08-480-551-30	Sequence 30, Appl	388	6	2.0	56	4	US-09-528-706-80	Sequence 80, Appl
316	6	2.0	12	2	US-08-378-709-31	Sequence 31, Appl	389	6	2.0	57	4	US-09-370-767-59181	Sequence 59181, A
317	6	2.0	12	2	US-08-612-842-32	Sequence 32, Appl	390	6	2.0	57	4	US-09-513-999C-6181	Sequence 6181, Ap
318	6	2.0	12	4	US-08-445-638-124	Sequence 124, App	391	6	2.0	61	4	US-09-513-999C-6181	Sequence 6181, Ap
319	6	2.0	12	4	US-09-428-082B-550	Sequence 550, App	392	6	2.0	61	4	US-09-072-634-10	Sequence 10, Appl

393	6	2.0	61	4	US-09-621-976-4027	Sequence 4027, Ap	466	6	2.0	108	4	US-09-839-542B-40	Sequence 40, Appl
394	6	2.0	63	4	US-09-270-767-58468	Sequence 58468, A	467	6	2.0	108	4	US-09-535-855-40	Sequence 40, Appl
395	6	2.0	64	4	US-09-252-991A-25121	Sequence 25121, A	468	6	2.0	108	4	US-09-902-540-16230	Sequence 16230, A
396	6	2.0	64	4	US-09-270-767-37216	Sequence 37216, A	469	6	2.0	112	4	US-09-489-039A-7374	Sequence 7374, Ap
397	6	2.0	64	4	US-09-270-767-39939	Sequence 39939, A	470	6	2.0	112	4	US-09-673-399A-234	Sequence 237, App
398	6	2.0	64	4	US-09-270-767-52433	Sequence 52433, A	471	6	2.0	112	4	US-09-621-976-6045	Sequence 6045, Ap
399	6	2.0	64	4	US-09-270-767-55156	Sequence 55156, A	472	6	2.0	113	4	US-09-106-568E-157	Sequence 157, App
400	6	2.0	64	4	US-09-248-796A-24762	Sequence 24762, A	473	6	2.0	113	4	US-09-248-796A-20113	Sequence 20113, A
401	6	2.0	65	4	US-09-621-976-7130	Sequence 7130, Ap	474	6	2.0	114	4	US-09-252-991A-25883	Sequence 25883, A
402	6	2.0	67	4	US-09-513-999C-7084	Sequence 7084, Ap	475	6	2.0	114	4	US-09-733-167A-5	Sequence 5, Appl1
403	6	2.0	68	3	US-09-007-905-50	Sequence 50, Appl1	476	6	2.0	114	4	US-09-270-767-57487	Sequence 57487, A
404	6	2.0	68	4	US-09-232-074-50	Sequence 50, Appl1	477	6	2.0	114	4	US-09-248-796A-28129	Sequence 28129, A
405	6	2.0	70	4	US-09-252-991A-27697	Sequence 27697, A	478	6	2.0	114	4	US-09-513-999C-7038	Sequence 7038, Ap
406	6	2.0	71	4	US-09-621-976-4052	Sequence 4052, Ap	479	6	2.0	117	4	US-09-489-039A-13048	Sequence 13048, A
407	6	2.0	71	4	US-09-302-540-13076	Sequence 13076, A	480	6	2.0	117	4	US-09-513-999C-6272	Sequence 6272, Ap
408	6	2.0	72	4	US-09-248-796A-23475	Sequence 23475, A	481	6	2.0	117	4	US-09-513-999C-6709	Sequence 6709, Ap
409	6	2.0	73	4	US-08-311-731A-296	Sequence 296, App	482	6	2.0	117	4	US-09-949-01E-8965	Sequence 8965, Ap
410	6	2.0	74	4	US-09-248-796A-24240	Sequence 24240, A	483	6	2.0	118	4	US-09-252-991A-28465	Sequence 28465, A
411	6	2.0	76	4	US-09-248-796A-21449	Sequence 21449, A	484	6	2.0	119	4	US-09-270-767-43255	Sequence 43255, A
412	6	2.0	76	4	US-09-248-796A-24505	Sequence 24505, A	485	6	2.0	120	4	US-09-252-991A-21271	Sequence 21271, A
413	6	2.0	77	4	US-09-270-767-57875	Sequence 57875, A	486	6	2.0	120	4	US-08-311-731A-411	Sequence 411, App
414	6	2.0	77	4	US-09-513-999C-4445	Sequence 4445, Ap	487	6	2.0	120	4	US-09-489-039A-7641	Sequence 7641, Ap
415	6	2.0	80	4	US-09-134-000C-3717	Sequence 3717, Ap	488	6	2.0	121	1	US-08-481-377-21	Sequence 21, Appl
416	6	2.0	80	4	US-09-621-976-5556	Sequence 5556, Ap	489	6	2.0	121	2	US-08-491-835-19	Sequence 19, Appl
417	6	2.0	81	4	US-09-502-540-15595	Sequence 15595, A	490	6	2.0	121	3	US-09-153-733A-21	Sequence 21, Appl
418	6	2.0	83	4	US-09-489-039A-11690	Sequence 11690, A	491	6	2.0	121	3	US-08-946-093A-19	Sequence 19, Appl
419	6	2.0	83	4	US-09-248-796A-25628	Sequence 25628, A	492	6	2.0	121	3	US-09-172-062-19	Sequence 19, Appl
420	6	2.0	83	4	US-09-302-540-11751	Sequence 11751, A	493	6	2.0	121	3	US-08-624-633-19	Sequence 19, Appl
421	6	2.0	84	4	US-09-902-540-13717	Sequence 13717, A	494	6	2.0	121	3	US-09-301-520D-19	Sequence 19, Appl
422	6	2.0	85	4	US-08-311-731A-100	Sequence 100, App	495	6	2.0	121	3	US-09-389-705-21	Sequence 21, Appl
423	6	2.0	85	4	US-09-841-879B-8	Sequence 8, Appl1	496	6	2.0	121	4	US-09-489-039A-11110	Sequence 11110, A
424	6	2.0	86	4	US-09-513-999C-7021	Sequence 7021, Ap	497	6	2.0	121	4	US-09-902-540-10057	Sequence 10057, A
425	6	2.0	87	4	US-09-489-039A-10564	Sequence 10564, A	498	6	2.0	121	5	PCT-US94-00666-21	Sequence 21, Appl
426	6	2.0	87	4	US-09-302-540-13177	Sequence 13177, A	499	6	2.0	121	5	PCT-US94-00666-19	Sequence 19, Appl
427	6	2.0	88	4	US-09-540-236-1943	Sequence 1943, Ap	500	6	2.0	122	1	US-08-581-528B-17	Sequence 17, Appl
428	6	2.0	89	4	US-09-599-360B-132	Sequence 132, App	501	6	2.0	122	1	US-08-455-555-23	Sequence 23, Appl
429	6	2.0	89	4	US-09-540-236-2401	Sequence 2401, Ap	502	6	2.0	122	2	US-08-525-598B-27	Sequence 27, Appl
430	6	2.0	90	4	US-09-252-991A-21131	Sequence 21131, A	503	6	2.0	122	2	US-08-581-528A-17	Sequence 17, Appl
431	6	2.0	91	4	US-09-252-991A-23967	Sequence 23967, A	504	6	2.0	122	3	US-09-097-616-17	Sequence 17, Appl
432	6	2.0	91	4	US-09-489-039A-11092	Sequence 11092, A	505	6	2.0	122	3	US-09-177-860A-27	Sequence 27, Appl
433	6	2.0	91	4	US-09-489-039A-11802	Sequence 11802, A	506	6	2.0	122	3	US-09-145-0067-23	Sequence 23, Appl
434	6	2.0	92	4	US-09-107-433-3651	Sequence 3651, Ap	507	6	2.0	122	4	US-09-378-238-37	Sequence 37, Appl
435	6	2.0	92	4	US-09-134-000C-4655	Sequence 4655, Ap	508	6	2.0	122	4	US-09-629-933-27	Sequence 27, Appl
436	6	2.0	93	4	US-09-489-039A-7356	Sequence 7356, Ap	509	6	2.0	122	4	US-09-686-344-45	Sequence 45, Appl
437	6	2.0	94	2	US-08-814-030-1	Sequence 1, Appl1	510	6	2.0	122	4	US-09-412-791D-17	Sequence 17, Appl
438	6	2.0	95	4	US-09-252-991A-19357	Sequence 19357, A	511	6	2.0	122	4	US-09-619-061-17	Sequence 17, Appl
439	6	2.0	95	4	US-09-270-767-59793	Sequence 59793, A	512	6	2.0	122	5	PCT-US94-00667-23	Sequence 23, Appl
440	6	2.0	95	4	US-09-248-796A-22091	Sequence 22091, A	513	6	2.0	122	5	PCT-US94-07782-17	Sequence 17, Appl
441	6	2.0	97	2	US-08-726-306A-128	Sequence 128, App	514	6	2.0	122	5	PCT-US94-07789-17	Sequence 17, Appl
442	6	2.0	97	4	US-08-311-731A-37	Sequence 37, Appl1	515	6	2.0	123	4	US-09-252-991A-28146	Sequence 28146, A
443	6	2.0	97	4	US-09-489-039A-8775	Sequence 8775, Ap	516	6	2.0	123	4	US-09-577-934A-3	Sequence 3, Appl1
444	6	2.0	98	4	US-09-615-192A-382	Sequence 382, App	517	6	2.0	123	4	US-09-270-767-33185	Sequence 33185, A
445	6	2.0	100	4	US-09-621-976-5449	Sequence 5449, Ap	518	6	2.0	123	4	US-09-270-767-54402	Sequence 54402, A
446	6	2.0	101	3	US-09-199-637A-77	Sequence 77, Appl	519	6	2.0	124	4	US-09-270-767-40657	Sequence 40657, A
447	6	2.0	101	3	US-09-199-637A-289	Sequence 289, App	520	6	2.0	124	4	US-09-270-767-55873	Sequence 55873, A
448	6	2.0	101	4	US-09-252-991A-21911	Sequence 21911, A	521	6	2.0	124	4	US-09-902-540-12036	Sequence 12036, A
449	6	2.0	101	4	US-09-248-796A-27051	Sequence 27051, A	522	6	2.0	125	4	US-09-199-637A-317	Sequence 317, App
450	6	2.0	101	4	US-09-513-999C-7871	Sequence 7871, Ap	523	6	2.0	125	4	US-09-252-991A-33028	Sequence 33028, A
451	6	2.0	104	4	US-09-621-976-5842	Sequence 5842, Ap	524	6	2.0	127	4	US-09-134-000C-4940	Sequence 4940, Ap
452	6	2.0	105	4	US-09-252-991A-26885	Sequence 26885, A	525	6	2.0	128	4	US-09-252-991A-32567	Sequence 32567, A
453	6	2.0	105	4	US-09-302-540-12948	Sequence 12948, A	526	6	2.0	128	4	US-09-640-211A-720	Sequence 720, App
454	6	2.0	106	3	US-09-083-351-14	Sequence 14, Appl1	527	6	2.0	129	4	US-09-252-991A-16731	Sequence 16731, A
455	6	2.0	106	3	US-09-083-351-15	Sequence 15, Appl1	528	6	2.0	129	4	US-09-640-211A-825	Sequence 825, App
456	6	2.0	106	3	US-09-083-352-14	Sequence 14, Appl1	529	6	2.0	130	1	US-08-455-550-9	Sequence 9, Appl1
457	6	2.0	106	3	US-09-083-352-15	Sequence 15, Appl1	530	6	2.0	131	4	US-09-252-991A-21357	Sequence 21357, A
458	6	2.0	106	4	US-09-198-452A-253	Sequence 253, App	531	6	2.0	131	4	US-09-270-767-61319	Sequence 61319, A
459	6	2.0	106	4	US-09-270-767-58597	Sequence 58597, A	532	6	2.0	131	4	US-08-534-976-4	Sequence 4, Appl1
460	6	2.0	106	4	US-09-248-796A-23643	Sequence 23643, A	533	6	2.0	132	2	US-08-954-470-4	Sequence 4, Appl1
461	6	2.0	106	4	US-09-612-809B-13	Sequence 13, Appl1	534	6	2.0	132	2	US-09-129-885A-4	Sequence 4, Appl1
462	6	2.0	107	4	US-09-612-809B-14	Sequence 14, Appl1	535	6	2.0	132	3	US-09-247-154-4	Sequence 4, Appl1
463	6	2.0	107	4	US-09-248-796A-23685	Sequence 23685, A	536	6	2.0	132	3	US-09-480-715-4	Sequence 4, Appl1
464	6	2.0	107	4	US-09-248-796A-27531	Sequence 27531, A	537	6	2.0	132	4	US-09-610-833-4	Sequence 4, Appl1
465	6	2.0	108	3	US-09-187-859-40	Sequence 40, Appl1	538	6	2.0	132	4	US-09-610-833-4	Sequence 4, Appl1

539	6	2.0	132	4	US-09-129-855A-4	Sequence 4, Appli	612	6	2.0	149	4	US-09-270-767-49997	Sequence 49997, A
540	6	2.0	133	4	US-09-252-991A-18533	Sequence 18533, A	613	6	2.0	150	4	US-09-252-991A-21785	Sequence 21785, A
541	6	2.0	133	4	US-09-252-991A-31987	Sequence 31987, A	614	6	2.0	151	4	US-09-252-991A-24676	Sequence 24676, A
542	6	2.0	133	4	US-09-134-000C-4871	Sequence 4871, Ap	615	6	2.0	151	4	US-09-621-876-5158	Sequence 5158, Ap
543	6	2.0	134	4	US-09-252-991A-19660	Sequence 19660, A	616	6	2.0	151	4	US-09-270-767-38747	Sequence 38747, A
544	6	2.0	134	4	US-09-252-991A-26710	Sequence 26710, A	617	6	2.0	151	4	US-09-270-767-53964	Sequence 53964, A
545	6	2.0	134	4	US-09-248-796A-25493	Sequence 25493, A	618	6	2.0	151	4	US-09-902-540-11681	Sequence 11681, A
546	6	2.0	135	4	US-09-252-991A-29208	Sequence 29208, A	619	6	2.0	151	4	US-09-302-540-13473	Sequence 13473, A
547	6	2.0	135	4	US-09-252-991A-31675	Sequence 31675, A	620	6	2.0	152	4	US-09-270-767-35128	Sequence 35128, A
548	6	2.0	136	4	US-09-252-991A-21384	Sequence 21384, A	621	6	2.0	152	4	US-09-370-767-50345	Sequence 50345, A
549	6	2.0	136	4	US-09-252-991A-31120	Sequence 31120, A	622	6	2.0	153	3	US-08-943-173-1	Sequence 1, Appli
550	6	2.0	136	4	US-09-270-767-57789	Sequence 57789, A	623	6	2.0	153	4	US-09-252-991A-24783	Sequence 24783, A
551	6	2.0	137	4	US-09-252-991A-17770	Sequence 17770, A	624	6	2.0	153	4	US-09-252-991A-30178	Sequence 30178, A
552	6	2.0	137	4	US-09-252-991A-24808	Sequence 24808, A	625	6	2.0	153	4	US-09-134-000C-5107	Sequence 5107, Ap
553	6	2.0	137	4	US-09-252-991A-26220	Sequence 26220, A	626	6	2.0	153	4	US-09-270-767-42492	Sequence 42492, A
554	6	2.0	138	1	US-08-698-551-4	Sequence 4, Appli	627	6	2.0	153	4	US-09-302-540-12154	Sequence 12154, A
555	6	2.0	138	2	US-08-602-228-4	Sequence 4, Appli	628	6	2.0	154	3	US-08-866-928B-5	Sequence 5, Appli
556	6	2.0	138	2	US-08-649-341A-4	Sequence 4, Appli	629	6	2.0	154	3	US-08-866-928B-6	Sequence 6, Appli
557	6	2.0	138	2	US-08-494-440B-4	Sequence 4, Appli	630	6	2.0	154	3	US-08-866-928B-7	Sequence 7, Appli
558	6	2.0	138	2	US-08-533-901B-4	Sequence 4, Appli	631	6	2.0	154	3	US-09-685-836-5	Sequence 5, Appli
559	6	2.0	138	2	US-08-839-032A-4	Sequence 4, Appli	632	6	2.0	154	4	US-09-685-836-6	Sequence 6, Appli
560	6	2.0	138	2	US-08-839-031A-4	Sequence 4, Appli	633	6	2.0	154	4	US-09-685-836-7	Sequence 7, Appli
561	6	2.0	138	3	US-09-185-258C-4	Sequence 4, Appli	634	6	2.0	154	4	US-09-252-991A-25607	Sequence 25607, A
562	6	2.0	138	4	US-09-252-991A-20026	Sequence 20026, A	635	6	2.0	154	4	US-09-252-991A-30329	Sequence 30329, A
563	6	2.0	138	4	US-09-252-991A-20131	Sequence 20131, A	636	6	2.0	154	4	US-09-252-991A-17892	Sequence 17892, A
564	6	2.0	138	4	US-09-902-540-14536	Sequence 14536, A	637	6	2.0	156	4	US-09-252-991A-25518	Sequence 25518, A
565	6	2.0	138	4	US-09-902-540-15833	Sequence 15833, A	638	6	2.0	156	4	US-09-489-039A-12749	Sequence 12749, A
566	6	2.0	138	5	PCT-US95-12724-4	Sequence 4, Appli	639	6	2.0	156	4	US-09-489-039A-12749	Sequence 12749, A
567	6	2.0	139	3	US-09-053-197A-40	Sequence 40, Appli	640	6	2.0	157	4	US-09-252-991A-17554	Sequence 17554, A
568	6	2.0	139	3	US-09-085-761A-40	Sequence 40, Appli	641	6	2.0	157	4	US-09-252-991A-30836	Sequence 30836, A
569	6	2.0	139	4	US-09-252-991A-19685	Sequence 19685, A	642	6	2.0	157	4	US-09-252-991A-31576	Sequence 31576, A
570	6	2.0	139	4	US-09-252-991A-21332	Sequence 21332, A	643	6	2.0	157	4	US-09-252-991A-31989	Sequence 31989, A
571	6	2.0	139	4	US-09-252-991A-23661	Sequence 23661, A	644	6	2.0	157	4	US-09-489-039A-9364	Sequence 9364, Ap
572	6	2.0	139	4	US-09-252-991A-28981	Sequence 28981, A	645	6	2.0	157	4	US-09-270-767-39506	Sequence 39506, A
573	6	2.0	139	4	US-09-252-991A-31379	Sequence 31379, A	646	6	2.0	157	4	US-09-270-767-54723	Sequence 54723, A
574	6	2.0	140	4	US-09-248-796A-15962	Sequence 15962, A	647	6	2.0	158	3	US-08-946-329A-66	Sequence 66, Appli
575	6	2.0	140	4	US-09-252-991A-23242	Sequence 23242, A	648	6	2.0	158	4	US-09-252-991A-26763	Sequence 26763, A
576	6	2.0	140	4	US-09-489-039A-13900	Sequence 13900, A	649	6	2.0	158	4	US-09-489-039A-10898	Sequence 10898, A
577	6	2.0	140	4	US-09-248-796A-25300	Sequence 25300, A	650	6	2.0	159	4	US-09-489-039A-8927	Sequence 8927, Ap
578	6	2.0	141	4	US-09-252-991A-21893	Sequence 21893, A	651	6	2.0	159	4	US-09-489-039A-9662	Sequence 9662, Ap
579	6	2.0	141	4	US-09-252-991A-23895	Sequence 23895, A	652	6	2.0	159	4	US-09-902-540-10781	Sequence 10781, A
580	6	2.0	141	4	US-09-270-767-31706	Sequence 31706, A	653	6	2.0	160	4	US-09-252-991A-17039	Sequence 17039, A
581	6	2.0	141	4	US-09-270-767-46923	Sequence 46923, A	654	6	2.0	160	4	US-09-252-991A-18043	Sequence 18043, A
582	6	2.0	141	4	US-09-513-999C-4215	Sequence 4215, Ap	655	6	2.0	160	4	US-09-252-991A-23275	Sequence 23275, A
583	6	2.0	142	4	US-09-252-991A-25603	Sequence 25603, A	656	6	2.0	160	4	US-09-270-767-33721	Sequence 33721, A
584	6	2.0	142	4	US-09-252-991A-28784	Sequence 28784, A	657	6	2.0	160	4	US-09-270-767-48938	Sequence 48938, A
585	6	2.0	142	4	US-09-270-767-45160	Sequence 45160, A	658	6	2.0	160	4	US-09-902-540-12994	Sequence 12994, A
586	6	2.0	142	4	US-09-107-433-4175	Sequence 4175, Ap	659	6	2.0	160	4	US-09-902-540-15069	Sequence 15069, A
587	6	2.0	143	4	US-09-252-991A-21012	Sequence 21012, A	660	6	2.0	161	4	US-09-252-991A-18142	Sequence 18142, A
588	6	2.0	143	4	US-09-252-991A-21367	Sequence 21367, A	661	6	2.0	161	4	US-09-252-991A-23452	Sequence 23452, A
589	6	2.0	143	4	US-09-252-991A-27046	Sequence 27046, A	662	6	2.0	161	4	US-09-252-991A-30023	Sequence 30023, A
590	6	2.0	143	4	US-09-252-991A-28392	Sequence 28392, A	663	6	2.0	161	4	US-09-198-452A-319	Sequence 319, App
591	6	2.0	143	4	US-09-252-991A-32985	Sequence 32985, A	664	6	2.0	161	4	US-09-489-039A-9917	Sequence 9917, Ap
592	6	2.0	144	4	US-09-252-991A-17046	Sequence 17046, A	665	6	2.0	161	4	US-09-513-999C-5070	Sequence 5070, Ap
593	6	2.0	144	4	US-09-252-991A-19305	Sequence 19305, A	666	6	2.0	162	4	US-09-252-991A-32101	Sequence 32101, A
594	6	2.0	144	4	US-09-270-767-48156	Sequence 48156, A	667	6	2.0	163	4	US-09-252-991A-17451	Sequence 17451, A
595	6	2.0	145	3	US-08-946-329A-55	Sequence 55, Appli	668	6	2.0	163	4	US-09-252-991A-22533	Sequence 22533, A
596	6	2.0	145	4	US-09-252-991A-21532	Sequence 21532, A	669	6	2.0	163	4	US-09-252-991A-27303	Sequence 27303, A
597	6	2.0	145	4	US-09-252-991A-25175	Sequence 25175, A	670	6	2.0	163	4	US-09-489-039A-9968	Sequence 9968, Ap
598	6	2.0	145	4	US-09-252-991A-31281	Sequence 31281, A	671	6	2.0	163	4	US-09-134-000C-3710	Sequence 3710, Ap
599	6	2.0	145	4	US-09-489-039A-10021	Sequence 10021, A	672	6	2.0	164	4	US-09-252-991A-16730	Sequence 16730, A
600	6	2.0	146	4	US-09-252-991A-23040	Sequence 23040, A	673	6	2.0	164	4	US-09-198-452A-427	Sequence 427, App
601	6	2.0	146	4	US-09-489-039A-7946	Sequence 7946, Ap	674	6	2.0	164	4	US-09-328-352-4685	Sequence 4685, Ap
602	6	2.0	147	3	US-08-065-844A-7	Sequence 7, Appli	675	6	2.0	164	4	US-09-270-767-59203	Sequence 59203, A
603	6	2.0	147	4	US-09-252-991A-28936	Sequence 28936, A	676	6	2.0	164	4	US-09-438-185A-410	Sequence 410, App
604	6	2.0	147	4	US-09-252-991A-29687	Sequence 29687, A	677	6	2.0	165	4	US-09-252-991A-24384	Sequence 24384, A
605	6	2.0	147	4	US-09-270-767-71829	Sequence 71829, A	678	6	2.0	165	4	US-09-248-796A-23180	Sequence 23180, A
606	6	2.0	147	4	US-09-270-767-47046	Sequence 47046, A	679	6	2.0	166	4	US-09-252-991A-27562	Sequence 27562, A
607	6	2.0	148	4	US-09-252-991A-26957	Sequence 26957, A	680	6	2.0	166	4	US-09-134-000C-3439	Sequence 3439, Ap
608	6	2.0	148	4	US-09-134-000C-37771	Sequence 37771, Ap	681	6	2.0	166	4	US-09-270-767-43161	Sequence 43161, A
609	6	2.0	149	4	US-09-252-991A-20244	Sequence 20244, A	682	6	2.0	166	4	US-09-270-767-45796	Sequence 45796, A
610	6	2.0	149	4	US-09-252-991A-22850	Sequence 22850, A	683	6	2.0	167	4	US-09-270-767-61415	Sequence 61415, A
611	6	2.0	149	4	US-09-270-767-34780	Sequence 34780, A	684	6	2.0	167	4	US-09-252-991A-17526	Sequence 17526, A

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686	6	2.0	168	4	US-09-252-991A-21273	Sequence 21273, A	759	6	2.0	190	4	US-09-252-991A-17851	Sequence 17851, A
687	6	2.0	168	4	US-09-252-991A-23198	Sequence 23198, A	760	6	2.0	190	4	US-09-252-991A-22679	Sequence 22679, A
688	6	2.0	168	4	US-09-252-991A-24947	Sequence 24947, A	761	6	2.0	190	4	US-09-252-991A-23624	Sequence 23624, A
689	6	2.0	168	4	US-09-252-991A-28064	Sequence 28064, A	762	6	2.0	190	4	US-09-270-767-33332	Sequence 33332, A
690	6	2.0	168	4	US-09-248-796A-20339	Sequence 20339, A	763	6	2.0	190	4	US-09-270-767-48549	Sequence 48549, A
691	6	2.0	168	4	US-09-902-540-12003	Sequence 12003, A	764	6	2.0	190	4	US-09-270-767-61626	Sequence 61626, A
692	6	2.0	168	4	US-09-252-991A-22544	Sequence 22544, A	765	6	2.0	190	4	US-09-107-433-4319	Sequence 4319, Ap
693	6	2.0	169	4	US-09-252-991A-25405	Sequence 25405, A	766	6	2.0	191	4	US-09-252-991A-19244	Sequence 19244, A
694	6	2.0	170	4	US-09-252-991A-19980	Sequence 19980, A	767	6	2.0	191	4	US-09-252-991A-19742	Sequence 19742, A
695	6	2.0	170	4	US-09-252-991A-29047	Sequence 29047, A	768	6	2.0	191	4	US-09-252-991A-24515	Sequence 24515, A
696	6	2.0	171	4	US-09-489-039A-8235	Sequence 8235, Ap	769	6	2.0	191	4	US-09-248-796A-24047	Sequence 24047, A
697	6	2.0	172	4	US-09-328-352-7411	Sequence 7411, Ap	770	6	2.0	192	4	US-09-540-236-3681	Sequence 3681, Ap
698	6	2.0	173	4	US-09-252-991A-18184	Sequence 18184, A	771	6	2.0	193	4	US-09-252-991A-23470	Sequence 23470, A
699	6	2.0	173	4	US-09-252-991A-22700	Sequence 22700, A	772	6	2.0	194	4	US-09-270-767-39426	Sequence 39426, A
700	6	2.0	173	4	US-09-252-991A-25439	Sequence 25439, A	773	6	2.0	194	4	US-09-270-767-54643	Sequence 54643, A
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702	6	2.0	173	4	US-09-328-352-7655	Sequence 7655, Ap	775	6	2.0	195	1	US-08-336-427-4	Sequence 4, Appl1
703	6	2.0	174	4	US-09-489-039A-8647	Sequence 8647, Ap	776	6	2.0	195	4	US-09-340-620A-49	Sequence 49, Appl
704	6	2.0	175	2	US-08-408-095-8	Sequence 8, Appl1	777	6	2.0	195	4	US-09-252-991A-30009	Sequence 30009, A
705	6	2.0	175	2	US-08-408-095-9	Sequence 9, Appl1	778	6	2.0	195	4	US-09-252-991A-30193	Sequence 30193, A
706	6	2.0	175	2	US-08-408-095-10	Sequence 10, Appl	779	6	2.0	195	4	US-09-270-767-41580	Sequence 41580, A
707	6	2.0	175	2	US-08-408-095-11	Sequence 11, Appl	780	6	2.0	195	4	US-09-841-879B-5	Sequence 5, Appl1
708	6	2.0	175	2	US-08-408-095-12	Sequence 12, Appl	781	6	2.0	196	4	US-09-252-991A-26457	Sequence 26457, A
709	6	2.0	175	2	US-08-408-095-14	Sequence 14, Appl	782	6	2.0	196	4	US-09-489-039A-9788	Sequence 9788, Ap
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712	6	2.0	175	4	US-09-710-379-1336	Sequence 1336, Ap	785	6	2.0	197	4	US-09-252-991A-33294	Sequence 33294, A
713	6	2.0	175	4	US-09-484-577A-54	Sequence 54, Appl	786	6	2.0	199	4	US-09-252-991A-13323	Sequence 13323, A
714	6	2.0	176	4	US-08-469-360A-51	Sequence 51, Appl	787	6	2.0	199	4	US-09-252-991A-22308	Sequence 22308, A
715	6	2.0	176	4	US-08-468-446-51	Sequence 51, Appl	788	6	2.0	199	4	US-09-252-991A-30363	Sequence 30363, A
716	6	2.0	176	4	US-08-467-344A-51	Sequence 51, Appl	789	6	2.0	199	4	US-09-252-991A-10326	Sequence 10326, A
717	6	2.0	176	4	US-08-424-550B-51	Sequence 51, Appl	790	6	2.0	199	4	US-09-949-016-10262	Sequence 10262, A
718	6	2.0	176	4	US-09-248-796A-23424	Sequence 23424, A	791	6	2.0	200	4	US-09-252-991A-20897	Sequence 20897, A
719	6	2.0	177	4	US-09-252-991A-21923	Sequence 21923, A	792	6	2.0	200	4	US-09-328-352-7205	Sequence 7205, Ap
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721	6	2.0	177	4	US-09-902-540-13376	Sequence 13376, A	794	6	2.0	201	4	US-09-252-991A-33202	Sequence 33202, A
722	6	2.0	178	4	US-09-252-991A-19068	Sequence 19068, A	795	6	2.0	201	4	US-09-248-796A-19314	Sequence 19314, A
723	6	2.0	178	4	US-09-252-991A-32482	Sequence 32482, A	796	6	2.0	202	4	US-09-252-991A-24790	Sequence 24790, A
724	6	2.0	178	4	US-09-252-991A-32741	Sequence 32741, A	797	6	2.0	202	4	US-09-710-279-11068	Sequence 11068, Ap
725	6	2.0	178	4	US-09-585-645A-19	Sequence 19, Appl	798	6	2.0	202	4	US-09-902-540-10636	Sequence 10636, A
726	6	2.0	179	3	US-08-483-533-33	Sequence 33, Appl	799	6	2.0	202	4	US-09-902-540-15190	Sequence 15190, A
727	6	2.0	179	3	US-09-283-471A-33	Sequence 33, Appl	800	6	2.0	203	3	US-09-299-041-8	Sequence 8, Appl1
728	6	2.0	179	4	US-09-270-767-32460	Sequence 32460, A	801	6	2.0	203	4	US-09-252-991A-20284	Sequence 20284, A
729	6	2.0	179	4	US-09-270-767-47677	Sequence 47677, A	802	6	2.0	203	4	US-09-252-991A-24035	Sequence 24035, A
730	6	2.0	180	4	US-09-252-991A-28297	Sequence 28297, A	803	6	2.0	203	4	US-09-252-991A-28879	Sequence 28879, A
731	6	2.0	181	4	US-09-252-991A-30481	Sequence 30481, A	804	6	2.0	203	4	US-09-543-681A-4741	Sequence 4741, Ap
732	6	2.0	181	4	US-09-328-352-7055	Sequence 7055, Ap	805	6	2.0	203	4	US-09-270-767-35326	Sequence 35326, A
733	6	2.0	181	4	US-09-489-039A-11004	Sequence 11004, A	806	6	2.0	203	4	US-09-270-767-30543	Sequence 30543, A
734	6	2.0	182	4	US-09-040-229B-4	Sequence 4, Appl1	807	6	2.0	204	4	US-09-252-991A-23103	Sequence 23103, A
735	6	2.0	182	4	US-09-252-991A-19696	Sequence 19696, A	808	6	2.0	204	4	US-09-252-991A-23105	Sequence 23105, A
736	6	2.0	182	4	US-09-252-991A-27971	Sequence 27971, A	809	6	2.0	204	4	US-09-489-039A-7474	Sequence 7474, Ap
737	6	2.0	182	4	US-09-252-991A-31478	Sequence 31478, A	810	6	2.0	205	4	US-09-252-991A-29378	Sequence 29378, A
738	6	2.0	182	4	US-09-543-681A-6272	Sequence 6272, Ap	811	6	2.0	205	4	US-09-270-767-43520	Sequence 43520, A
739	6	2.0	182	4	US-09-248-796A-17553	Sequence 17553, A	812	6	2.0	205	4	US-09-107-433-3118	Sequence 3118, Ap
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741	6	2.0	183	4	US-09-252-991A-22355	Sequence 22355, A	814	6	2.0	206	4	US-09-252-991A-26202	Sequence 26202, A
742	6	2.0	183	4	US-09-252-991A-32179	Sequence 32179, A	815	6	2.0	207	4	US-09-252-991A-33043	Sequence 33043, A
743	6	2.0	183	6	5168049-4	Patent No. 5168049	816	6	2.0	208	4	US-09-328-352-6009	Sequence 6009, Ap
744	6	2.0	183	6	5168049-4	Patent No. 5168049	817	6	2.0	208	4	US-09-134-000C-3698	Sequence 3698, Ap
745	6	2.0	184	3	US-08-759-628-10	Sequence 10, Appl	818	6	2.0	208	4	US-09-710-279-1084	Sequence 1084, Ap
746	6	2.0	184	4	US-09-252-991A-17955	Sequence 17955, A	819	6	2.0	208	4	US-09-949-016-7529	Sequence 7529, Ap
747	6	2.0	184	4	US-09-252-991A-20944	Sequence 20944, A	820	6	2.0	209	4	US-09-252-991A-16676	Sequence 16676, A
748	6	2.0	185	3	US-09-218-363-15	Sequence 15, Appl	821	6	2.0	209	4	US-09-248-796A-16078	Sequence 16078, A
749	6	2.0	185	4	US-09-252-991A-20685	Sequence 20685, A	822	6	2.0	209	4	US-09-248-796A-19096	Sequence 19096, A
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752	6	2.0	186	4	US-09-252-991A-27151	Sequence 27151, A	825	6	2.0	211	2	US-08-164-292B-2	Sequence 2, Appl1
753	6	2.0	186	4	US-09-252-991A-28295	Sequence 28295, A	826	6	2.0	211	2	US-08-708-958-2	Sequence 2, Appl1
754	6	2.0	186	4	US-09-489-039A-11500	Sequence 11500, A	827	6	2.0	211	3	US-08-845-623-2	Sequence 2, Appl1
755	6	2.0	187	4	US-09-252-991A-18467	Sequence 18467, A	828	6	2.0	211	3	US-08-815-937-2	Sequence 2, Appl1
756	6	2.0	187	4	US-09-252-991A-21931	Sequence 21931, A	829	6	2.0	211	3	US-09-103-330-2	Sequence 2, Appl1
757	6	2.0	187	4	US-09-248-796A-16116	Sequence 16116, A	830	6	2.0	211	3	US-09-435-243-2	Sequence 2, Appl1

831	6	2.0	211	3	US-09-323-872A-12	Sequence 12, Appl	904	6	2.0	233	2	US-08-458-568A-4	Sequence 4, Appl
832	6	2.0	211	4	US-09-252-991A-24927	Sequence 24927, A	905	6	2.0	233	3	US-08-871-572B-8	Sequence 8, Appl
833	6	2.0	211	4	US-09-252-991A-26393	Sequence 26393, A	906	6	2.0	233	4	US-09-252-991A-22617	Sequence 22617, A
834	6	2.0	211	4	US-09-072-433-21	Sequence 21, Appl	907	6	2.0	233	4	US-09-252-991A-25021	Sequence 25021, A
835	6	2.0	211	4	US-09-394-142B-4	Sequence 14, Appl	908	6	2.0	233	4	US-09-252-991A-25339	Sequence 25339, A
836	6	2.0	211	4	US-09-949-016-11438	Sequence 11438, A	909	6	2.0	233	4	US-09-902-540-11845	Sequence 11845, A
837	6	2.0	211	4	US-09-902-540-15438	Sequence 15438, A	910	6	2.0	233	4	US-09-902-540-16165	Sequence 16165, A
838	6	2.0	212	4	US-09-252-991A-24512	Sequence 24512, A	911	6	2.0	233	3	US-09-199-637A-61	Sequence 61, Appl
839	6	2.0	212	4	US-09-252-991A-11401	Sequence 31401, A	912	6	2.0	234	4	US-09-252-991A-29466	Sequence 29466, A
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841	6	2.0	212	4	US-09-248-796A-15317	Sequence 15317, A	914	6	2.0	235	4	US-09-252-991A-31578	Sequence 31578, A
842	6	2.0	213	4	US-09-252-991A-24240	Sequence 24240, A	915	6	2.0	235	4	US-09-198-452A-930	Sequence 930, App
843	6	2.0	213	4	US-09-252-991A-27051	Sequence 27051, A	916	6	2.0	236	3	US-09-230-156A-22	Sequence 22, Appl
844	6	2.0	213	4	US-09-248-796A-26548	Sequence 26548, A	917	6	2.0	236	4	US-09-252-991A-26334	Sequence 26334, A
845	6	2.0	214	4	US-09-252-991A-19407	Sequence 19407, A	918	6	2.0	236	4	US-09-252-991A-26346	Sequence 26346, A
846	6	2.0	214	4	US-09-252-991A-24368	Sequence 24368, A	919	6	2.0	237	1	US-08-910-973-13	Sequence 13, Appl
847	6	2.0	214	4	US-09-252-991A-25326	Sequence 25326, A	920	6	2.0	237	4	US-09-499-227-13	Sequence 13, Appl
848	6	2.0	214	4	US-08-722-570-2	Sequence 2, Appl	921	6	2.0	237	4	US-09-252-991A-17927	Sequence 17927, A
849	6	2.0	214	4	US-08-932-411A-2	Sequence 2, Appl	922	6	2.0	237	4	US-09-252-991A-32341	Sequence 32341, A
850	6	2.0	214	4	US-09-758-282B-19	Sequence 19, Appl	923	6	2.0	238	4	US-09-140-749-51	Sequence 51, Appl
851	6	2.0	214	4	US-09-758-282B-10	Sequence 20, Appl	924	6	2.0	238	4	US-09-270-767-43802	Sequence 43802, A
852	6	2.0	214	4	US-09-577-304A-19	Sequence 19, Appl	925	6	2.0	239	4	US-09-252-991A-25700	Sequence 25700, A
853	6	2.0	214	4	US-09-577-304A-20	Sequence 20, Appl	926	6	2.0	239	4	US-09-438-185A-866	Sequence 866, App
854	6	2.0	215	4	US-09-252-991A-23297	Sequence 23297, A	927	6	2.0	240	4	US-09-252-991A-16592	Sequence 16592, A
855	6	2.0	215	4	US-09-949-016-9485	Sequence 9485, Ap	928	6	2.0	240	4	US-09-252-991A-22559	Sequence 22559, A
856	6	2.0	216	4	US-09-252-991A-18666	Sequence 18666, A	929	6	2.0	240	4	US-09-252-991A-23507	Sequence 23507, A
857	6	2.0	216	4	US-09-252-991A-33048	Sequence 33048, A	930	6	2.0	240	4	US-09-583-110-2970	Sequence 2970, Ap
858	6	2.0	216	4	US-09-489-039A-7265	Sequence 7265, Ap	931	6	2.0	241	4	US-09-252-991A-21735	Sequence 21735, A
859	6	2.0	217	4	US-09-252-991A-30942	Sequence 30942, A	932	6	2.0	241	4	US-09-252-991A-32554	Sequence 32554, A
860	6	2.0	217	4	US-09-369-247-113	Sequence 113, App	933	6	2.0	241	4	US-09-640-211A-753	Sequence 753, App
861	6	2.0	217	4	US-09-270-767-45127	Sequence 45127, A	934	6	2.0	242	4	US-09-252-991A-19021	Sequence 19021, A
862	6	2.0	217	4	US-09-484-577A-37	Sequence 37, Appl	935	6	2.0	242	4	US-09-252-991A-21615	Sequence 21615, A
863	6	2.0	217	4	US-09-902-540-11063	Sequence 12063, A	936	6	2.0	242	4	US-09-583-110-4354	Sequence 4354, Ap
864	6	2.0	218	4	US-09-252-991A-22136	Sequence 22136, A	937	6	2.0	242	4	US-09-248-796A-16872	Sequence 16872, A
865	6	2.0	218	4	US-09-252-991A-25922	Sequence 25922, A	938	6	2.0	242	4	US-09-107-433-4338	Sequence 4338, Ap
866	6	2.0	218	4	US-09-252-991A-35922	Sequence 35922, A	939	6	2.0	243	4	US-09-252-991A-30374	Sequence 30374, A
867	6	2.0	218	4	US-09-602-787A-566	Sequence 566, App	940	6	2.0	243	4	US-09-489-039A-8634	Sequence 8468, Ap
868	6	2.0	219	3	US-09-134-001C-4581	Sequence 4581, Ap	941	6	2.0	243	4	US-09-902-540-16197	Sequence 16197, A
869	6	2.0	219	4	US-09-252-991A-28209	Sequence 28209, A	942	6	2.0	244	1	US-08-910-973-33	Sequence 22, Appl
870	6	2.0	219	4	US-09-270-767-44585	Sequence 44585, A	943	6	2.0	244	4	US-09-499-227-22	Sequence 22, Appl
871	6	2.0	220	4	US-09-252-991A-28993	Sequence 28993, A	944	6	2.0	244	4	US-09-252-991A-32454	Sequence 32454, A
872	6	2.0	221	4	US-09-252-991A-27841	Sequence 27841, A	945	6	2.0	244	4	US-08-722-570-1	Sequence 1, Appl
873	6	2.0	221	4	US-09-252-991A-31566	Sequence 31566, A	946	6	2.0	244	4	US-09-328-352-5597	Sequence 5597, Ap
874	6	2.0	221	4	US-09-252-991A-32684	Sequence 32684, A	947	6	2.0	244	4	US-08-932-411A-1	Sequence 1, Appl
875	6	2.0	222	4	US-09-252-991A-32198	Sequence 32198, A	948	6	2.0	244	4	US-08-932-411A-14	Sequence 14, Appl
876	6	2.0	222	4	US-09-489-039A-7232	Sequence 7232, Ap	949	6	2.0	245	3	US-08-483-533-42	Sequence 42, Appl
877	6	2.0	223	3	US-08-857-534-12	Sequence 12, Appl	950	6	2.0	245	3	US-09-283-471A-42	Sequence 42, Appl
878	6	2.0	223	3	US-09-206-676C-1	Sequence 1, Appl	951	6	2.0	245	4	US-08-465-260A-39	Sequence 39, Appl
879	6	2.0	223	4	US-09-252-991A-23081	Sequence 23081, A	952	6	2.0	245	4	US-09-252-991A-26027	Sequence 26027, A
880	6	2.0	223	4	US-09-613-298-12	Sequence 12, Appl	953	6	2.0	245	4	US-08-488-446-39	Sequence 39, Appl
881	6	2.0	223	4	US-09-902-540-14920	Sequence 14920, A	954	6	2.0	245	4	US-08-467-344A-39	Sequence 39, Appl
882	6	2.0	223	5	PCT-US95-04971-12	Sequence 12, Appl	955	6	2.0	245	4	US-09-270-767-33751	Sequence 33751, A
883	6	2.0	224	4	US-09-602-787A-556	Sequence 556, App	956	6	2.0	245	4	US-09-270-767-48968	Sequence 48968, A
884	6	2.0	224	4	US-09-270-767-44784	Sequence 44784, A	957	6	2.0	245	4	US-08-424-550B-39	Sequence 39, Appl
885	6	2.0	224	4	US-09-949-016-11101	Sequence 11101, A	958	6	2.0	246	4	US-09-252-991A-16586	Sequence 16586, A
886	6	2.0	224	4	US-09-902-540-12540	Sequence 12540, A	959	6	2.0	246	4	US-09-583-110-4242	Sequence 4242, Ap
887	6	2.0	225	4	US-09-252-991A-21601	Sequence 21601, A	960	6	2.0	247	2	US-08-851-974-1	Sequence 1, Appl
888	6	2.0	225	4	US-09-252-991A-24245	Sequence 24245, A	961	6	2.0	247	2	US-08-851-974-4	Sequence 4, Appl
889	6	2.0	225	4	US-09-252-991A-25503	Sequence 25503, A	962	6	2.0	247	2	US-09-213-350-1	Sequence 1, Appl
890	6	2.0	225	4	US-09-902-540-12361	Sequence 12361, A	963	6	2.0	247	3	US-09-213-350-4	Sequence 4, Appl
891	6	2.0	225	4	US-09-902-540-12694	Sequence 12694, A	964	6	2.0	247	3	US-08-961-083-170	Sequence 170, App
892	6	2.0	226	3	US-09-206-676C-2	Sequence 2, Appl	965	6	2.0	247	4	US-09-252-991A-23672	Sequence 23672, A
893	6	2.0	226	4	US-09-252-991A-30602	Sequence 30602, A	966	6	2.0	247	4	US-09-536-784A-170	Sequence 170, App
894	6	2.0	226	4	US-09-270-767-44368	Sequence 44368, A	967	6	2.0	247	4	US-09-944-016-6457	Sequence 6457, Ap
895	6	2.0	226	4	US-09-248-796A-14964	Sequence 14964, A	968	6	2.0	247	4	US-09-902-540-10732	Sequence 10732, A
896	6	2.0	227	4	US-09-543-681A-7769	Sequence 7769, Ap	969	6	2.0	248	4	US-09-452-239-6	Sequence 6, Appl
897	6	2.0	228	4	US-09-438-185A-131	Sequence 131, App	970	6	2.0	248	4	US-09-252-991A-20899	Sequence 20899, A
898	6	2.0	229	4	US-09-252-991A-29511	Sequence 29511, A	971	6	2.0	248	4	US-09-252-991A-30100	Sequence 30100, A
899	6	2.0	229	4	US-09-248-796A-28098	Sequence 28098, A	972	6	2.0	248	4	US-09-602-787A-90	Sequence 90, Appl
900	6	2.0	230	4	US-09-252-991A-33122	Sequence 33122, A	973	6	2.0	248	4	US-09-270-767-43329	Sequence 43329, A
901	6	2.0	230	4	US-09-489-039A-12375	Sequence 12375, A	974	6	2.0	248	4	US-09-248-796A-16880	Sequence 16880, A
902	6	2.0	231	4	US-09-252-991A-27366	Sequence 27366, A	975	6	2.0	248	4	US-09-248-796A-19941	Sequence 19941, A
903	6	2.0	231	4	US-09-198-452A-207	Sequence 207, App	976	6	2.0	248	4	US-09-902-540-12538	Sequence 12538, A

TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-859-167-6

Query Match 4.3%; Score 13; DB 3; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCDIRLRVRAEYC 207
|||||
DB 192 TCDIRLRVRAEYC 204

RESULT 4

US-09-109-273-4
Sequence 4, Application US/09109273
Patent No. 6063760
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760rls
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,273
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,167
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TTU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-109-273-4

Query Match 4.3%; Score 13; DB 3; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCDIRLRVRAEYC 207
|||||
DB 192 TCDIRLRVRAEYC 204

RESULT 5

US-09-109-273-6
Sequence 6, Application US/09109273
Patent No. 6063760
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6063760rls
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/109,273
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,167
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TTU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-109-273-6

Query Match 4.3%; Score 13; DB 3; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCDIRLRVRAEYC 207
|||||
DB 192 TCDIRLRVRAEYC 204

RESULT 6

US-09-276-993-4
Sequence 4, Application US/09276993
Patent No. 6207801
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: FADD-LIKE ANTI-APOPTOTIC MOLECULES, METHODS OF
TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801rls
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

Query Match 4.3%; Score 13; DB 3; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCDIRLRVRAEYC 207
|||||
DB 192 TCDIRLRVRAEYC 204


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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/276,993
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,167
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-276-993-4

Query Match      4.3%; Score 13; DB 3; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      195 TCDIRLRVRAEYC 207
DB      192 TCDIRLRVRAEYC 204

RESULT 7
US-09-276-993-6
; Sequence 6, Application US/09276993
; Patent No. 6207801
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: FADD-Like Anti-Apoptotic Molecules, Methods Of
; TITLE OF INVENTION: USING THE SAME, AND COMPOSITIONS FOR AND METHODS
; TITLE OF INVENTION: OF MAKING THE SAME
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6207801rls
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/276,993
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,167
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-276-993-6

Query Match      4.3%; Score 13; DB 3; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      195 TCDIRLRVRAEYC 207
DB      192 TCDIRLRVRAEYC 204

RESULT 8
US-09-723-450-4
; Sequence 4, Application US/09723450
; Patent No. 6576751
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: Fadd-Like Anti-Apoptotic Molecules, Methods Of Using The Same, An
; TITLE OF INVENTION: Compositions For And Methods Of Making The Same
; FILE REFERENCE: TJU2445
; CURRENT APPLICATION NUMBER: US/09/723,450
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/276,993
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/859,167
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: No. 6576751el Sequence
; US-09-723-450-4

Query Match      4.3%; Score 13; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      195 TCDIRLRVRAEYC 207
DB      192 TCDIRLRVRAEYC 204

RESULT 9
US-09-723-450-6
; Sequence 6, Application US/09723450
; Patent No. 6576751
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: Fadd-Like Anti-Apoptotic Molecules, Methods Of Using The Same, An
; TITLE OF INVENTION: Compositions For And Methods Of Making The Same
; FILE REFERENCE: TJU2445
; CURRENT APPLICATION NUMBER: US/09/723,450
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/276,993
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/859,167
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Artificial Sequence
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FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: No. 6576751el Sequence
US-09-723-450-6

Query Match 4.3%; Score 13; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCDIRLRVRAEYC 207
Db 192 TCDIRLRVRAEYC 204

RESULT 10
US-09-733-167A-1
Sequence 1, Application US/09733167A
Patent No. 6696547
GENERAL INFORMATION:
APPLICANT: Peter, Marcus
TITLE OF INVENTION: Protein for Regulation of Apoptosis
FILE REFERENCE: 4121-120
CURRENT APPLICATION NUMBER: US/09/733,167A
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: PCT/DE99/01712
PRIOR FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: German Patent Application No. 6696547 198 25 621.3
PRIOR FILING DATE: 1998-06-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 318
TYPE: PRT
ORGANISM: Homo sapiens
US-09-733-167A-1

Query Match 4.3%; Score 13; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCDIRLRVRAEYC 207
Db 192 TCDIRLRVRAEYC 204

RESULT 11
US-09-733-167A-3
Sequence 3, Application US/09733167A
Patent No. 6696547
GENERAL INFORMATION:
APPLICANT: Peter, Marcus
APPLICANT: Kramer, Peter
TITLE OF INVENTION: Protein for Regulation of Apoptosis
FILE REFERENCE: 4121-120
CURRENT APPLICATION NUMBER: US/09/733,167A
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: PCT/DE99/01712
PRIOR FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: German Patent Application No. 6696547 198 25 621.3
PRIOR FILING DATE: 1998-06-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 318
TYPE: PRT
ORGANISM: Mus musculus
US-09-733-167A-3

Query Match 4.3%; Score 13; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 TCDIRLRVRAEYC 207
Db 192 TCDIRLRVRAEYC 204

RESULT 12
US-09-252-991A-30543
Sequence 30543, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30543
LENGTH: 91
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30543

Query Match 3.0%; Score 9; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 RRRRGAPA 177
Db 5 RRRRGAPA 13

RESULT 13
US-09-602-777A-230
Sequence 230, Application US/09602777A
Patent No. 6831165
GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Krogger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Habenhauer, Gregor
TITLE OF INVENTION: CORYNBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
FILE REFERENCE: BGI-128CP
CURRENT APPLICATION NUMBER: US/09/602,777A
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: DE 19931636.8
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932125.6
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932126.4
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932127.2
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932128.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932129.9
PRIOR FILING DATE: 1999-07-19
PRIOR APPLICATION NUMBER: DE 19932226.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932920.6
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19932922.2
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19932924.9
PRIOR FILING DATE: 1999-07-14


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; PRIOR APPLICATION NUMBER: DE 19932928.1
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932930.3
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932933.8
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932935.4
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932973.7
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933002.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933003.4
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941390.8
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941391.6
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 230
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-602-777A-230

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Query Match          3.0%; Score 9; DB 4; Length 336;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      282 EALREAVGR 290
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        58 EALREAVGR 66

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RESULT 14
US-09-252-991A-18973
; Sequence 18973, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18973
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18973

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Query Match          3.0%; Score 9; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      171 RRGAPAP 179
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        119 RRGAPAP 127

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RESULT 15
US-09-252-991A-25124
; Sequence 25124, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25124
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25124

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Query Match          3.0%; Score 9; DB 4; Length 386;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      167 GARRRRRGA 175
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        171 GARRRRRGA 179

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Search completed: February 12, 2005, 16:39:45
Job time : 35 secs

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A:Cross-references: EMBL:X15423; NID:G6897; PIDN:CAA33463.1; PID:G6898
A:Experimental source: var. Bristol
R:Benian, G.M.; Kiffe, J.E.; Neckelmann, N.; Moerman, D.G.; Waterston, R.H.
Nature 342, 43-50, 1969
A:Title: Sequence of an unusually large protein implicated in regulation of myosin activity
A:Reference number: S06797; MUID:90044042; PMID:2812002
A:Accession: S06797
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 806-1175,1178-1998, 'Y', 2000-3040, 'I', 3042-3335, 'I', 3337-5693,5696-6359, 'I', 6
A:Cross-references: EMBL:X15423
A:Experimental source: var. Bristol
R:Benian, G.M.; L'Hernault, S.W.; Morris, M.E.
Genetics 134, 1097-1104, 1993
A:Title: Additional sequence complexity in the muscle gene, unc-22, and its encoded protein
A:Reference number: S57218; MUID:93387664; PMID:8397135
A:Accession: S57218
A:Molecule type: DNA
A:Residues: 2-99,108-194, 'Q', 196-206,374-468,658-753 <BEN4>
A:Experimental source: var. Bristol
R:White, S.
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A:Reference number: Z20442
A:Accession: T27934
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 'MGIPGKKCKQ', 19-6839 <W1>
A:Cross-references: EMBL:Z73897; PIDN:CAA98064.1; GSPDB:GN00022; CESP:ZK617.1a
A:Experimental source: clone ZK617
R:Haris, B.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z20458
A:Accession: T28030
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 'MGIPGKKCKQ', 19-6839 <W12>
A:Cross-references: EMBL:Z73899; PIDN:CAA98081.1; GSPDB:GN00022; CESP:ZK617.1a
A:Experimental source: clone ZK829
C:Comment: Lack of unc-22 leads to a constant twitching of the body muscles.
C:Genetics:
A:Gene: unc-22; CESP:ZK617.1a
A:Map position: 4
A:Introns: 18/3; 69/3; 143/2; 176/3; 264/2; 387/3; 413/2; 471/1; 516/3; 550/3; 582/3; 60
152/3; 6691/3; 6776/1; 6808/3
C:Superfamily: ATP; fibronectin type III repeat homology; immunoglobulin homology;
C:Keywords: ATP; autophosphorylation; duplication; muscle; phosphotransferase; serine/th
R:806-899,899-990,991-1083,1084-1175,1178-1273,1474-1567,1770-1864,2065-2158,2258-2450,2
96-5790,6263-6356,6386-6478,6541-6635,6649-6742,6745-6838/Region: motif 2 2259-2357,2451-2
F,1274-1372,1373-1473,1568-1670,1671-1769,1865-1964,1965-2065,2159-2258,2259-2357,2451-2
F,2425-4313,4314-4415,4416-4516,4612-4710,4711-4811,4908-5009,5010-5109,5110-5210,5399-
F,5940-6197/Domain: protein kinase homology <KIN>
F,5948-5956/Region: protein kinase ATP-binding motif
F,5971/Active site: Lys #status predicted

Query Match 6.8%; Score 106; DB 2; Length 6839;
Best Local Similarity 22.9%; Pred. No. 25;
Matches 72; Conservative 37; Mismatches 131; Indels 74; Gaps 13;

QY 4 SSGTAPPCWEEDECDIYGMISLHMFEEVVGQLTCELELLAFLIDEAPGAGGLARAR 63
DB 136 SASITPVAKMKMDGVPLSMGGL-YHAIFSDLDQTYLCOLEI-----RGPSSSDA-GQYR 187
QY 64 SGLLELLLELRGGCGESNLRLLGQLRLVLAHDDLPHLARKR-----RRPV 110
DB 188 CNI-----RNDGFTN-----ANLALNFEEDPSEERQERKRSTASPRSSRGPSRPS 235
QY 111 SPERYSTGTSSSKRT-----EGSCRR--RRSSSSANSQOGWETG-----S 151
DB 236 SPKSKMKREGPTKTLKREGSPSKLRSRTSTPVNEEVSQESRSRSTDKMEVDQVS 295
QY 152 PPTKQRRSRGSPSGARRRRGAPR--AFQOQSEPARPSSEKVTCDIRLRYAEXCE 208
DB 296 GASKRKPGLDLPFGDEKTLRAGSPSTRKSPRSKASPTPSRKGSSAGAGAGTTGASAS 355

QY 209 HGPALEQGVAS-----RRPOLAROLDVFGQATAVLRSDGVCIDIKFSELSYL 259
DB 356 ATSATSGSASSDASRDKYTRPPIVL-----EASRSQTRGIRGGSVLEVQWCHSST 407
QY 260 DAFWGDYLSGALLQ 273
DB 408 IIEW--YRDGTLVR 419

RESULT 8
127935
hypothetical protein ZK617.1b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27935; T28031
R:White, S.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z20442
A:Accession: T27935
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7160 <W1>
A:Cross-references: UNIPROT:Q23551; EMBL:Z73897; PIDN:CAA98065.1; GSPDB:GN00022; CESP:ZK
R:Haris, B.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z20458
A:Accession: T28031
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7160 <W12>
A:Cross-references: EMBL:Z73899; PIDN:CAA98082.1; GSPDB:GN00022; CESP:ZK617.1b
A:Experimental source: clone ZK829
C:Genetics:
A:Gene: CESP:ZK617.1b
A:Map position: 4
A:Introns: 10/3; 61/3; 135/2; 168/3; 256/2; 379/3; 405/2; 463/1; 508/3; 542/3; 574/3; 59
3067/1; 3141/3; 3269/1; 6473/3; 7012/3; 7097/1; 7129/3
C:Superfamily: twitchin; fibronectin type III repeat homology; immunoglobulin homology;

Query Match 6.8%; Score 106; DB 2; Length 7160;
Best Local Similarity 22.9%; Pred. No. 27;
Matches 72; Conservative 37; Mismatches 131; Indels 74; Gaps 13;

QY 4 SSGTAPPCWEEDECDIYGMISLHMFEEVVGQLTCELELLAFLIDEAPGAGGLARAR 63
DB 128 SASITPVAKMKMDGVPLSMGGL-YHAIFSDLDQTYLCOLEI-----RGPSSSDA-GQYR 179
QY 64 SGLLELLLELRGGCGESNLRLLGQLRLVLAHDDLPHLARKR-----RRPV 110
DB 180 CNI-----RNDGFTN-----ANLALNFEEDPSEERQERKRSTASPRSSRGPSRPS 227
QY 111 SPERYSTGTSSSKRT-----EGSCRR--RRSSSSANSQOGWETG-----S 151
DB 228 SPKSKMKREGPTKTLKREGSPSKLRSRTSTPVNEEVSQESRSRSTDKMEVDQVS 287
QY 152 PPTKQRRSRGSPSGARRRRGAPR--AFQOQSEPARPSSEKVTCDIRLRYAEXCE 208
DB 288 GASKRKPGLDLPFGDEKTLRAGSPSTRKSPRSKASPTPSRKGSSAGAGAGTTGASAS 347
QY 209 HGPALEQGVAS-----RRPOLAROLDVFGQATAVLRSDGVCIDIKFSELSYL 259
DB 348 ATSATSGSASSDASRDKYTRPPIVL-----EASRSQTRGIRGGSVLEVQWCHSST 399
QY 260 DAFWGDYLSGALLQ 273
DB 400 IIEW--YRDGTLVR 411

RESULT 9
T00062
hypothetical protein KIAA0434 - human (fragment)

C.Species: Homo sapiens (man)
C.Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C.Accession: T00062
R.Ishikawa, K.; Nagase, T.; Nakajima, D.; Seki, N.; Ohira, M.; Miyajima, N.; Tanaka, A.;
submitted to the EMBL Data Library, October 1997
A.Description: Prediction of the coding sequences of unidentified human genes. VIII. The
A.Reference number: Z14082
A.Accession: T00062
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-1571 <ISH>
A.Cross-references: UNIPROT:O43161; EMBL:AB007894; NID:G2662148; PIDN:BAA23707.1; PID:G2
A.Experimental source: brain; clone HH2165
C.Genetics:
A.Note: KIAA0434

Query Match 6.8%; Score 105.5; DB 2; Length 1571;
Best Local Similarity 24.5%; Pred. No. 6.3;
Matches 46; Conservative 25; Mismatches 70; Indels 47; Gaps 7;

QY 53 PGAGGLARARSGLELLELERRGCGESNLRLLGQ-----LLRVLAHDLPHLA 103
DB 1275 PHDEGGPGHNAKE-----HHGDHGRISGHTGEPRRAKPHAKDLGHEARPH-S 1328
QY 104 RKRPRPVSPERYSYGTSSSKRTGSCRRRRQSS--SANSQCGWETGSPPTKRQRRS 160
DB 1329 QPSSAPAMPKKGQPGYSSAEYSOPS---RASSAVHNASDKSGSRQAHSGPALQ--S 1382
QY 161 RRRPBGARRRRRCAPAAQQOSEPRAPRSEKVTCDILRVRAEYCEHGPALGQVARS 220
DB 1383 KAEPAQAPQOLGQRAAPGPGQSQSPS-----SRQIPSGAASR 1419
QY 221 RPOALARQ 228
DB 1420 QPQTQQQQ 1427

RESULT 10

T46359
hypothetical protein DKF2p434K1316.1 - human (fragment)
C.Species: Homo sapiens (man)
C.Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C.Accession: T46359
R.Kocher, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A.Reference number: Z23037
A.Accession: T46359
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-658 <AAA>
A.Cross-references: UNIPROT:Q9NTP9; EMBL:AL137291
A.Experimental source: adult testis; clone DKF2p434K1316
C.Genetics:
A.Note: DKF2p434K1316.1

Query Match 6.7%; Score 103.5; DB 2; Length 658;
Best Local Similarity 28.9%; Pred. No. 3.7;
Matches 59; Conservative 18; Mismatches 74; Indels 53; Gaps 10;

QY 59 LARARSGLELLELERRGQ-----CGESNLRLLGQLRVLAHDLPHLARRRRPVSP 113
DB 21 LEQVSSGLHRLRLQRFQQAHEWYDEGFARLAG--AGPGREAVLALALARR--APE 73
QY 114 RYSYGT-----SSSKRTGSCRRRRSSSANSQCGWETGSPPTKRQRRS 161
DB 74 P-SAGTPEPMALALDLSPPALRWGRQARQ--ELERRIQHLEENSPGVRRRRAD 131
QY 162 GRPSCGARRRRRG-----APAAQQOSEPAR-----PSSEGVTCIDILRVRAEYCE 208
DB 132 GASGGAQMGPRSPSPSLSSLLPSSPGPRAPASHCSLAPCE-----DYEE 178
QY 209 HGPALEQGVASRRPA-LARQUDV 231

DB 179 EGPRLAEPAGRRPPRAVLIRGLEV 202

RESULT 11

T09219
basal transcription factor SNAPc large chain SNAP190 - human
C.Species: Homo sapiens (man)
C.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 16-Aug-2004
C.Accession: T09219
R.Wong, M.W.; Henry, R.W.; Ma, B.; Kobayashi, R.; Klages, N.; Matchias, P.; Strublin, M.;
Wol, Cell. Biol. 18, 368-377, 1998
A>Title: The large subunit of basal transcription factor SNAPc is a Myb domain protein
A.Reference number: Z16616; MUID:98078693; PMID:9418884
A.Accession: T09219
A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA
A.Residues: 1-1469 <WON>
A.Cross-references: UNIPROT:Q9Y6P7; EMBL:AF032387; NID:G2641556; PIDN:AA02972.1; PID:G2
A.Experimental source: tissue type fetal cell teratocarcinoma
C.Genetics:
A.Gene: SNAP190

C.Function: transcription factor; required for transcription of snRNA genes
C.Superfamily: myb DNA-binding repeat homology
C.Keywords: DNA binding; RNA biosynthesis; transcription factor
F.396-447/Domain: myb DNA-binding repeat homology <MYB>

Query Match 6.7%; Score 103.5; DB 2; Length 1469;
Best Local Similarity 24.3%; Pred. No. 8.3;
Matches 59; Conservative 32; Mismatches 75; Indels 77; Gaps 12;

QY 50 DEAPAGGLARARSGLELLELERRGCGESNLRLLGQLRVLAHDL-----LP 100
DB 429 EEPGRSAQCRDRLRLRLHPSLK-----GRNLEBEOLLEILIKYGVGHAKTASELP 484
QY 101 H-----LARKRRPVSPERYSYGTSSSKRTGSCRRRRQSSSAN 141
DB 485 HRSGSQCLSKWKIMGKQGLRRRRRARHVSVRS--STSSGSSGSSGSSSSSSSS 542
QY 142 -----SQCGWENG--SP-----PTKRQRRSGRPGSGARRRRGAPAA--- 178
DB 543 EDEPEQAQAGEGDRALLSPYMPVMDMLWPA--RSTSQPMRGAGAWLGGPAASTLS 599
QY 179 PQOSEPARPSSB-----GKVTCDILRVRAEYCEHGPALGQVARS-----RQAL 225
DB 600 PPKSSASQGSKEASTTAAAPGETSFVQVPARA---HGPVRSQAQSHSADTRPAGA 655
QY 226 ARQ 228
DB 656 EKQ 658

RESULT 12

T02345
hypothetical protein KIAA0324 - human (fragment)

C.Species: Homo sapiens (man)
C.Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C.Accession: T02345

R.Ricke, D.O.; Bruce, D.; Mundt, M.; Doggett, N.; Munk, C.; Saunders, E.; Robinson, D.;
re, J.; White, S.; Ueng, S.; Tatum, O.; Campbell, C.; Fawcett, J.; Deaven, L.
submitted to the EMBL Data Library, March 1998
A.Description: Sequencing of human chromosome 16p13.3.
A.Reference number: Z14664

A.Accession: T02345
A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA
A.Residues: 1-1791 <RIC>

A.Cross-references: UNIPROT:O60382; EMBL:AC004493; NID:G2996648; PIDN:AA008453.1; PID:G2
C.Genetics:
A.Map position: 16
A.Introns: 1610/2; 1706/2
A.Note: KIAA0324

	Query Match	6.7%;	Score 103.5;	DB 2;	Length 1791;	
	Best Local Similarity	29.3%;	Pred. No. 10;			
	Matches	41;	Conservative	17;	Mismatches	59; Indels 23; Gaps 5;
Oy	100	PHLARKRR-----PVSPERYSYGTS-----SSSKRTGSCRRRROSSSANSQOQOMETG	150			
	:	:	:	:	:	:
Dd	983	PPVTRRRSRKPTPVTRRRSRSTSPITRRRSRSTSVTRRRRSRSTSPVTRRRSRST	1042			
Oy	151	SPPYTKQRGRSGRGCGARRRRGAPAPPOOSSEARPSBSGYTCIDRLVRAVCENG	210			
	:	:	:	:	:	:
Dd	1043	SPVTRRRRSRK--TPPAIRRRRSRSTPLPRRRSRSP-----LAIRRRSRST	1090			
Oy	211	PALEGVAS--RRPOLARQ	228			
	:	:	:	:	:	:
Dd	1091	PTARGKSLTRSPPAIRRR	1110			

RESULT 13

synapsin I splice form a - human
C:Species: Homo sapiens (man)
C:Date: 17-Aug-1990 #sequence_revision 17-Aug-1990 #text_change 09-Jul-2004
C:Accession: A35363; B35363; A35805
R:Stuehlf, T.C.
J Biol. Chem. 265, 7849-7852, 1990
A:Title: The structure of the human synapsin I gene and protein.
A:Reference number: A35363; MUID:90243651; PMID:2110562
A:Accession: A35363
A:Molecule type: DNA
A:Residues: 1-705 <SUE>
A:Cross-references: UNIPROT:P17600; GB:M58371; GB:J05431
A:Accession: B35363
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-659, 'KASPAQAQP' <SU2>
A:Cross-references: GB:M58378; GB:J05431
R:Saerwald, A.; Hoesehe, C.; Oeschwald, R.; Killmann, M.W.
J Biol. Chem. 265, 14932-14937, 1990
A:Title: The 5'-flanking region of the synapsin I gene. A G+C-rich, TATA- and CAAT-less
A:Reference number: A35805; MUID:90368667; PMID:2118519
A:Accession: A35805
A:Molecule type: DNA
A:Residues: 1-125 <SAU>
A:Cross-references: GB:M55301; NID:9338655; PIDD:AAA60608.1; PID:9553654; GB:J05630
C:Genetics:
A:Gene: GDB:SYN1
A:Cross-references: GDB:119606; OMIM:313440
A:Map position: Xp11.23-Xp11.23
C:Keywords: actin binding; alternative splicing; phosphoprotein

	Query Match	6.6%; Score 102.5; DB 2; Length 705;
	Best Local Similarity	23.7%; Pred. No. 4.7;
	Matches	57; Conservative 32; Mismatches 87; Indels 65; Gaps 10;
QY	31 EVVGGQLTECEHLLAFLLDEAPGAAGLARSGLLEELPERGQCCESLRLLG---	87
DB	362 ELFGG-LDICAVEAL-----HGKDGSDHILEVV-----GSMPILGDHQ	399
QY	88 ----OLLRVLAAHDLLPHLARRRRPVSPERYSYGTSS-----SKTEGSCRRR	133
DB	400 DEKDQIVELVNKKMAQALPRQRDASPGFSGHSQTSPSALPLGRQTSQQPAPPAQO	459
QY	134 ROSSSSANNGOOQWETGSPPTKRQ-----RARGPSGAGARRRRRGAR-AAAPQOOS	183
DB	460 RPPPOGPPROPBPGRGPPLQORPPPOGOHLISGLGPASPULFORLPSTSAPOQA	519
QY	184 EPARPSESEKVTCDIILRVRAEYCENHPALEGV---ASRRPOLA-----ROLDVFQG	234
DB	520 SQAAPRTQOGR-----QSRPVAGGPAPRAPAPAPSPSQRAGPQATRTQTSVSGP	572
QY	235 A 235	
DB	573 A 573	

RESULT 14

hypothetical 119.5K protein (uvra region) - Micrococcus luteus
N/Alternate names: ORF 1 protein
C/Species: Micrococcus luteus, Micrococcus lysodeikticus
C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 04-Feb-2000
C/Accession: J00405
R/Shiota, S.; Nakayama, H.
Mol. Gen. Genet. 217, 332-340, 1989
A/Title: Micrococcus luteus homolog of the Escherichia coli uvra gene: identification of
A/Reference number: S04781; MUID:89364717; PMID:2549377
A/Accession: J00405
A/Molecule type: DNA
A/Residues: 1-1106 <SH1>
A/Cross-references: EMBL:X15867
A/Note: this reading frame extends between two stop codons and does not begin with a start
A/Note: the gene encoding this protein overlaps uvra gene
C/Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;

[illegible]

RESULT 15

A:Accession: A55335
 A:Reference number: A55335; MUID:95074156; PMID:7527040
 A:Article: Isolation and characterization of MRF-1, a brain-derived DNA-binding protein with myelin regulatory factor 1 - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 03-Aug-1995
 C:Accession: A55335
 R:Haque, N.S.; Buchberg, A.M.; Khalil, K. J. Biol. Chem. 269, 31149-31156, 1994
 A:Title: Isolation and characterization of MRF-1, a brain-derived DNA-binding protein with myelin regulatory factor 1 - mouse (fragment)
 A:Accession: A55335
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-274 <HAO>
 A:Cross-references: GB:U14648
 A:Note: authors translated the codon CGC for residue 192 as Cys

```

Query Match 6.5%; Score 101.5; DB 2; Length 274;
Best Local Similarity 28.5%; Pred. No. 2.1;
Matches 39; Conservative 18; Mismatches 51; Indels 29; Gaps 6

QY 87 GQLLEY-LARDHLEPHLARKRRRPVSPERY---SYGTSSSKR-----TEGSCRRRRQGS 137
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 138 GHELVALQVLRVRRPDSHNRGPF-PPRRYGGGCGRRSSPPRPAALIAKPEWSRRKPPR 196
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 138 SSANSQGGWETGSGPPTKQRR-----SGRPGSGARRRRRGAPAPQGGSE-- 184
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db	197	YSRKSRSRTRSRSRSTSKSRARSKSKSSVSRSRSRSRSRSRSPPPVSKRESKSR	256
Qy	185	-----PARPSEKVT	195
Db	257	SRKSPPKSPREGEVS	273

Search completed: February 12, 2005, 16:30:28
Job time : 24 secs

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OM protein - protein search, using SW model

Run on: February 12, 2005, 16:38:00 ; Search time 15 Seconds
(without alignments)
755.515 Million cell updates/sec

Title: US-10-030-271-2
Perfect score: 303
Sequence: 1 MALSGSTPAFCWEDECLDY.....LREAVGRAVRLVSYDEAD 303

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 147297 seqs, 37401721 residues

Word size : 0

Total number of hits satisfying chosen parameters: 147297

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	2.6	439	6	US-10-450-763-51705 Sequence 51705, A
2	8	2.6	439	6	US-10-450-763-54383 Sequence 54383, A
3	8	2.6	712	6	US-10-450-763-30700 Sequence 30700, A
4	8	2.6	805	6	US-10-450-763-54385 Sequence 54385, A
5	8	2.6	1066	6	US-10-450-763-54384 Sequence 54384, A
6	8	2.6	1089	6	US-10-450-763-53691 Sequence 53691, A
7	8	2.6	1125	6	US-10-450-763-51707 Sequence 51707, A
8	8	2.6	1127	6	US-10-489-448-2732 Sequence 2732, Ap
9	8	2.6	1131	6	US-10-450-763-51706 Sequence 51706, A
10	8	2.6	1142	6	US-10-450-763-54386 Sequence 54386, A
11	8	2.6	1292	6	US-10-489-448-997 Sequence 997, App
12	8	2.6	1388	6	US-10-450-763-51703 Sequence 51703, A
13	7	2.3	33	6	US-10-699-562-21 Sequence 21, Appl
14	7	2.3	41	6	US-10-450-763-32943 Sequence 32943, A
15	7	2.3	64	6	US-10-450-763-52787 Sequence 52787, A
16	7	2.3	113	6	US-10-450-763-49753 Sequence 49753, A
17	7	2.3	122	7	US-11-031-175-10858 Sequence 10858, A
18	7	2.3	164	7	US-11-031-175-14156 Sequence 14156, A
19	7	2.3	164	7	US-11-031-175-15953 Sequence 15953, A
20	7	2.3	171	7	US-11-031-175-13213 Sequence 13213, A
21	7	2.3	225	7	US-11-027-399-3301 Sequence 3301, Ap
22	7	2.3	225	7	US-11-027-843-3301 Sequence 3301, Ap
23	7	2.3	225	7	US-11-027-878-3301 Sequence 3301, Ap
24	7	2.3	225	7	US-11-028-169-3301 Sequence 3301, Ap
25	7	2.3	225	7	US-11-028-204-3301 Sequence 3301, Ap

26	7	2.3	225	7	US-11-027-877-3301 Sequence 3301, Ap
27	7	2.3	225	7	US-11-027-879-3301 Sequence 3301, Ap
28	7	2.3	225	7	US-11-028-149-3301 Sequence 3301, Ap
29	7	2.3	225	7	US-11-027-802-3301 Sequence 3301, Ap
30	7	2.3	225	7	US-11-027-890-3301 Sequence 3301, Ap
31	7	2.3	225	7	US-11-027-892-3301 Sequence 3301, Ap
32	7	2.3	225	7	US-11-028-099-3301 Sequence 3301, Ap
33	7	2.3	225	7	US-11-028-197-3301 Sequence 3301, Ap
34	7	2.3	225	7	US-11-027-844-3301 Sequence 3301, Ap
35	7	2.3	225	7	US-11-028-050-3301 Sequence 3301, Ap
36	7	2.3	225	7	US-11-028-457-3301 Sequence 3301, Ap
37	7	2.3	225	7	US-11-027-891-3301 Sequence 3301, Ap
38	7	2.3	225	7	US-11-028-291-3301 Sequence 3301, Ap
39	7	2.3	225	7	US-11-028-458-3301 Sequence 3301, Ap
40	7	2.3	264	1	PCT-US04-17965-1054 Sequence 1054, Ap
41	7	2.3	264	1	PCT-US04-17965-2068 Sequence 2068, Ap
42	7	2.3	264	1	PCT-US04-17965-3604 Sequence 3604, Ap
43	7	2.3	294	8	US-60-643-717-7253 Sequence 7253, Ap
44	7	2.3	298	8	US-60-643-717-7823 Sequence 7823, Ap
45	7	2.3	300	7	US-11-031-175-14290 Sequence 14290, A
46	7	2.3	302	8	US-60-643-717-18643 Sequence 18643, A
47	7	2.3	355	7	US-11-031-175-15046 Sequence 15046, A
48	7	2.3	382	8	US-60-643-717-4153 Sequence 4153, Ap
49	7	2.3	382	8	US-60-643-717-14833 Sequence 14833, A
50	7	2.3	382	8	US-60-643-717-18949 Sequence 18949, A
51	7	2.3	386	8	US-60-643-717-12030 Sequence 12030, A
52	7	2.3	387	8	US-60-643-717-12515 Sequence 12515, A
53	7	2.3	403	7	US-11-031-175-11445 Sequence 11445, A
54	7	2.3	439	6	US-10-450-763-42544 Sequence 42544, A
55	7	2.3	505	6	US-10-450-763-34076 Sequence 34076, A
56	7	2.3	551	8	US-60-643-717-2548 Sequence 2548, Ap
57	7	2.3	551	8	US-60-643-717-6872 Sequence 6872, Ap
58	7	2.3	569	6	US-10-450-763-33216 Sequence 33216, A
59	7	2.3	574	6	US-10-450-763-33565 Sequence 33565, A
60	7	2.3	591	6	US-10-450-763-47629 Sequence 47629, A
61	7	2.3	602	8	US-60-643-717-11276 Sequence 11276, A
62	7	2.3	619	7	US-11-031-175-11405 Sequence 14059, A
63	7	2.3	684	6	US-10-450-763-44485 Sequence 44485, A
64	7	2.3	690	6	US-10-863-245A-2 Sequence 2, Appl1
65	7	2.3	690	6	US-10-863-245A-18 Sequence 18, Appl1
66	7	2.3	694	8	US-60-643-717-18622 Sequence 18622, A
67	7	2.3	710	6	US-10-450-763-50473 Sequence 50473, A
68	7	2.3	731	7	US-11-031-175-13763 Sequence 13763, A
69	7	2.3	731	8	US-60-643-717-12386 Sequence 12386, A
70	7	2.3	749	8	US-60-643-717-9435 Sequence 9435, Ap
71	7	2.3	752	6	US-10-450-763-58459 Sequence 58459, A
72	7	2.3	755	1	PCT-US04-17965-1405 Sequence 1405, Ap
73	7	2.3	775	8	US-60-643-717-5553 Sequence 5553, Ap
74	7	2.3	1035	6	US-10-450-763-35678 Sequence 35678, A
75	7	2.3	1037	7	US-11-031-175-9845 Sequence 9845, Ap
76	7	2.3	1099	7	US-11-033-545-5451 Sequence 5451, App
77	7	2.3	1100	7	US-11-033-545-344 Sequence 344, App
78	7	2.3	1524	6	US-10-450-763-60700 Sequence 60700, A
79	7	2.3	2108	8	US-60-643-717-5434 Sequence 5434, Ap
80	6	2.0	15	6	US-10-817-970-2016 Sequence 2016, Ap
81	6	2.0	19	6	US-10-699-562-11 Sequence 11, Appl1
82	6	2.0	22	6	US-10-699-562-9 Sequence 9, Appl1
83	6	2.0	28	6	US-10-450-763-49931 Sequence 49931, A
84	6	2.0	31	7	US-11-026-433-19 Sequence 19, Appl1
85	6	2.0	37	6	US-10-450-763-33582 Sequence 33582, A
86	6	2.0	40	7	US-11-042-241-236 Sequence 236, App
87	6	2.0	46	6	US-10-450-763-38359 Sequence 38359, A
88	6	2.0	50	6	US-10-450-763-44143 Sequence 44143, A
89	6	2.0	50	7	US-11-031-175-10534 Sequence 10534, A
90	6	2.0	54	6	US-10-699-562-22 Sequence 22, Appl1
91	6	2.0	54	6	US-10-450-763-47626 Sequence 47626, A
92	6	2.0	57	6	US-10-450-763-59101 Sequence 59101, A
93	6	2.0	62	6	US-10-450-763-55230 Sequence 55230, A
94	6	2.0	64	6	US-10-450-763-38358 Sequence 38358, A
95	6	2.0	65	6	US-10-450-763-35166 Sequence 35166, A
96	6	2.0	65	6	US-10-450-763-46258 Sequence 46258, A
97	6	2.0	65	6	US-10-450-763-54312 Sequence 54312, A
98	6	2.0	65	6	US-10-489-448-1889 Sequence 1889, A

99	6	2.0	US-10-450-763-50892	Sequence 50892, A	172	6	2.0	150	6	US-10-489-448-3360	Sequence 3360, Ap
100	6	2.0	US-10-450-763-56851	Sequence 56851, A	173	6	2.0	151	7	US-11-031-175-11681	Sequence 11681, A
101	6	2.0	US-11-031-175-13076	Sequence 13076, A	174	6	2.0	151	7	US-11-031-175-13473	Sequence 13473, A
102	6	2.0	US-10-450-763-54318	Sequence 54318, A	175	6	2.0	153	7	US-11-031-175-12154	Sequence 12154, A
103	6	2.0	US-11-031-643-42	Sequence 42, Ap1	176	6	2.0	155	1	PCT-US04-43356-135	Sequence 135, App
104	6	2.0	US-11-031-490-42	Sequence 42, Ap1	177	6	2.0	155	1	PCT-US04-43356-137	Sequence 137, App
105	6	2.0	US-10-450-763-56859	Sequence 56859, A	178	6	2.0	155	6	US-10-450-763-53914	Sequence 53914, A
106	6	2.0	US-10-450-763-49874	Sequence 49874, A	179	6	2.0	155	7	US-11-021-949-135	Sequence 135, App
107	6	2.0	US-10-450-763-46477	Sequence 46477, A	180	6	2.0	155	7	US-11-021-949-137	Sequence 137, App
108	6	2.0	US-11-031-175-15595	Sequence 15595, A	181	6	2.0	156	6	US-10-450-763-18290	Sequence 18290, Ap
109	6	2.0	PCT-US05-00040-7	Sequence 7, App1	182	6	2.0	156	8	US-60-643-717-4345	Sequence 4345, Ap
110	6	2.0	US-11-031-175-11751	Sequence 11751, A	183	6	2.0	158	8	US-60-643-717-6836	Sequence 6836, Ap
111	6	2.0	US-11-031-175-13717	Sequence 13717, A	184	6	2.0	159	7	US-11-031-175-10781	Sequence 10781, A
112	6	2.0	US-10-450-763-41733	Sequence 41733, A	185	6	2.0	160	6	US-10-450-763-44237	Sequence 44237, A
113	6	2.0	US-10-450-763-58648	Sequence 58648, A	186	6	2.0	160	7	US-11-031-175-12994	Sequence 12994, A
114	6	2.0	US-11-031-175-11177	Sequence 13177, A	187	6	2.0	160	7	US-11-031-175-15069	Sequence 15069, A
115	6	2.0	US-10-450-763-56812	Sequence 56812, A	188	6	2.0	164	6	US-10-450-763-30837	Sequence 30837, A
116	6	2.0	US-10-450-763-46990	Sequence 46990, A	189	6	2.0	164	6	US-10-489-448-2854	Sequence 2854, Ap
117	6	2.0	US-10-450-763-56868	Sequence 56868, A	190	6	2.0	165	6	US-10-450-763-53865	Sequence 53865, A
118	6	2.0	US-10-450-763-57565	Sequence 57565, A	191	6	2.0	168	7	US-11-031-175-12003	Sequence 12003, A
119	6	2.0	US-10-489-448-2863	Sequence 2863, Ap	192	6	2.0	168	8	US-60-643-717-6603	Sequence 6603, Ap
120	6	2.0	US-10-450-763-56849	Sequence 56849, A	193	6	2.0	168	8	US-60-643-717-6637	Sequence 6637, Ap
121	6	2.0	US-10-450-763-35724	Sequence 35724, A	194	6	2.0	170	6	US-10-450-763-54535	Sequence 54535, A
122	6	2.0	US-10-450-763-46475	Sequence 46475, A	195	6	2.0	175	6	US-60-643-717-10236	Sequence 10236, A
123	6	2.0	PCT-US04-43356-195	Sequence 46475, A	196	6	2.0	177	6	US-10-450-763-39793	Sequence 39793, A
124	6	2.0	PCT-US04-09510-1260	Sequence 195, App	197	6	2.0	177	7	US-11-031-175-13376	Sequence 13376, A
125	6	2.0	US-11-021-949-195	Sequence 1260, Ap	198	6	2.0	180	6	US-10-450-763-46969	Sequence 46969, A
126	6	2.0	PCT-US04-09510-1192	Sequence 1192, Ap	199	6	2.0	182	6	US-10-450-763-56901	Sequence 56901, A
127	6	2.0	PCT-US04-09510-1210	Sequence 1210, Ap	200	6	2.0	182	6	US-11-031-175-11219	Sequence 11219, A
128	6	2.0	PCT-US04-09510-1257	Sequence 1257, Ap	201	6	2.0	182	7	US-11-031-175-11219	Sequence 11219, A
129	6	2.0	PCT-US04-09510-1259	Sequence 1259, Ap	202	6	2.0	184	6	US-10-450-763-56222	Sequence 56222, A
130	6	2.0	PCT-US04-09510-1262	Sequence 1262, Ap	203	6	2.0	185	6	US-10-450-763-43248	Sequence 43248, A
131	6	2.0	US-10-450-763-56635	Sequence 56635, A	204	6	2.0	185	7	US-11-027-399-5249	Sequence 5249, Ap
132	6	2.0	US-10-489-448-3034	Sequence 3034, Ap	205	6	2.0	185	7	US-11-027-843-5249	Sequence 5249, Ap
133	6	2.0	US-11-031-175-12948	Sequence 12948, A	206	6	2.0	185	7	US-11-027-878-5249	Sequence 5249, Ap
134	6	2.0	US-10-450-763-59788	Sequence 59788, A	207	6	2.0	185	7	US-11-028-169-5249	Sequence 5249, Ap
135	6	2.0	US-10-450-763-45938	Sequence 45938, A	208	6	2.0	185	7	US-11-028-204-5249	Sequence 5249, Ap
136	6	2.0	US-11-031-175-16230	Sequence 16230, A	209	6	2.0	185	7	US-11-027-879-5249	Sequence 5249, Ap
137	6	2.0	US-10-450-763-56850	Sequence 56850, A	210	6	2.0	185	7	US-11-027-819-5249	Sequence 5249, Ap
138	6	2.0	US-10-450-763-56866	Sequence 56866, A	211	6	2.0	185	7	US-11-028-149-5249	Sequence 5249, Ap
139	6	2.0	US-10-489-448-1169	Sequence 1169, Ap	212	6	2.0	185	7	US-11-027-802-5249	Sequence 5249, Ap
140	6	2.0	US-10-450-763-56893	Sequence 56893, A	213	6	2.0	185	7	US-11-027-880-5249	Sequence 5249, Ap
141	6	2.0	US-10-450-763-30915	Sequence 30915, A	214	6	2.0	185	7	US-11-027-892-5249	Sequence 5249, Ap
142	6	2.0	US-10-450-763-33598	Sequence 33598, A	215	6	2.0	185	7	US-11-028-099-5249	Sequence 5249, Ap
143	6	2.0	US-10-450-763-48461	Sequence 48461, A	216	6	2.0	185	7	US-11-028-197-5249	Sequence 5249, Ap
144	6	2.0	US-10-450-763-4631	Sequence 4631, A	217	6	2.0	185	7	US-11-027-884-5249	Sequence 5249, Ap
145	6	2.0	US-10-450-763-31996	Sequence 31996, A	218	6	2.0	185	7	US-11-028-050-5249	Sequence 5249, Ap
146	6	2.0	US-10-450-763-32086	Sequence 32086, A	219	6	2.0	185	7	US-11-028-457-5249	Sequence 5249, Ap
147	6	2.0	US-10-450-763-50726	Sequence 50726, A	220	6	2.0	185	7	US-11-027-891-5249	Sequence 5249, Ap
148	6	2.0	US-10-450-763-47370	Sequence 47370, A	221	6	2.0	185	7	US-11-028-291-5249	Sequence 5249, Ap
149	6	2.0	US-11-031-175-10057	Sequence 10057, A	222	6	2.0	185	7	US-11-028-458-5249	Sequence 5249, Ap
150	6	2.0	US-10-450-763-56670	Sequence 56670, A	223	6	2.0	186	6	US-10-450-763-53866	Sequence 53866, A
151	6	2.0	US-10-450-763-56886	Sequence 56886, A	224	6	2.0	186	6	US-10-450-763-38643	Sequence 38643, A
152	6	2.0	US-10-450-763-56847	Sequence 56847, A	225	6	2.0	189	6	US-60-643-717-9978	Sequence 9978, Ap
153	6	2.0	US-11-031-175-12036	Sequence 12036, A	226	6	2.0	190	8	US-60-643-717-11266	Sequence 11266, A
154	6	2.0	US-10-489-448-3218	Sequence 3218, Ap	227	6	2.0	194	7	US-11-031-175-10343	Sequence 10343, Ap
155	6	2.0	US-10-450-763-49020	Sequence 49020, A	228	6	2.0	194	8	US-60-643-717-6741	Sequence 6741, A
156	6	2.0	US-10-450-763-33789	Sequence 33789, A	229	6	2.0	196	8	US-10-450-763-47420	Sequence 47420, Ap
157	6	2.0	US-10-489-448-1137	Sequence 1137, Ap	230	6	2.0	197	6	US-60-643-717-4170	Sequence 4170, Ap
158	6	2.0	US-10-450-763-48571	Sequence 48571, A	231	6	2.0	197	8	US-60-643-717-7170	Sequence 7170, Ap
159	6	2.0	US-10-450-763-51259	Sequence 51259, A	232	6	2.0	197	8	US-60-643-717-14429	Sequence 14429, A
160	6	2.0	US-10-450-763-46449	Sequence 46449, A	233	6	2.0	198	6	US-10-450-763-52565	Sequence 52565, A
161	6	2.0	US-10-450-763-49716	Sequence 49716, A	234	6	2.0	198	6	US-10-489-448-1119	Sequence 1119, Ap
162	6	2.0	US-10-450-763-40374	Sequence 40374, A	235	6	2.0	198	8	US-60-643-717-18072	Sequence 18072, A
163	6	2.0	US-10-489-448-2880	Sequence 2880, Ap	236	6	2.0	199	8	US-60-643-717-6233	Sequence 6233, Ap
164	6	2.0	US-10-450-763-30551	Sequence 30551, A	237	6	2.0	200	8	US-60-643-717-6500	Sequence 6500, Ap
165	6	2.0	US-10-489-448-2810	Sequence 2810, Ap	238	6	2.0	202	7	US-11-031-175-10636	Sequence 10636, A
166	6	2.0	US-11-031-175-14536	Sequence 14536, A	239	6	2.0	202	7	US-11-031-175-15190	Sequence 15190, A
167	6	2.0	US-10-450-763-56857	Sequence 56857, A	240	6	2.0	203	8	US-60-643-717-9910	Sequence 9910, App
168	6	2.0	US-10-450-763-56857	Sequence 56857, A	241	6	2.0	203	8	US-10-489-448-2926	Sequence 2926, Ap
169	6	2.0	US-11-040-661-40	Sequence 40, Ap1	242	6	2.0	205	6	US-10-450-763-33788	Sequence 33788, Ap
170	6	2.0	US-10-450-763-38063	Sequence 38063, A	243	6	2.0	205	6	US-60-643-717-4680	Sequence 4680, Ap
171	6	2.0			244	6	2.0	207	6	US-10-450-763-50498	Sequence 50498, A

245	6	2.0	207	8	US-60-643-717-14300	Sequence 14300, A	318	6	2.0	242	7	US-11-028-457-4354	Sequence 4354, Ap
246	6	2.0	211	7	US-11-031-175-15438	Sequence 15438, A	319	6	2.0	242	7	US-11-027-891-4354	Sequence 4354, Ap
247	6	2.0	213	6	US-10-450-763-44696	Sequence 44696, A	320	6	2.0	242	7	US-11-028-291-4354	Sequence 4354, Ap
248	6	2.0	215	6	US-10-450-763-56887	Sequence 56887, A	321	6	2.0	242	7	US-11-028-454-4354	Sequence 4354, Ap
249	6	2.0	217	8	US-11-031-175-12063	Sequence 12063, A	322	6	2.0	243	1	PCT-US04-43366-136	Sequence 136, App
250	6	2.0	217	8	US-60-643-717-10078	Sequence 10078, A	323	6	2.0	243	7	US-11-021-944-136	Sequence 136, App
251	6	2.0	217	8	US-60-643-717-17367	Sequence 17367, A	324	6	2.0	243	7	US-11-031-175-16197	Sequence 16197, A
252	6	2.0	218	6	US-10-450-763-58871	Sequence 58871, A	325	6	2.0	244	6	US-10-450-763-60492	Sequence 60492, A
253	6	2.0	218	7	US-11-047-224-10	Sequence 10, Appl	326	6	2.0	246	6	US-10-450-763-31092	Sequence 31092, A
254	6	2.0	223	6	US-10-489-448-3453	Sequence 3453, Ap	327	6	2.0	246	7	US-11-027-399-4242	Sequence 4242, Ap
255	6	2.0	223	7	US-11-031-175-14920	Sequence 14920, A	328	6	2.0	246	7	US-11-027-843-4242	Sequence 4242, Ap
256	6	2.0	224	6	US-10-450-763-48306	Sequence 48306, A	329	6	2.0	246	7	US-11-027-878-4242	Sequence 4242, Ap
257	6	2.0	224	7	US-11-031-175-12540	Sequence 12540, A	330	6	2.0	246	7	US-11-028-166-4242	Sequence 4242, Ap
258	6	2.0	225	7	US-11-031-175-12561	Sequence 12561, A	331	6	2.0	246	7	US-11-028-204-4242	Sequence 4242, Ap
259	6	2.0	225	7	US-11-031-175-12694	Sequence 12694, A	332	6	2.0	246	7	US-11-027-877-4242	Sequence 4242, Ap
260	6	2.0	226	6	US-10-450-763-53953	Sequence 53953, A	333	6	2.0	246	7	US-11-027-879-4242	Sequence 4242, Ap
261	6	2.0	226	6	US-10-450-763-58728	Sequence 58728, Ap	334	6	2.0	246	7	US-11-028-149-4242	Sequence 4242, Ap
262	6	2.0	226	6	US-10-489-448-2889	Sequence 2889, Ap	335	6	2.0	246	7	US-11-027-802-4242	Sequence 4242, Ap
263	6	2.0	228	6	US-10-450-763-35177	Sequence 35177, A	336	6	2.0	246	7	US-11-027-899-4242	Sequence 4242, Ap
264	6	2.0	229	6	US-10-450-763-53966	Sequence 53966, A	337	6	2.0	246	7	US-11-027-899-4242	Sequence 4242, Ap
265	6	2.0	229	6	US-60-643-717-13646	Sequence 13646, A	338	6	2.0	246	7	US-11-028-099-4242	Sequence 4242, Ap
266	6	2.0	230	6	US-10-450-763-41579	Sequence 41579, A	339	6	2.0	246	7	US-11-028-197-4242	Sequence 4242, Ap
267	6	2.0	230	6	US-10-450-763-54248	Sequence 54248, A	340	6	2.0	246	7	US-11-027-844-4242	Sequence 4242, Ap
268	6	2.0	231	6	US-10-450-763-35550	Sequence 35550, A	341	6	2.0	246	7	US-11-028-050-4242	Sequence 4242, Ap
269	6	2.0	233	7	US-11-031-175-11845	Sequence 11845, A	342	6	2.0	246	7	US-11-028-457-4242	Sequence 4242, Ap
270	6	2.0	233	7	US-11-031-175-16165	Sequence 16165, A	343	6	2.0	246	7	US-11-027-891-4242	Sequence 4242, Ap
271	6	2.0	233	8	US-60-643-717-4918	Sequence 4918, Ap	344	6	2.0	246	7	US-11-028-291-4242	Sequence 4242, Ap
272	6	2.0	234	7	US-11-031-175-14877	Sequence 14877, A	345	6	2.0	246	7	US-11-028-454-4242	Sequence 4242, Ap
273	6	2.0	234	8	US-60-643-717-2865	Sequence 2865, Ap	346	6	2.0	247	1	PCT-US04-42360-679	Sequence 679, App
274	6	2.0	234	8	US-60-643-717-2946	Sequence 2946, Ap	347	6	2.0	247	7	US-11-031-175-10732	Sequence 10732, A
275	6	2.0	235	8	US-60-643-717-3555	Sequence 3555, Ap	348	6	2.0	248	6	US-10-450-763-38064	Sequence 38064, A
276	6	2.0	235	6	US-10-489-448-1001	Sequence 1001, Ap	349	6	2.0	248	7	US-11-031-175-13538	Sequence 13538, A
277	6	2.0	236	6	US-10-450-763-53622	Sequence 53622, A	350	6	2.0	248	7	US-11-031-175-16714	Sequence 16714, A
278	6	2.0	236	6	US-10-450-763-57806	Sequence 57806, A	351	6	2.0	251	8	US-60-643-717-4830	Sequence 4830, Ap
279	6	2.0	236	7	US-11-031-175-10625	Sequence 10625, A	352	6	2.0	251	8	US-60-643-717-12695	Sequence 12695, A
280	6	2.0	239	1	PCT-US04-17965-842	Sequence 842, App	353	6	2.0	253	6	US-10-450-763-37316	Sequence 37316, A
281	6	2.0	239	6	US-10-450-763-54491	Sequence 54491, A	354	6	2.0	254	6	US-10-450-763-56437	Sequence 56437, A
282	6	2.0	240	7	US-11-027-399-2970	Sequence 2970, Ap	355	6	2.0	255	1	PCT-US04-17965-2016	Sequence 2016, Ap
283	6	2.0	240	7	US-11-027-843-2970	Sequence 2970, Ap	356	6	2.0	258	6	US-10-717-666A-59	Sequence 59, Appl
284	6	2.0	240	7	US-11-027-878-2970	Sequence 2970, Ap	357	6	2.0	259	6	US-10-450-763-38102	Sequence 38102, A
285	6	2.0	240	7	US-11-028-169-2970	Sequence 2970, Ap	358	6	2.0	259	7	US-11-031-175-12875	Sequence 12875, A
286	6	2.0	240	7	US-11-028-204-2970	Sequence 2970, Ap	359	6	2.0	262	8	US-60-643-717-13969	Sequence 13969, A
287	6	2.0	240	7	US-11-027-877-2970	Sequence 2970, Ap	360	6	2.0	263	6	US-10-450-763-34078	Sequence 34078, A
288	6	2.0	240	7	US-11-027-879-2970	Sequence 2970, Ap	361	6	2.0	263	7	US-11-031-175-15616	Sequence 15616, A
289	6	2.0	240	7	US-11-028-149-2970	Sequence 2970, Ap	362	6	2.0	264	7	US-11-027-399-3617	Sequence 3617, Ap
290	6	2.0	240	7	US-11-027-802-2970	Sequence 2970, Ap	363	6	2.0	264	7	US-11-027-843-3617	Sequence 3617, Ap
291	6	2.0	240	7	US-11-027-890-2970	Sequence 2970, Ap	364	6	2.0	264	7	US-11-027-878-3617	Sequence 3617, Ap
292	6	2.0	240	7	US-11-027-892-2970	Sequence 2970, Ap	365	6	2.0	264	7	US-11-028-169-3617	Sequence 3617, Ap
293	6	2.0	240	7	US-11-028-099-2970	Sequence 2970, Ap	366	6	2.0	264	7	US-11-028-204-3617	Sequence 3617, Ap
294	6	2.0	240	7	US-11-028-197-2970	Sequence 2970, Ap	367	6	2.0	264	7	US-11-027-887-3617	Sequence 3617, Ap
295	6	2.0	240	7	US-11-027-844-2970	Sequence 2970, Ap	368	6	2.0	264	7	US-11-027-879-3617	Sequence 3617, Ap
296	6	2.0	240	7	US-11-028-050-2970	Sequence 2970, Ap	369	6	2.0	264	7	US-11-028-149-3617	Sequence 3617, Ap
297	6	2.0	240	7	US-11-028-457-2970	Sequence 2970, Ap	370	6	2.0	264	7	US-11-027-802-3617	Sequence 3617, Ap
298	6	2.0	240	7	US-11-027-891-2970	Sequence 2970, Ap	371	6	2.0	264	7	US-11-027-889-3617	Sequence 3617, Ap
299	6	2.0	240	7	US-11-028-291-2970	Sequence 2970, Ap	372	6	2.0	264	7	US-11-027-899-3617	Sequence 3617, Ap
300	6	2.0	240	7	US-11-028-458-2970	Sequence 2970, Ap	373	6	2.0	264	7	US-11-028-099-3617	Sequence 3617, Ap
301	6	2.0	242	8	US-60-643-717-17851	Sequence 17851, A	374	6	2.0	264	7	US-11-028-197-3617	Sequence 3617, Ap
302	6	2.0	242	7	US-10-489-448-3475	Sequence 3475, Ap	375	6	2.0	264	7	US-11-027-844-3617	Sequence 3617, Ap
303	6	2.0	242	7	US-11-027-399-4354	Sequence 4354, Ap	376	6	2.0	264	7	US-11-028-050-3617	Sequence 3617, Ap
304	6	2.0	242	7	US-11-027-843-4354	Sequence 4354, Ap	377	6	2.0	264	7	US-11-028-457-3617	Sequence 3617, Ap
305	6	2.0	242	7	US-11-027-878-4354	Sequence 4354, Ap	378	6	2.0	264	7	US-11-027-889-3617	Sequence 3617, Ap
306	6	2.0	242	7	US-11-028-169-4354	Sequence 4354, Ap	379	6	2.0	264	7	US-11-028-291-3617	Sequence 3617, Ap
307	6	2.0	242	7	US-11-028-204-4354	Sequence 4354, Ap	380	6	2.0	264	7	US-11-028-459-3617	Sequence 3617, Ap
308	6	2.0	242	7	US-11-027-877-4354	Sequence 4354, Ap	381	6	2.0	267	8	US-60-643-717-6282	Sequence 6282, Ap
309	6	2.0	242	7	US-11-027-879-4354	Sequence 4354, Ap	382	6	2.0	269	7	US-11-031-175-12511	Sequence 12511, A
310	6	2.0	242	7	US-11-028-149-4354	Sequence 4354, Ap	383	6	2.0	270	6	US-10-450-763-38644	Sequence 38644, A
311	6	2.0	242	7	US-11-027-802-4354	Sequence 4354, Ap	384	6	2.0	270	6	US-10-450-763-54320	Sequence 54320, A
312	6	2.0	242	7	US-11-027-890-4354	Sequence 4354, Ap	385	6	2.0	270	6	US-10-489-448-3356	Sequence 3356, Ap
313	6	2.0	242	7	US-11-027-892-4354	Sequence 4354, Ap	386	6	2.0	272	7	US-11-031-175-13063	Sequence 13063, A
314	6	2.0	242	7	US-11-028-099-4354	Sequence 4354, Ap	387	6	2.0	272	6	US-10-489-448-1331	Sequence 1431, Ap
315	6	2.0	242	7	US-11-028-197-4354	Sequence 4354, Ap	388	6	2.0	272	7	US-11-031-175-15379	Sequence 15379, A
316	6	2.0	242	7	US-11-027-844-4354	Sequence 4354, Ap	389	6	2.0	274	6	US-10-450-763-38440	Sequence 38440, A
317	6	2.0	242	7	US-11-028-050-4354	Sequence 4354, Ap	390	6	2.0	275	1	PCT-US04-17965-847	Sequence 847, App

391	2.0	275	8	US-60-643-717-12609	Sequence 12609, A	464	2.0	304	1	PCT-US04-42360-448	Sequence 448, App
392	2.0	277	6	US-10-450-763-37953	Sequence 37953, A	465	2.0	304	7	US-11-031-175-14957	Sequence 14957, A
393	2.0	277	6	US-10-450-763-42217	Sequence 42217, A	466	2.0	304	7	US-10-450-763-44200	Sequence 34200, A
394	2.0	278	6	US-10-450-763-51810	Sequence 51810, A	467	2.0	305	6	US-10-450-763-40763	Sequence 40763, A
395	2.0	278	7	US-11-031-175-10783	Sequence 10783, A	468	2.0	305	6	US-10-450-763-57400	Sequence 57400, A
396	2.0	278	7	US-11-031-175-12602	Sequence 12602, A	469	2.0	307	6	US-10-450-763-55114	Sequence 55114, A
397	2.0	279	6	US-10-450-763-47976	Sequence 47976, A	470	2.0	307	8	US-60-643-717-2813	Sequence 2813, App
398	2.0	280	6	US-10-450-763-39441	Sequence 39441, A	471	2.0	308	7	US-11-031-175-15489	Sequence 15489, A
399	2.0	280	7	US-11-031-175-11498	Sequence 11498, A	472	2.0	309	8	US-60-643-717-15347	Sequence 15347, A
400	2.0	282	6	US-10-450-763-46262	Sequence 46262, A	473	2.0	310	6	US-10-489-448-1665	Sequence 1665, App
401	2.0	283	7	US-11-027-399-3190	Sequence 3190, App	474	2.0	310	7	US-11-031-175-15686	Sequence 15686, A
402	2.0	283	7	US-11-027-883-3190	Sequence 3190, App	475	2.0	313	7	US-11-023-805-4	Sequence 4, App11
403	2.0	283	7	US-11-027-878-3190	Sequence 3190, App	476	2.0	315	7	US-11-031-175-12484	Sequence 12484, A
404	2.0	283	7	US-11-028-169-3190	Sequence 3190, App	477	2.0	317	7	US-11-031-175-10988	Sequence 10988, A
405	2.0	283	7	US-11-028-204-3190	Sequence 3190, App	478	2.0	319	8	US-60-643-717-16444	Sequence 16444, A
406	2.0	283	7	US-11-027-877-3190	Sequence 3190, App	479	2.0	320	7	US-60-643-717-17357	Sequence 17357, A
407	2.0	283	7	US-11-027-879-3190	Sequence 3190, App	480	2.0	322	7	US-11-031-175-12125	Sequence 12125, A
408	2.0	283	7	US-11-028-149-3190	Sequence 3190, App	481	2.0	323	7	US-11-031-175-12207	Sequence 12207, A
409	2.0	283	7	US-11-027-880-3190	Sequence 3190, App	482	2.0	328	6	PCT-US04-30360-7	Sequence 7, App11
410	2.0	283	7	US-11-027-890-3190	Sequence 3190, App	483	2.0	328	6	US-10-450-763-40679	Sequence 40679, A
411	2.0	283	7	US-11-027-892-3190	Sequence 3190, App	484	2.0	328	6	US-10-450-763-55900	Sequence 55900, A
412	2.0	283	7	US-11-028-099-3190	Sequence 3190, App	485	2.0	328	6	US-10-489-448-1150	Sequence 1150, App
413	2.0	283	7	US-11-028-197-3190	Sequence 3190, App	486	2.0	330	1	PCT-US04-42360-2094	Sequence 2094, App
414	2.0	283	7	US-11-027-844-3190	Sequence 3190, App	487	2.0	332	6	US-10-450-763-33797	Sequence 33797, A
415	2.0	283	7	US-11-028-050-3190	Sequence 3190, App	488	2.0	332	6	US-10-450-763-37114	Sequence 37114, A
416	2.0	283	7	US-11-028-457-3190	Sequence 3190, App	489	2.0	333	7	US-60-643-717-17357	Sequence 17357, A
417	2.0	283	7	US-11-028-891-3190	Sequence 3190, App	490	2.0	333	7	US-10-450-763-50659	Sequence 50659, A
418	2.0	283	7	US-11-028-291-3190	Sequence 3190, App	491	2.0	333	7	US-11-031-175-10638	Sequence 10638, A
419	2.0	283	7	US-11-031-175-14951	Sequence 14951, A	492	2.0	333	7	US-11-047-224-8	Sequence 8, App11
420	2.0	283	7	US-11-028-458-3190	Sequence 3190, App	493	2.0	335	7	US-11-031-175-15208	Sequence 15208, A
421	2.0	284	6	US-10-450-763-57707	Sequence 57707, A	494	2.0	336	8	US-60-643-717-12181	Sequence 12181, A
422	2.0	287	6	US-10-450-763-55316	Sequence 55316, A	495	2.0	338	6	US-10-450-763-55341	Sequence 55341, A
423	2.0	288	6	US-11-031-175-10097	Sequence 10097, A	496	2.0	338	7	US-11-021-835-135	Sequence 135, App
424	2.0	289	6	US-10-450-763-41030	Sequence 41030, A	497	2.0	340	7	US-11-031-175-10905	Sequence 10905, A
425	2.0	289	6	US-60-643-717-6903	Sequence 6903, App	498	2.0	340	7	US-11-031-175-12586	Sequence 12586, A
426	2.0	289	8	US-60-643-717-15213	Sequence 15213, A	499	2.0	343	6	US-10-450-763-31832	Sequence 31832, A
427	2.0	290	6	US-10-450-763-46646	Sequence 46646, A	500	2.0	344	7	US-11-032-643-44	Sequence 44, App1
428	2.0	291	6	US-10-450-763-57633	Sequence 57633, A	501	2.0	345	7	US-11-032-643-44	Sequence 44, App1
429	2.0	291	8	US-60-643-717-15360	Sequence 15360, A	502	2.0	347	8	US-60-643-717-18557	Sequence 18557, A
430	2.0	292	7	US-11-027-399-4530	Sequence 4530, App	503	2.0	348	7	US-11-031-175-11383	Sequence 11383, A
431	2.0	292	7	US-11-027-843-4530	Sequence 4530, App	504	2.0	348	8	US-60-643-717-1716	Sequence 1716, App
432	2.0	292	7	US-11-027-878-4530	Sequence 4530, App	505	2.0	348	8	US-60-643-717-2027	Sequence 2027, App
433	2.0	292	7	US-11-028-169-4530	Sequence 4530, App	506	2.0	348	8	US-60-643-717-3417	Sequence 3417, App
434	2.0	292	7	US-11-028-204-4530	Sequence 4530, App	507	2.0	348	8	US-60-643-717-4094	Sequence 4094, App
435	2.0	292	7	US-11-027-877-4530	Sequence 4530, App	508	2.0	348	8	US-60-643-717-4679	Sequence 4679, App
436	2.0	292	7	US-11-027-879-4530	Sequence 4530, App	509	2.0	348	8	US-60-643-717-4927	Sequence 4927, App
437	2.0	292	7	US-11-028-149-4530	Sequence 4530, App	510	2.0	348	8	US-60-643-717-5923	Sequence 5923, App
438	2.0	292	7	US-11-027-802-4530	Sequence 4530, App	511	2.0	348	8	US-60-643-717-5928	Sequence 5928, App
439	2.0	292	7	US-11-027-890-4530	Sequence 4530, App	512	2.0	348	8	US-60-643-717-6593	Sequence 6593, App
440	2.0	292	7	US-11-027-892-4530	Sequence 4530, App	513	2.0	348	8	US-60-643-717-6598	Sequence 6598, App
441	2.0	292	7	US-11-028-197-4530	Sequence 4530, App	514	2.0	348	8	US-60-643-717-10962	Sequence 10962, App
442	2.0	292	7	US-11-028-194-4530	Sequence 4530, App	515	2.0	352	7	US-11-031-175-12834	Sequence 12834, App
443	2.0	292	7	US-11-027-844-4530	Sequence 4530, App	516	2.0	352	8	US-60-643-717-5885	Sequence 5885, App
444	2.0	292	7	US-11-028-050-4530	Sequence 4530, App	517	2.0	354	7	US-11-031-175-15411	Sequence 15411, A
445	2.0	292	7	US-11-028-457-4530	Sequence 4530, App	518	2.0	356	6	US-10-450-763-34005	Sequence 34005, A
446	2.0	292	7	US-11-027-891-4530	Sequence 4530, App	519	2.0	359	7	US-11-031-175-16822	Sequence 16822, A
447	2.0	292	7	US-11-028-291-4530	Sequence 4530, App	520	2.0	359	8	US-60-643-717-14419	Sequence 14419, A
448	2.0	292	7	US-11-031-175-13893	Sequence 13893, A	521	2.0	361	8	US-60-643-717-7014	Sequence 7014, App
449	2.0	292	7	US-11-028-458-4530	Sequence 4530, App	522	2.0	364	6	US-10-450-763-40366	Sequence 40366, App
450	2.0	294	8	US-60-643-717-3105	Sequence 3105, App	523	2.0	364	7	US-11-031-175-11265	Sequence 11265, A
451	2.0	294	8	US-60-643-717-6614	Sequence 6614, App	524	2.0	368	6	US-10-450-763-42483	Sequence 42483, A
452	2.0	294	8	US-60-643-717-15418	Sequence 15418, A	525	2.0	368	7	US-11-031-175-11925	Sequence 11925, A
453	2.0	295	8	US-60-643-717-13568	Sequence 13568, App	526	2.0	368	7	US-11-047-224-2	Sequence 2, App11
454	2.0	297	6	US-10-450-763-59513	Sequence 59513, A	527	2.0	368	8	US-60-643-717-3568	Sequence 3568, App
455	2.0	297	8	US-60-643-717-14416	Sequence 14416, A	528	2.0	368	8	US-60-643-717-15048	Sequence 15048, A
456	2.0	299	8	US-60-643-717-13515	Sequence 13515, A	529	2.0	369	1	PCT-US04-42360-850	Sequence 850, App
457	2.0	299	8	US-60-643-717-660	Sequence 660, App	530	2.0	369	8	US-60-643-717-9402	Sequence 9402, App
458	2.0	300	1	PCT-US05-00638-87	Sequence 87, App1	531	2.0	370	1	PCT-US04-30360-101	Sequence 101, App
459	2.0	300	6	US-10-450-763-54319	Sequence 54319, A	532	2.0	371	8	US-60-643-717-5901	Sequence 5901, App
460	2.0	301	8	US-60-643-717-3038	Sequence 3038, App	533	2.0	371	8	US-60-643-717-11272	Sequence 11272, A
461	2.0	301	8	US-60-643-717-5654	Sequence 5654, App	534	2.0	373	6	US-10-450-763-46345	Sequence 46345, App
462	2.0	301	8	US-60-643-717-7902	Sequence 7902, App	535	2.0	373	8	US-60-643-717-6576	Sequence 6576, App
463	2.0	302	8	US-60-643-717-13840	Sequence 13840, A	536	2.0	373	8	US-60-643-717-17538	Sequence 17538, A

537	6	2.0	374	6	US-10-489-448-2999	Sequence 2999, Ap	610	2.0	426	7	US-11-031-175-10978	Sequence 10978, A
538	6	2.0	374	8	US-60-643-717-5932	Sequence 5932, Ap	611	2.0	429	8	US-60-643-717-5189	Sequence 5189, Ap
539	6	2.0	374	8	US-60-643-717-9485	Sequence 9485, Ap	612	2.0	434	6	US-10-450-763-32277	Sequence 32277, A
540	6	2.0	375	7	US-11-031-175-14394	Sequence 14394, A	613	2.0	434	7	US-11-031-175-10958	Sequence 10958, A
541	6	2.0	375	8	US-60-643-717-1707	Sequence 1707, Ap	614	2.0	434	8	US-11-031-175-10908	Sequence 10908, A
542	6	2.0	375	8	US-60-643-717-2794	Sequence 2794, Ap	615	2.0	437	7	US-60-643-717-9680	Sequence 9680, Ap
543	6	2.0	375	8	US-60-643-717-5930	Sequence 5930, Ap	616	2.0	437	8	US-60-643-717-14362	Sequence 14362, A
544	6	2.0	375	8	US-60-643-717-6601	Sequence 6601, Ap	617	2.0	442	8	US-60-643-717-6458	Sequence 6458, Ap
545	6	2.0	375	8	US-60-643-717-9511	Sequence 9511, Ap	618	2.0	446	7	US-11-031-175-13540	Sequence 13540, A
546	6	2.0	375	8	US-60-643-717-16384	Sequence 16384, A	619	2.0	447	7	US-11-031-175-14760	Sequence 14760, A
547	6	2.0	376	6	US-10-450-763-41149	Sequence 41149, A	620	2.0	448	8	US-60-643-717-14877	Sequence 14877, Ap
548	6	2.0	377	7	US-11-031-175-13599	Sequence 13599, A	621	2.0	449	6	US-10-450-763-31298	Sequence 31298, A
549	6	2.0	377	8	US-60-643-717-6577	Sequence 6577, Ap	622	2.0	452	7	US-11-031-175-99072	Sequence 99072, Ap
550	6	2.0	378	6	US-10-450-763-50320	Sequence 50320, A	623	2.0	453	8	US-60-643-717-6026	Sequence 6026, Ap
551	6	2.0	379	6	US-10-450-763-37352	Sequence 37352, A	624	2.0	453	6	US-10-450-763-45646	Sequence 45646, A
552	6	2.0	380	6	US-10-450-763-44602	Sequence 44602, A	625	2.0	453	6	US-10-450-763-47618	Sequence 47618, A
553	6	2.0	380	6	US-60-643-717-1824	Sequence 1824, Ap	626	2.0	453	6	US-10-450-763-55856	Sequence 55856, A
554	6	2.0	381	1	PCT-US03-35712-117	Sequence 117, App	627	2.0	455	8	US-60-643-717-2044	Sequence 2044, Ap
555	6	2.0	381	1	PCT-US04-42360-1613	Sequence 1613, Ap	628	2.0	455	6	US-10-489-448-1403	Sequence 1403, Ap
556	6	2.0	381	8	US-60-643-717-410	Sequence 410, App	629	2.0	455	6	US-10-489-448-1427	Sequence 1427, Ap
557	6	2.0	382	6	US-10-450-763-36402	Sequence 36402, A	630	2.0	455	7	US-11-027-399-3305	Sequence 3905, Ap
558	6	2.0	384	8	US-60-643-717-6210	Sequence 6210, Ap	631	2.0	455	7	US-11-027-843-3305	Sequence 3905, Ap
559	6	2.0	384	8	US-60-643-717-18207	Sequence 18207, A	632	2.0	455	7	US-11-027-878-3305	Sequence 3905, Ap
560	6	2.0	385	6	US-10-450-763-52155	Sequence 52155, A	633	2.0	455	7	US-11-028-169-3305	Sequence 3905, Ap
561	6	2.0	385	6	US-10-489-448-3232	Sequence 3232, Ap	634	2.0	455	7	US-11-028-204-3305	Sequence 3905, Ap
562	6	2.0	385	6	US-10-489-448-3233	Sequence 3233, Ap	635	2.0	455	7	US-11-027-877-3305	Sequence 3905, Ap
563	6	2.0	385	7	US-11-031-175-10094	Sequence 10094, A	636	2.0	455	7	US-11-027-879-3305	Sequence 3905, Ap
564	6	2.0	386	7	US-11-031-175-13651	Sequence 13651, A	637	2.0	455	7	US-11-028-149-3305	Sequence 3905, Ap
565	6	2.0	392	6	US-10-450-763-36946	Sequence 36946, A	638	2.0	455	7	US-11-027-890-3305	Sequence 3905, Ap
566	6	2.0	392	7	US-11-031-175-13511	Sequence 13511, A	639	2.0	455	7	US-11-027-890-3305	Sequence 3905, Ap
567	6	2.0	392	8	US-60-643-717-14734	Sequence 14734, A	640	2.0	455	7	US-11-028-099-3305	Sequence 3905, Ap
568	6	2.0	393	8	US-60-643-717-8850	Sequence 8850, Ap	641	2.0	455	7	US-11-028-197-3305	Sequence 3905, Ap
569	6	2.0	393	8	US-60-643-717-11131	Sequence 11131, A	642	2.0	455	7	US-11-028-844-3305	Sequence 3905, Ap
570	6	2.0	394	7	US-10-450-763-54735	Sequence 54735, A	643	2.0	455	7	US-11-028-050-3305	Sequence 3905, Ap
571	6	2.0	395	6	US-10-450-763-54732	Sequence 54732, A	644	2.0	455	7	US-11-027-891-3305	Sequence 3905, Ap
572	6	2.0	395	6	US-10-450-763-54735	Sequence 54735, A	645	2.0	455	7	US-11-028-456-3305	Sequence 3905, Ap
573	6	2.0	398	6	US-10-489-448-1694	Sequence 1694, Ap	646	2.0	455	7	US-11-028-291-3305	Sequence 3905, Ap
574	6	2.0	398	8	US-60-643-717-14646	Sequence 14646, Ap	647	2.0	455	7	US-10-450-763-48210	Sequence 48210, A
575	6	2.0	399	6	US-10-450-763-48134	Sequence 48134, A	648	2.0	458	6	PCT-US04-42360-50	Sequence 50, Appl
576	6	2.0	399	6	US-60-643-717-5245	Sequence 5245, Ap	649	2.0	459	1	US-11-031-175-15589	Sequence 15589, A
577	6	2.0	401	6	US-10-450-763-43518	Sequence 43518, A	650	2.0	460	7	US-60-643-717-12512	Sequence 12512, A
578	6	2.0	401	6	US-10-450-763-51116	Sequence 51116, A	651	2.0	461	8	US-10-450-763-16075	Sequence 16075, A
579	6	2.0	402	6	US-10-450-763-59706	Sequence 59706, A	652	2.0	462	7	US-10-450-763-57381	Sequence 57381, A
580	6	2.0	402	6	US-10-450-763-59702	Sequence 59702, A	653	2.0	463	6	US-10-450-763-52882	Sequence 52882, A
581	6	2.0	403	6	US-10-450-763-59706	Sequence 59706, A	654	2.0	464	6	US-60-643-717-6546	Sequence 6546, A
582	6	2.0	403	6	US-10-450-763-48692	Sequence 48692, A	655	2.0	464	6	US-60-643-717-3519	Sequence 3519, A
583	6	2.0	405	8	US-11-031-175-15722	Sequence 15722, A	656	2.0	465	8	US-60-643-717-3616	Sequence 3616, Ap
584	6	2.0	405	8	US-60-643-717-838	Sequence 838, App	657	2.0	466	8	US-10-450-763-46828	Sequence 46828, A
585	6	2.0	406	7	US-11-031-175-11121	Sequence 11121, A	658	2.0	466	8	US-60-643-717-18786	Sequence 18786, A
586	6	2.0	408	8	US-60-643-717-9181	Sequence 9181, Ap	659	2.0	466	8	PCT-US04-17965-2191	Sequence 2191, Ap
587	6	2.0	410	6	US-10-450-763-47658	Sequence 47658, A	660	2.0	470	1	US-10-450-763-49220	Sequence 49220, A
588	6	2.0	411	6	US-10-450-763-38787	Sequence 38787, A	661	2.0	470	6	US-11-031-175-11254	Sequence 11254, A
589	6	2.0	411	8	US-60-643-717-11943	Sequence 11943, A	662	2.0	476	8	US-11-027-879-3355	Sequence 3355, Ap
590	6	2.0	412	1	PCT-US04-42360-350	Sequence 350, App	663	2.0	477	7	US-11-027-877-3355	Sequence 3355, Ap
591	6	2.0	412	1	PCT-US04-42360-430	Sequence 430, App	664	2.0	477	6	US-10-450-763-33946	Sequence 33946, A
592	6	2.0	412	7	US-11-031-175-9713	Sequence 9713, Ap	665	2.0	472	6	US-10-450-763-55894	Sequence 55894, A
593	6	2.0	412	7	US-60-643-717-7950	Sequence 7950, Ap	666	2.0	473	6	US-10-450-763-35119	Sequence 35119, A
594	6	2.0	412	8	US-60-643-717-12491	Sequence 12491, A	667	2.0	473	8	US-60-643-717-706	Sequence 706, App
595	6	2.0	413	8	US-11-031-175-16100	Sequence 16100, A	668	2.0	476	7	US-11-028-204-3355	Sequence 3355, Ap
596	6	2.0	413	8	US-60-643-717-18360	Sequence 18360, A	669	2.0	476	8	US-11-027-879-3355	Sequence 3355, Ap
597	6	2.0	414	8	US-60-643-717-10629	Sequence 10629, A	670	2.0	477	7	US-11-027-879-3355	Sequence 3355, Ap
598	6	2.0	415	8	US-60-643-717-14045	Sequence 14045, A	671	2.0	477	7	US-11-027-880-3355	Sequence 3355, Ap
599	6	2.0	417	8	US-60-643-717-3162	Sequence 3162, Ap	672	2.0	477	7	US-11-027-890-3355	Sequence 3355, Ap
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604	6	2.0	421	7	US-11-031-175-10569	Sequence 10569, A	677	2.0	477	7	US-11-027-890-3355	Sequence 3355, Ap
605	6	2.0	422	7	US-11-031-175-15649	Sequence 15649, A	678	2.0	477	7	US-11-027-890-3355	Sequence 3355, Ap
606	6	2.0	423	8	US-60-643-717-1518	Sequence 1518, Ap	679	2.0	477	7	US-11-028-099-3355	Sequence 3355, Ap
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686	6	2.0	477	7	US-11-027-891-3555	Sequence 3555, Ap
687	6	2.0	477	7	US-11-028-291-3555	Sequence 3555, Ap
688	6	2.0	477	7	US-11-031-175-15889	Sequence 15889, A
689	6	2.0	477	7	US-11-028-458-3555	Sequence 3555, Ap
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693	6	2.0	478	6	US-60-643-717-5125	Sequence 5125, Ap
694	6	2.0	482	7	US-11-031-175-16249	Sequence 16249, A
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698	6	2.0	486	1	PCT-US04-17965-1240	Sequence 1240, Ap
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706	6	2.0	493	6	US-10-450-763-51308	Sequence 51308, A
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713	6	2.0	503	1	PCT-US04-06979-599	Sequence 599, Ap
714	6	2.0	503	1	PCT-US04-42360-326	Sequence 326, Ap
715	6	2.0	504	1	PCT-US04-42360-326	Sequence 326, Ap
716	6	2.0	504	6	US-10-450-763-45233	Sequence 45233, A
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719	6	2.0	507	6	US-10-450-763-50792	Sequence 50792, A
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723	6	2.0	512	8	US-60-643-717-7704	Sequence 7704, Ap
724	6	2.0	512	8	US-60-643-717-14010	Sequence 14010, A
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736	6	2.0	526	6	US-10-450-763-48433	Sequence 48433, A
737	6	2.0	526	8	US-60-643-717-1303	Sequence 1303, Ap
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739	6	2.0	528	8	US-60-643-717-638	Sequence 638, Ap
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741	6	2.0	528	8	US-60-643-717-4546	Sequence 4546, Ap
742	6	2.0	528	8	US-60-643-717-12306	Sequence 12306, A
743	6	2.0	528	8	US-60-643-717-13170	Sequence 13170, A
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746	6	2.0	529	8	US-60-643-717-17272	Sequence 17272, A
747	6	2.0	530	8	US-10-450-763-60048	Sequence 60048, A
748	6	2.0	531	8	US-60-643-717-10740	Sequence 10740, A
749	6	2.0	533	8	US-60-643-717-5938	Sequence 5938, Ap
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753	6	2.0	539	6	US-10-450-763-59645	Sequence 59645, A
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755	6	2.0	539	7	US-11-031-175-11952	Sequence 11952, A
756	6	2.0	539	8	US-60-643-717-575	Sequence 575, Ap
757	6	2.0	542	8	US-60-643-717-3348	Sequence 3348, Ap
758	6	2.0	542	1	PCT-US04-42360-347	Sequence 347, Ap
759	6	2.0	543	1	PCT-US04-42360-2234	Sequence 2234, Ap
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761	6	2.0	545	7	US-11-031-175-10533	Sequence 10533, A
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763	6	2.0	546	6	US-10-450-763-45232	Sequence 45232, A
764	6	2.0	547	6	US-10-450-763-49217	Sequence 49217, A
765	6	2.0	549	7	US-11-031-175-14387	Sequence 14387, A
766	6	2.0	550	8	US-60-643-717-7000	Sequence 7000, Ap
767	6	2.0	550	8	US-60-643-717-13768	Sequence 13768, Ap
768	6	2.0	551	8	US-60-643-717-4563	Sequence 4563, Ap
769	6	2.0	551	8	US-60-643-717-11068	Sequence 11068, A
770	6	2.0	552	8	US-60-643-717-6008	Sequence 6008, Ap
771	6	2.0	552	8	US-60-643-717-9253	Sequence 9253, Ap
772	6	2.0	553	8	US-60-643-717-1772	Sequence 1772, Ap
773	6	2.0	554	7	US-11-031-175-14972	Sequence 14972, Ap
774	6	2.0	555	6	US-10-450-763-46906	Sequence 46906, A
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776	6	2.0	556	6	US-60-643-717-17275	Sequence 17275, A
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779	6	2.0	561	6	US-10-450-763-33378	Sequence 33378, A
780	6	2.0	561	6	US-60-643-717-558	Sequence 558, Ap
781	6	2.0	562	6	US-10-450-763-45932	Sequence 45932, A
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783	6	2.0	562	8	US-60-643-717-15103	Sequence 15103, A
784	6	2.0	563	6	US-10-450-763-51317	Sequence 51317, A
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788	6	2.0	567	8	US-60-643-717-3138	Sequence 3138, Ap
789	6	2.0	567	8	US-60-643-717-6863	Sequence 6863, Ap
790	6	2.0	567	8	US-60-643-717-1898	Sequence 1898, Ap
791	6	2.0	574	8	US-60-643-717-1848	Sequence 1848, A
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795	6	2.0	583	6	US-10-450-763-18031	Sequence 18031, A
796	6	2.0	583	7	US-11-031-175-14031	Sequence 14031, A
797	6	2.0	583	7	US-11-031-175-14460	Sequence 14460, A
798	6	2.0	583	8	US-60-643-717-1848	Sequence 1848, A
799	6	2.0	586	8	US-60-643-717-17736	Sequence 17736, A
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803	6	2.0	595	7	US-11-031-175-18334	Sequence 18334, A
804	6	2.0	597	7	US-11-031-175-16436	Sequence 16436, A
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808	6	2.0	606	6	US-10-450-763-38590	Sequence 38590, A
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813	6	2.0	620	7	US-11-031-175-11179	Sequence 11179, A
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815	6	2.0	621	6	US-10-489-448-1744	Sequence 1744, Ap
816	6	2.0	625	6	US-10-489-448-1513	Sequence 1513, Ap
817	6	2.0	627	8	US-60-643-717-13548	Sequence 13548, A
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819	6	2.0	632	8	US-60-643-717-14510	Sequence 14510, A
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821	6	2.0	637	8	US-60-643-717-5269	Sequence 5269, Ap
822	6	2.0	643	6	US-10-489-448-1613	Sequence 1613, Ap
823	6	2.0	649	8	US-60-643-717-9713	Sequence 9713, Ap
824	6	2.0	653	6	US-10-450-763-48711	Sequence 48711, A
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827	6	2.0	658	6	US-10-450-763-43779	Sequence 43779, A
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834	6	2.0	673	7	US-11-027-843-2860	Sequence 2860, App	907	6	2.0	765	6	US-10-450-763-58874	Sequence 58874, A
835	6	2.0	673	7	US-11-027-878-2860	Sequence 2860, App	908	6	2.0	767	8	US-60-643-717-5052	Sequence 5052, App
836	6	2.0	673	7	US-11-028-169-2860	Sequence 2860, App	909	6	2.0	772	1	PCT-US04-17965-1190	Sequence 1190, App
837	6	2.0	673	7	US-11-028-204-2860	Sequence 2860, App	910	6	2.0	772	8	US-60-643-717-12573	Sequence 12573, A
838	6	2.0	673	7	US-11-027-877-2860	Sequence 2860, App	911	6	2.0	773	8	US-60-643-717-1018	Sequence 1018, App
839	6	2.0	673	7	US-11-027-879-2860	Sequence 2860, App	912	6	2.0	774	8	US-60-643-717-2433	Sequence 2433, App
840	6	2.0	673	7	US-11-028-149-2860	Sequence 2860, App	913	6	2.0	777	6	US-10-489-448-1621	Sequence 1621, App
841	6	2.0	673	7	US-11-027-802-2860	Sequence 2860, App	914	6	2.0	783	7	US-11-031-175-11405	Sequence 11405, A
842	6	2.0	673	7	US-11-027-890-2860	Sequence 2860, App	915	6	2.0	784	8	US-60-643-717-5362	Sequence 5362, App
843	6	2.0	673	7	US-11-027-892-2860	Sequence 2860, App	916	6	2.0	792	7	US-11-031-175-16475	Sequence 16475, A
844	6	2.0	673	7	US-11-028-099-2860	Sequence 2860, App	917	6	2.0	802	6	US-10-450-763-54216	Sequence 54216, A
845	6	2.0	673	7	US-11-028-197-2860	Sequence 2860, App	918	6	2.0	802	7	US-11-031-175-14060	Sequence 14060, A
846	6	2.0	673	7	US-11-027-844-2860	Sequence 2860, App	919	6	2.0	804	6	US-10-450-763-45931	Sequence 45931, A
847	6	2.0	673	7	US-11-028-050-2860	Sequence 2860, App	920	6	2.0	805	6	US-10-489-448-1202	Sequence 1202, App
848	6	2.0	673	7	US-11-028-457-2860	Sequence 2860, App	921	6	2.0	819	6	US-10-450-763-49219	Sequence 49219, A
849	6	2.0	673	7	US-11-027-891-2860	Sequence 2860, App	922	6	2.0	819	8	US-60-643-717-16439	Sequence 16439, A
850	6	2.0	673	7	US-11-028-291-2860	Sequence 2860, App	923	6	2.0	820	6	US-10-450-763-47402	Sequence 47402, A
851	6	2.0	673	7	US-11-028-458-2860	Sequence 2860, App	924	6	2.0	821	6	US-10-489-448-1200	Sequence 1200, App
852	6	2.0	677	6	US-10-450-763-37731	Sequence 37731, A	925	6	2.0	828	7	US-11-031-175-10903	Sequence 10903, A
853	6	2.0	677	6	US-11-031-175-12985	Sequence 12985, A	926	6	2.0	830	8	US-60-643-717-9807	Sequence 9807, App
854	6	2.0	678	7	US-11-031-175-13408	Sequence 13408, A	927	6	2.0	831	5	US-09-684-305-5	Sequence 5, App1
855	6	2.0	680	6	US-10-450-763-60525	Sequence 60525, A	928	6	2.0	832	5	US-09-684-305-4	Sequence 4, App1
856	6	2.0	682	6	US-10-450-763-52417	Sequence 52417, A	929	6	2.0	833	5	US-09-684-305-8	Sequence 8, App1
857	6	2.0	683	6	US-10-717-665A-71	Sequence 71, App1	930	6	2.0	833	5	US-09-684-305-107	Sequence 107, App
858	6	2.0	684	1	PCT-US05-00638-125	Sequence 125, App	931	6	2.0	833	5	US-09-684-305-130	Sequence 130, App
859	6	2.0	684	7	US-11-027-399-5255	Sequence 5255, App	932	6	2.0	833	5	US-09-684-305-132	Sequence 132, App
860	6	2.0	684	7	US-11-027-843-5255	Sequence 5255, App	933	6	2.0	834	5	US-09-684-305-6	Sequence 6, App1
861	6	2.0	684	7	US-11-027-878-5255	Sequence 5255, App	934	6	2.0	834	5	US-09-684-305-160	Sequence 160, App
862	6	2.0	684	7	US-11-028-169-5255	Sequence 5255, App	935	6	2.0	836	5	US-09-684-305-162	Sequence 162, App
863	6	2.0	684	7	US-11-028-204-5255	Sequence 5255, App	936	6	2.0	836	5	US-09-684-305-164	Sequence 164, App
864	6	2.0	684	7	US-11-027-877-5255	Sequence 5255, App	937	6	2.0	836	6	US-10-450-763-31083	Sequence 31083, A
865	6	2.0	684	7	US-11-027-879-5255	Sequence 5255, App	938	6	2.0	836	6	US-10-875-094-8	Sequence 8, App1
866	6	2.0	684	7	US-11-028-149-5255	Sequence 5255, App	939	6	2.0	836	6	US-10-875-094-11	Sequence 11, App1
867	6	2.0	684	7	US-11-027-802-5255	Sequence 5255, App	940	6	2.0	837	7	US-11-025-609-317	Sequence 317, App
868	6	2.0	684	7	US-11-027-890-5255	Sequence 5255, App	941	6	2.0	837	7	US-11-033-545-380	Sequence 380, App
869	6	2.0	684	7	US-11-027-892-5255	Sequence 5255, App	942	6	2.0	840	6	US-10-450-763-39157	Sequence 39157, A
870	6	2.0	684	7	US-11-028-099-5255	Sequence 5255, App	943	6	2.0	842	6	US-10-875-094-15	Sequence 15, App1
871	6	2.0	684	7	US-11-028-197-5255	Sequence 5255, App	944	6	2.0	842	6	US-10-875-094-20	Sequence 20, App1
872	6	2.0	684	7	US-11-027-844-5255	Sequence 5255, App	945	6	2.0	842	6	US-10-875-094-23	Sequence 23, App1
873	6	2.0	684	7	US-11-028-050-5255	Sequence 5255, App	946	6	2.0	842	6	US-10-875-094-26	Sequence 26, App1
874	6	2.0	684	7	US-11-028-457-5255	Sequence 5255, App	947	6	2.0	847	6	US-10-450-763-47696	Sequence 47696, A
875	6	2.0	684	7	US-11-027-891-5255	Sequence 5255, App	948	6	2.0	849	6	US-10-931-719-10	Sequence 10, App1
876	6	2.0	684	7	US-11-028-458-5255	Sequence 5255, App	949	6	2.0	849	7	US-11-033-545-564	Sequence 564, App
877	6	2.0	684	7	US-11-028-458-5255	Sequence 5255, App	950	6	2.0	852	6	US-10-450-763-44045	Sequence 44045, A
878	6	2.0	686	6	US-10-450-763-37057	Sequence 37057, A	951	6	2.0	853	7	US-11-031-175-14044	Sequence 14044, A
879	6	2.0	686	6	US-10-450-763-47359	Sequence 47359, A	952	6	2.0	853	8	US-60-643-717-2104	Sequence 2104, App
880	6	2.0	686	6	US-10-450-763-38589	Sequence 38589, A	953	6	2.0	853	8	US-60-643-717-10173	Sequence 10173, A
881	6	2.0	686	6	US-10-489-448-1612	Sequence 1612, App	954	6	2.0	856	6	US-10-489-448-1220	Sequence 1220, App
882	6	2.0	687	1	PCT-US04-23166A-604	Sequence 604, App	955	6	2.0	862	1	PCT-US04-42360-1312	Sequence 1312, App
883	6	2.0	697	1	PCT-US04-23166A-748	Sequence 748, App	956	6	2.0	864	6	US-10-489-448-1042	Sequence 1042, App
884	6	2.0	699	7	US-11-025-607-12	Sequence 12, App1	957	6	2.0	868	6	US-10-450-763-54786	Sequence 54786, A
885	6	2.0	700	7	US-11-031-175-11872	Sequence 11872, A	958	6	2.0	876	8	US-60-643-717-765	Sequence 765, App
886	6	2.0	705	6	US-10-450-763-48643	Sequence 48643, A	959	6	2.0	888	6	US-10-450-763-34028	Sequence 34028, A
887	6	2.0	705	6	US-10-450-763-59189	Sequence 59189, A	960	6	2.0	891	5	US-09-785-085C-8	Sequence 8, App1
888	6	2.0	710	6	US-10-450-763-52854	Sequence 52854, A	961	6	2.0	894	6	US-10-485-555-16	Sequence 16, App1
889	6	2.0	724	6	US-10-450-763-50942	Sequence 50942, A	962	6	2.0	896	6	US-10-450-763-52997	Sequence 52997, A
890	6	2.0	725	6	US-10-450-763-48665	Sequence 48665, A	963	6	2.0	897	7	US-11-031-175-15636	Sequence 15636, A
891	6	2.0	726	8	US-10-450-763-58870	Sequence 58870, A	964	6	2.0	900	6	US-10-450-763-30870	Sequence 30870, A
892	6	2.0	726	8	US-60-643-717-17584	Sequence 17584, A	965	6	2.0	903	7	US-11-031-175-11595	Sequence 11595, A
893	6	2.0	728	6	US-10-450-763-33993	Sequence 33993, A	966	6	2.0	908	8	US-60-643-717-9942	Sequence 9942, App
894	6	2.0	731	6	US-10-852-335A-104	Sequence 104, App	967	6	2.0	908	8	US-60-643-717-9951	Sequence 9951, App
895	6	2.0	733	7	US-11-031-175-13857	Sequence 13857, A	968	6	2.0	909	6	US-10-936-061-80	Sequence 80, App1
896	6	2.0	745	5	US-09-785-085C-5	Sequence 5, App1	969	6	2.0	909	6	US-10-936-062-80	Sequence 80, App1
897	6	2.0	745	5	US-11-031-175-10275	Sequence 10275, A	970	6	2.0	914	6	US-10-489-448-1914	Sequence 1914, App
898	6	2.0	748	6	US-10-937-758A-41	Sequence 41, App1	971	6	2.0	917	6	US-10-450-763-36655	Sequence 36655, A
899	6	2.0	748	7	US-11-031-175-10617	Sequence 10617, A	972	6	2.0	917	6	US-10-450-763-39139	Sequence 39139, A
900	6	2.0	749	8	US-60-643-717-2384	Sequence 2384, App	973	6	2.0	928	7	US-11-031-175-13048	Sequence 13048, A
901	6	2.0	749	8	US-60-643-717-7219	Sequence 7219, App	974	6	2.0	931	6	US-10-450-763-48926	Sequence 48926, A


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975 6 2.0 933 6 US-10-450-763-46103 Sequence 46103, A
976 6 2.0 943 6 US-10-450-763-41229 Sequence 41229, A
977 6 2.0 947 6 US-10-450-763-52541 Sequence 52541, A
978 6 2.0 950 8 US-60-643-717-15310 Sequence 15310, A
979 6 2.0 960 8 US-60-643-717-17814 Sequence 17814, A
980 6 2.0 963 6 US-10-489-448-1176 Sequence 1176, Ap
981 6 2.0 967 6 US-10-450-763-38693 Sequence 38693, A
982 6 2.0 978 1 PCT-US04-42360-364 Sequence 364, App
983 6 2.0 991 6 US-10-450-763-53804 Sequence 53804, A
984 6 2.0 993 6 US-11-033-545-332 Sequence 332, App
985 6 2.0 994 6 US-10-717-665A-38 Sequence 38, App1
986 6 2.0 1000 7 US-10-450-763-38471 Sequence 38471, A
987 6 2.0 1013 6 US-10-450-763-38471 Sequence 38471, A
988 6 2.0 1015 1 PCT-US05-00638-99 Sequence 99, App1
989 6 2.0 1016 6 US-10-450-763-39144 Sequence 39144, A
990 6 2.0 1016 6 US-10-852-335A-164 Sequence 164, App
991 6 2.0 1025 1 PCT-US04-42360-391 Sequence 391, App
992 6 2.0 1025 8 US-60-643-717-16057 Sequence 16057, A
993 6 2.0 1037 6 US-10-450-763-46107 Sequence 46107, A
994 6 2.0 1058 6 US-10-450-763-33212 Sequence 33212, A
995 6 2.0 1058 7 US-11-031-175-15976 Sequence 15976, A
996 6 2.0 1060 7 US-11-031-175-9866 Sequence 9866, Ap
997 6 2.0 1065 6 US-10-450-763-53805 Sequence 53805, A
998 6 2.0 1074 6 US-10-450-763-55007 Sequence 55007, A
999 6 2.0 1086 8 US-60-643-717-3535 Sequence 3535, Ap
1000 6 2.0 1090 6 US-10-450-763-56527 Sequence 56527, A
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ALIGNMENTS

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RESULT 1
US-10-450-763-51705
; Sequence 51705, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 51705
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (67)..(107)
; OTHER INFORMATION: lysyl oxidase copper-binding region proteins domain
; OTHER INFORMATION: identified by eMATRIX, accession number BL00926G, p-value=2.950e-
; OTHER INFORMATION: 09, raw score of 12.21
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (61)..(117)
; OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolase family domain
; OTHER INFORMATION: identified by Pfam, accession name UCH-2, E-value=7.7e-11, Pfam
; OTHER INFORMATION: score of 49.4
US-10-450-763-51705
```

```
Query Match 2.6%; Score 8; DB 6; Length 439;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 43 ELIAFLD 50
Db 122 ELIAFLD 129
```

```
RESULT 2
US-10-450-763-54383
; Sequence 54383, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 54383
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (67)..(107)
; OTHER INFORMATION: lysyl oxidase copper-binding region proteins domain
; OTHER INFORMATION: identified by eMATRIX, accession number BL00926G, p-value=2.950e-
; OTHER INFORMATION: 09, raw score of 12.21
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (61)..(117)
; OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolase family domain
; OTHER INFORMATION: identified by Pfam, accession name UCH-2, E-value=7.7e-11, Pfam
; OTHER INFORMATION: score of 49.4
US-10-450-763-54383
```

```
Query Match 2.6%; Score 8; DB 6; Length 439;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 43 ELIAFLD 50
Db 122 ELIAFLD 129

RESULT 3
US-10-450-763-30700
; Sequence 30700, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 30700
; LENGTH: 712
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (287)..(305)
; OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolases family 2 proteins
; OTHER INFORMATION: domain identified by eMATRIX, accession number BL00972A, p-value-
; OTHER INFORMATION: 8.500e-20, raw score of 11.93
```



```
/ FEATURE:
/ NAME/KEY: DOMAIN
/ LOCATION: (286)..(317)
/ OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolases fam11 domain
/ OTHER INFORMATION: identified by Pfam, accession name UCH-1, E-value=9.8e-17, Pfam
/ OTHER INFORMATION: score of 69.0
US-10-450-763-30700
```

```
Query Match
Best Local Similarity 2.6%; Score 8; DB 6; Length 712;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 43 ELLAFLLD 50
Db 380 ELLAFLLD 387
```

```
RESULT 4
US-10-450-763-54385
; Sequence 54385, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT FILING DATE: 2003-06-11
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
SEQ ID NO 54385
LENGTH: 805
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (552)..(570)
OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolases family 2 proteins
OTHER INFORMATION: domain identified by eMATRIX, accession number BL00972A, p-value=
OTHER INFORMATION: 7.120e-18, raw score of 11.93
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (551)..(582)
OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolases fam11 domain
OTHER INFORMATION: identified by Pfam, accession name UCH-1, E-value=6.8e-13, Pfam
OTHER INFORMATION: score of 56.3
US-10-450-763-54385
```

```
Query Match
Best Local Similarity 2.6%; Score 8; DB 6; Length 805;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 43 ELLAFLLD 50
Db 645 ELLAFLLD 652
```

```
RESULT 5
US-10-450-763-54384
; Sequence 54384, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT FILING DATE: 2003-06-11
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
```

```
/ PRIOR FILING DATE: 2000-03-31
/ PRIOR APPLICATION NUMBER: 09/649,167
/ PRIOR FILING DATE: 2000-08-23
/ NUMBER OF SEQ ID NOS: 60736
/ SOFTWARE: Custom
SEQ ID NO 54384
LENGTH: 1066
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (622)..(640)
OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolases family 2 proteins
OTHER INFORMATION: domain identified by eMATRIX, accession number BL00972A, p-value=
OTHER INFORMATION: 7.120e-18, raw score of 11.93
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (622)..(653)
OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolases fam11 domain
OTHER INFORMATION: identified by Pfam, accession name UCH-1, E-value=6.8e-13, Pfam
OTHER INFORMATION: score of 56.3
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1066)
OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-54384
```

```
Query Match
Best Local Similarity 2.6%; Score 8; DB 6; Length 1066;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 43 ELLAFLLD 50
Db 715 ELLAFLLD 722
```

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RESULT 6
US-10-450-763-53691
; Sequence 53691, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT FILING DATE: 2003-06-11
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
SEQ ID NO 53691
LENGTH: 1089
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (994)..(1019)
OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolases family 2 proteins
OTHER INFORMATION: domain identified by eMATRIX, accession number BL00972D, p-value=
OTHER INFORMATION: 7.750e-19, raw score of 22.55
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (991)..(1051)
OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolase family domain
OTHER INFORMATION: identified by Pfam, accession name UCH-2, E-value=1.1e-26, Pfam
OTHER INFORMATION: score of 102.0
US-10-450-763-53691
```

```
Query Match
Best Local Similarity 2.6%; Score 8; DB 6; Length 1089;
```


Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ELLAFILD 50
|||||

Db 309 ELLAFILD 316

RESULT 7
US-10-450-763-51707
; Sequence 51707, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 51707
; LENGTH: 1125
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (254)..(1272)
; OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolases family 2 proteins
; OTHER INFORMATION: domain identified by eMATRIX, accession number BL00972A, p-value=
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1125)
; OTHER INFORMATION: 7.120e-18, raw score of 11.93
US-10-450-763-51707

Query Match 2.6%; Score 8; DB 6; Length 1125;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ELLAFILD 50
|||||

Db 347 ELLAFILD 354

RESULT 8
US-10-489-448-2732
; Sequence 2732, Application US/10489448
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyun
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Ghosh, Malabika
; APPLICANT: Ma, Yungang
; APPLICANT: Asundi, Vinod
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 810CIP PCT
; CURRENT APPLICATION NUMBER: US/10/489,448

CURRENT FILING DATE: 1004-03-10
; PRIOR APPLICATION NUMBER: US 60/324,631
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3476
; SOFTWARE: pc_fl_genes Version 6.0
; SEQ ID NO 2732
; LENGTH: 1127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-489-448-2732

Query Match 2.6%; Score 8; DB 6; Length 1127;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ELLAFILD 50
|||||

Db 347 ELLAFILD 354

RESULT 9
US-10-450-763-51706
; Sequence 51706, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 51706
; LENGTH: 1131
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (66)..(113)
; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,
; OTHER INFORMATION: accession number BL00226D, p-value=5.979e-24, raw score of 19.10
US-10-450-763-51706

Query Match 2.6%; Score 8; DB 6; Length 1131;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 ELLAFILD 50
|||||

Db 862 ELLAFLLD 869

RESULT 10

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US-10-450-763-54386
; Sequence 54386, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: HySeq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 54386
; LENGTH: 1142
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (76)..(123)
; OTHER INFORMATION: Intermediate filaments proteins domain identified by eMATRIX,
; OTHER INFORMATION: accession number BL00226D, p-value=5.979e-24, raw score of 19.10
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(121)
; OTHER INFORMATION: Intermediate filament protein domain identified by Pfam,
; OTHER INFORMATION: accession name filament_E-value=1.3e-17, Pfam score of 70.0
US-10-450-763-54386
```

Query Match

Best Local Similarity 2.6%; Score 8; DB 6; Length 1142;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 ELLAFLLD 50
Db 873 ELLAFLLD 880

RESULT 11

```
US-10-489-448-997
; Sequence 997, Application US/10489448
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Ma, Yundong
; APPLICANT: Asundi, Vinod
; APPLICANT: Wang, Zhilwei
; APPLICANT: Wang, Gezhi
; APPLICANT: Haley-Vicente, Dana
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 810CIP PCT
; CURRENT APPLICATION NUMBER: US/10/489,448
; PRIOR FILING DATE: 1004-03-10
; PRIOR APPLICATION NUMBER: US 60/324,631
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/488,725
```

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; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PAM.
```

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; SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 997
; LENGTH: 1292
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-489-448-997
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Query Match

Best Local Similarity 2.6%; Score 8; DB 6; Length 1292;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 ELLAFLLD 50
Db 516 ELLAFLLD 523

RESULT 12

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US-10-450-763-51703
; Sequence 51703, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: HySeq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 51703
; LENGTH: 1388
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1293)..(1318)
; OTHER INFORMATION: Ubiquitin carboxyl-terminal hydrolase family 2 proteins
; OTHER INFORMATION: domain identified by eMATRIX, accession number BL00972D, p-value=
; OTHER INFORMATION: score of 102.0
US-10-450-763-51703
```

Query Match 2.6%; Score 8; DB 6; Length 1388;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 43 ELAFLD 50
Db 645 ELAFLD 652

RESULT 13
US-10-699-562-21
; Sequence 21, Application US/10699562
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: JIANG, Tao
; APPLICANT: TSIEN, Roger Y.
; TITLE OF INVENTION: PEPTIDES WHOSE UPTAKE BY CELLS IS
; TITLE OF INVENTION: CONTROLLABLE
; FILE REFERENCE: 39754-0974A US
; CURRENT APPLICATION NUMBER: US/10/699,562
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polypeptide
; NAME/KEY: UNSURE
; LOCATION: 16, 32
; OTHER INFORMATION: aminocaproic acid linker
US-10-699-562-21

Query Match 2.3%; Score 7; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 167 GARRRR 173
Db 24 GARRRR 30

RESULT 14
US-10-450-763-32943
; Sequence 32943, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hysq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 32943
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-763-32943

Query Match 2.3%; Score 7; DB 6; Length 41;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 163 RPSGAR 169
Db 28 RPSGAR 34

RESULT 15
US-10-450-763-52787
; Sequence 52787, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hysq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 52787
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(64)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-52787

Query Match 2.3%; Score 7; DB 6; Length 64;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 SSANSQ 144
Db 52 SSANSQ 58

Search completed: February 12, 2005, 16:43:14
Job time : 26 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 12, 2005, 15:26:59 / Search time 71 Seconds
(without alignments)
2185.352 Million cell updates/sec

Title: US-10-030-271-2

Perfect score: 1550

Sequence: 1 MALSGSTPAFCWEDECDLY.....LREAVGREAVRLVVSDEAD 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: uniprot_03:*
2: uniprot_sprot:*
3: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	99.5	326	1 DED2_HUMAN	Q8WKF8 homo sapien
2	1401	90.4	330	1 DED2_MOUSE	Q8WKF8 mus musculu
3	672.5	43.4	369	2 Q919M3	Q919M3 brachydanio
4	636.5	41.1	404	2 Q6DHM2	Q6DHM2 brachydanio
5	614.5	39.6	318	1 DED2_HUMAN	Q75618 homo sapien
6	610.5	39.4	318	1 DED2_MOUSE	Q922K0 ratuus norv
7	608.5	39.3	318	1 DED2_MOUSE	Q922K0 ratuus norv
8	398	25.7	243	2 Q6GNZ8	Q6GNZ8 xenopus lae
9	349.5	22.5	244	2 Q6DHV2	Q6DHV2 brachydanio
10	253.5	16.4	168	2 Q8BRM9	Q8BRM9 mus musculu
11	116.5	7.5	531	2 Q7XU10	Q7XU10 oryza sativ
12	116	7.5	526	2 Q9ZRH9	Q9ZRH9 oryza sativ
13	115.5	7.5	476	2 Q6TRY3	Q6TRY3 human papil
14	115.5	7.5	5072	2 Q6UD66	Q6UD66 toxoplasma
15	114.5	7.4	381	2 Q73JY6	Q73JY6 mycobacteri
16	114.5	7.4	601	2 Q62185	Q62185 caenorhabdi
17	114	7.4	3084	2 Q8U211	Q8U211 pseudorhabdi
18	113.5	7.3	599	2 Q96NPI	Q96NPI homo sapien
19	113.5	7.3	725	1 ATU DROME	Q94546 drosophila
20	113.5	7.3	758	2 Q8N5H8	Q8N5H8 homo sapien
21	110.5	7.1	285	2 Q8LWS9	Q8LWS9 oryza sativ
22	110	7.1	878	2 Q8L7M3	Q8L7M3 arabidopsis
23	110	7.1	891	2 Q9ZM08	Q9ZM08 arabidopsis
24	110	7.1	894	2 Q9FYB2	Q9FYB2 arabidopsis
25	110	7.1	1310	2 Q9H7L6	Q9H7L6 homo sapien
26	109.5	7.1	1546	2 Q8TER5	Q8TER5 homo sapien
27	109.5	7.1	708	2 Q96JH4	Q96JH4 homo sapien
28	109.5	7.1	6620	2 Q96MA2	Q96MA2 homo sapien
29	109	7.0	1585	2 Q9UEM8	Q9UEM8 homo sapien
30	109	7.0	2303	2 Q9S596	Q9S596 homo sapien
31	108.5	7.0	374	2 Q9VHC0	Q9VHC0 drosophila

32	108.5	7.0	483	1 VE2 HPV14	P36783 human papil
33	108.5	7.0	3924	1 ANK2_HUMAN	Q01484 homo sapien
34	108	7.0	549	2 Q7XPT7	Q7XPT7 oryza sativ
35	108	7.0	581	2 Q9RU45	Q9RU45 deinococcus
36	107.5	6.9	220	2 Q6P366	Q6P366 xenopus tro
37	107.5	6.9	595	2 Q8S108	Q8S108 oryza sativ
38	107.5	6.9	323	2 Q7R429	Q7R429 giardia lam
39	106.5	6.9	231	2 Q8N922	Q8N922 homo sapien
40	106.5	6.9	238	2 Q6Y219	Q6Y219 oryza sativ
41	106.5	6.9	1040	2 Q8NHN2	Q8NHN2 homo sapien
42	106.5	6.9	2607	2 Q8BT18	Q8BT18 mus musculu
43	106	6.8	1469	2 Q6PD04	Q6PD04 mus musculu
44	106	6.8	6839	2 Q23550	Q23550 caenorhabdi
45	106	6.8	7158	2 Q23551	Q23551 caenorhabdi

ALIGNMENTS

RESULT 1

DEDD2_HUMAN STANDARD; PRT; 326 AA.

AC Q8WKF8; Q8NBR2; Q8NES1; Q8TRA8; Q96D35;

DT 05-JUL-2004 (Rel. 44, Created)

DT 05-JUL-2004 (Rel. 44, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE DNA-binding death effector domain-containing protein 2 (DED-containing protein FLAME-3).

GN Name=DEDD2; Synonym=FLAME3;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, AND INTERACTION WITH CASP8.

RX MEDLINE=21850646; PubMed=11741985; DOI=10.1074/jbc.M10749200;

RA Roth M., Steiner-Liwen F., Pawlowski K., Godzik A., Reed J.C.;

RT "Identification and characterization of DED2, a death effector domain-containing protein."

RT J. Biol. Chem. 277:7501-7508(2002).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, SUBCELLULAR LOCATION, AND INTERACTIONS WITH CASP8 AND GTP3C3.

RX MEDLINE=21961615; PubMed=11965497; DOI=10.1038/ej/cdd/4401038;

RA Zhan Y., Hegde R., Srinivasula S.M., Fernandes-Alnemri T., Alnemri E.S.;

RT "Death effector domain-containing proteins DEDD and FLAME-3 form nuclear complexes with the FTRIC102 subunit of human transcription factor IIC."

RT Cell Death Differ. 9:439-447(2002).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RX MEDLINE=2220288; PubMed=12235123; DOI=10.1083/jcb.200112124;

RA Lee J.C., Schickling O., Stegh A.H., Oshima R.G., Dinadate D., Cohen G.M., Peter M.R.;

RT "DEDD regulates degradation of intermediate filaments during apoptosis."

RT J. Cell Biol. 158:1051-1066(2002).

RN [4]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RX TISSUE=Testis; Carcinoma;

RX PubMed=14702039; DOI=10.1038/ng1285;

OT Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa K., Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., Tanai H., Kimata M., Watanabe M., Hirooka S., Chiba Y.,

RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Horita T.,
 RA Kusano Y., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
 RA Nomura Y., Togiya S., Komai F., Hara R., Takenuchi K., Arita M.,
 RA Imose N., Mueshino K., Yuki H., Oshima A., Sasaki N., Aotake S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Higashigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi T.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Omori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Oktani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senda T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RN Nat. Genet. 36:40-45(2004).
 [5]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Brain, and Lung;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cavaletto T.L., Schetz T.E.,
 RA Brownstein M.J., Ueidi T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullenbach P.H.,
 RA Boeck S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield J.S.N., Krzywicki M.T., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [6]
 RP INTERACTIONS WITH CASP8 AND CASP10.
 RX PubMed=12527898; DOI=10.1038/sj.onc.1206099;
 RA Alcivar A., Hu S., Tang J., Yang X.,
 RT "DED2 and DED2 associate with caspase-8/10 and signal cell death.";
 RT Oncogene 22:291-297(2003).
 CC -1- FUNCTION: May play a critical role in death receptor-induced
 CC apoptosis and may target Casp8 and Casp10 to the nucleus. May
 CC regulate degradation of intermediate filaments during apoptosis.
 CC May play a role in the general transcription machinery in the
 CC nucleus and might be an important regulator of the activity of
 CC GTF3C3.
 CC -1- SUBUNIT: Interacts with CASP8, CASP10 and GTF3C3. Homodimerizes
 CC and heterodimerizes with DED2.
 CC -1- SUBCELLULAR LOCATION: Nuclear; accumulated in subnuclear
 CC structures resembling nucleoli.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q8WXR8-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8WXR8-2; Sequence=VSP_010312;
 CC -1- TISSUE SPECIFICITY: Expressed in most tissues. High levels were
 CC found in liver, kidney, heart, ovary, spleen, testes, skeletal
 CC muscle and peripheral blood leukocytes. Expression was absent or
 CC low in colon and small intestine. Expression is relatively high in
 CC the tumor cell lines chronic myelogenous leukemia K-562 and the
 CC colorectal adenocarcinoma SW480. Expression is moderate in the

CC cervical carcinoma HeLa, the Burkitt's lymphoma Raji, the lung
 CC carcinoma A549, and the melanoma G361. In contrast, two leukemia
 CC cell lines, HL-60 (promyelocytic leukemia) and MOLT-4
 CC (lymphoblastic leukemia), show relatively low levels.
 CC -1- DOMAIN: Interacts with Casp8 and Casp10 are mediated by the DED
 CC domain.
 CC -1- SIMILARITY: Contains 1 death effector (DED) domain.
 CC CAUTION: Ref.5 (AAH13372) sequence differs from that shown due to
 CC a frameshift in position 186.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC DR EMBL; AF443591; AAL48220.1; -;
 CC DR EMBL; AF457575; AAM10835.1; -;
 CC DR EMBL; AY125488; AAM95240.1; -;
 CC DR EMBL; AK075328; BAC11551.1; -;
 CC DR EMBL; BC013372; AAH13372.2; ALT_FRAME.
 CC DR EMBL; BC027930; AAH27930.1; -;
 CC DR Genew; HGNC:24450; DED2.
 CC DR H-InvDB; HIX0015171; -;
 CC DR InterPro; IPR011029; DEATH_like.
 CC DR InterPro; IPR001875; DED.
 CC DR Pfam; PF01335; DED, 1.
 CC DR SMART; SMO0031; DED, 1.
 CC DR PROSITE; PS50168; DED, 1.
 CC KW Alternative splicing; Apoptosis; DNA-binding; Nuclear protein;
 CC Transcription regulation.
 CC FT DOMAIN 25 104
 CC FT DOMAIN 104 109
 CC FT DOMAIN 155 173
 CC FT VARSPLIC 145 149
 CC FT CONFLICT 27 27 H -> N (in Ref. 2).
 CC FT CONFLICT 56 56 A -> G (in Ref. 2).
 CC FT CONFLICT 79 79 D -> G (in Ref. 4).
 CC FT CONFLICT 207 207 C -> R (in Ref. 2).
 CC FT CONFLICT 230 230 Missing (in Ref. 5; AAH13372).
 CC SQ SEQUENCE 326 AA; 36178 MW; 3E7B0B307C6870CD CRC64;
 CC -----
 CC Query Match 99.5%; Score 1543; DB 1; Length 326;
 CC Best Local Similarity 99.7%; Pred. No. 6-5e-105;
 CC Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC 1 MALGSPAPCPMEDECDYVGMILSRHMFVVGQULTECELELLAFLDPAAGLA 60
 CC 1 MALGSPAPCPMEDECDYVGMILSRHMFVVGQULTECELELLAFLDPAAGLA 60
 CC 61 PARSGLELLLERRGCGESNRLQLGLVRLARHDLPLHAKRRRPPVSPERYSTG 120
 CC 61 PARSGLELLLERRGCGESNRLQLGLVRLARHDLPLHAKRRRPPVSPERYSTG 120
 CC 61 PARSGLELLLERRGCGESNRLQLGLVRLARHDLPLHAKRRRPPVSPERYSTG 120
 CC 121 SSSKRTTSSCRRRRSSSSANSQOGWETSPPKRRGRSGRGARRRRRGAAPAPQ 180
 CC 121 SSSKRTTSSCRRRRSSSSANSQOGWETSPPKRRGRSGRGARRRRRGAAPAPQ 180
 CC 121 SSSKRTTSSCRRRRSSSSANSQOGWETSPPKRRGRSGRGARRRRRGAAPAPQ 180
 CC 181 QOSEPARSSSGKTYCDIRLVRARVECHGAPALGCVASRRPQALARQDVFQATAVLR 240
 CC 181 QOSEPARSSSGKTYCDIRLVRARVECHGAPALGCVASRRPQALARQDVFQATAVLR 240
 CC 181 QOSEPARSSSGKTYCDIRLVRARVECHGAPALGCVASRRPQALARQDVFQATAVLR 240
 CC 241 SRDGSVVCIDIKFSELSTLDFPWCDDYSGALLQALRGVFLTEALREAVGRAVLLVSD 300
 CC 241 SRDGSVVCIDIKFSELSTLDFPWCDDYSGALLQALRGVFLTEALREAVGRAVLLVSD 300
 CC 301 EAD 303
 CC 301 EAD 303
 CC 301 EAD 303

RESULT 2
DED2_MOUSE
ID DED2_MOUSE STANDARD: PRT; 330 AA.
AC Q8QZV0, Q8QZV1.
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE DNA-binding death effector domain-containing protein 2 (DED-containing protein FLAME-3).
CN Name=DED2; Synonym=Flame3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6J;
RX MEDLINE=21961615; PubMed=11965497; DOI=10.1038/sj/cdd/4401038;
RA Zhan Y., Hegde R., Srinivasula S.M., Fernandes-Alnemri T., Alnemri E.S.;
RT "Death effector domain-containing proteins DEDD and FLAME-3 form nuclear complexes with the Ffl1C102 subunit of human transcription factor IIC.";
RT Cell Death Differ. 9:439-447(2002).
RL [2]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP PubMed=12527898; DOI=10.1038/sj.onc.1206099;
RX Alciivar A., Hu S., Tang J., Yang X.;
RT "DED and DED2 associate with caspase-8/10 and signal cell death.";
RT Oncogene 22:291-297(2003).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Retina;
RX MEDLINE=22288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strussberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schaller G.D., Altschul S.F., Zeeberg K.F., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., Mewan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.N., Krzywinski M.J., Skalka U., Smalls D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: May play a critical role in death receptor-induced apoptosis and may target CASP8 and CASP10 to the nucleus. May regulate degradation of intermediate filaments during apoptosis. May play a role in the general transcription machinery in the nucleus and might be an important regulator of the activity of GTF3C3.
CC -1- SUBUNIT: Interacts with CASP8, CASP10 and GTF3C3. Homodimerizes and heterodimerizes with DEDD (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear, accumulated in subnuclear structures resembling nucleoli (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q8QZV0-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8QZV0-2; Sequence=VSP_010313; VSP_010314;
CC Note=No experimental confirmation available;

CC -1- TISSUE SPECIFICITY: Expression is high in liver, heart, kidney, and testis but low in brain, spleen, lung, and skeletal muscle.
CC -1- DOMAIN: Interacts with CASP8 and CASP10 are mediated by the DED domain (By similarity).
CC -1- SIMILARITY: Contains 1 death effector (DED) domain.
CC -----
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CC -----
CC EMBL; AF545756; AAM10836.1; -;
CC EMBL; AF543541; AAN3179.1; -;
CC EMBL; BC037043; AAH37043.1; -;
CC MGD; MGI:1914629; 2410050E11RLK.
CC InterPro; IPR011029; DEATH_like.
CC InterPro; IPR011875; DED.
CC Pfam; PF01335; DED; 1.
CC SMART; SM00031; DED; 1.
CC PROSITE; PS50168; DED; 1.
CC KW Alternative splicing; Apoptosis; DNA-binding; Nuclear protein; Transcription regulation.
CC FT DOMAIN 25 104
CC FT DOMAIN 104 109
CC FT DOMAIN 156 174
CC FT VARSPLIC 1 171
CC FT FT
CC FT VARSPLIC 172 200
CC FT FT
CC FT FT
CC SQ SEQUENCE 330 AA; 36786 MW; 889BCAF9E01304B0 CRC64;
Query Match 90.4%; Score 1401; DB 1; Length 330;
Best Local Similarity 91.5%; Pred. No. 1.6e-94;
Matches 281; Conservative 5; Mismatches 17; Indels 4; Gaps 2;
QY 1 MALSGSTPAPCWEDECDIDYGMLSLHMFVVGQLTRECEIELLAFLIDEAPGAAGIA 60
DB 1 MALSGSTPAPEWEDECDIDYGMLSLHMFVVGQLTRECEIELLAFLIDEAPGAGIA 60
QY 61 RARSGLELLELEERGGCGESNLRLLGQLRLVLAARDLPHLARRRRPVSPERYSGT- 119
DB 61 RARSGLELLELEERGGCGESNLRLLGQLRLVLAARDLPHLARRRRPVSPERYSGT- 120
QY 120 SSSSRRTESGCRRRRSSSSANSQCGOWETGSPPTKRRRRSGRRPGARRRRGAPAP 179
DB 121 SSSSRRTESGCRRRRSSSSANSQCGOWETGSPPTKRRRRSGRRPGARRRRGAPAP 180
QY 180 ---QCGSEPARPPSSGKTYTCIDRLRVRAYCEHGFALFGVARRPPALAROLDVFGQT 236
DB 181 QCHQHCHQHOELGRPSSSGKTYTCIDRLRVRAYCEHGFALFGVARRPPALAROLDVFGQT 240
QY 237 AVLRGRDLSGVVCDIKFSELSYLDLFWKGDYLSGALLQRLRGVFTLEALREAVGREAVYLL 296
DB 241 AVLRGRDLSGVVCDIKFSELSYLDLFWKGDYLSGALLQRLRGVFTLEALREAVGREAVYLL 300
QY 297 VSVDEAD 303
DB 301 VSVDEAD 307
RESULT 3
Q919M3 PRELIMINARY; PRT; 369 AA.
AC Q919M3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Dedd1.


```

GN Name=dedd1;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20373792; PubMed=10917738;
RA Indhara N., Nunez G.;
RT "Genes with homology to mammalian apoptosis regulators identified in
RT zebrafish."
RL Cell Death Differ. 7:509-510(2000).
DR EMBL; AF232226; AAF66963.1; -
DR ZFIN; ZDB-GENE-000616-2; dedd1.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR01875; DED.
DR Pfam; PF01335; DED; 1.
DR PROSITE; PS50168; DED; 1.
SQ SEQUENCE 369 AA; 42244 MW; 73B09E9B17EEC247 CRC64;

Query Match 43.4%; Score 672.5; DB 2; Length 369;
Best Local Similarity 45.6%; Pred. No. 3.5e-41;
Matches 156; Conservative 36; Mismatches 91; Indels 59; Gaps 7;

QY 12 WEDECDLYYGMLSHRMFEVVGQLTE-CELELLAFILDER-----P 53
DB 13 WEETECLSYETLTSLHETFEIVGSQLTETCGE-VAFILDEYTPGKAPLDPEGWTEJLP 71
QY 54 GAAG-----GLARSSGELLELELRRGCGGSNRL 85
DB 72 GPDSPQANTPCPRLLKSWQKQPOKEGCSIASRRKPSGVYELLLELRRGLSPANLRP 131
QY 86 LGQLRLVLRHDLPLHARKRRRPVSPERSYSGTSSSKRTGSCRRRRQSSSSANSQOG 145
DB 132 LLQQLRLITRHDVLPFVSGQKRRRTVSPEKQIDPEVDFRQDREVGSNMTNIPSFENTODH 191
QY 146 QMETGS---PPTKQRRSRGRPSGARGRRRRGAPAAQOQSEPARPSEGVTCIDILR 201
DB 192 HMRASGSSMTSASSNRRKRGHHMSRSR--GPEIOPSTP-----NKVTCIDILR 243
QY 202 VRAECERGPALGEGVASRRPQALARQLDFGQATVLRSDIGSVCDIKFSELSYIDA 261
DB 244 VRAEISEHSALRGFPSPDKPPLRQPELFRASULLRTRDLSIVCDIKSKLTINDT 303
QY 262 FWGDYLSGALLQALRGVLTLEALREAVGREAVRLIVSDEAD 303
DB 304 FWPDMYSGALLKALKGVFITDLSIRAAQGVRLIVSVDOYD 345

RESULT 4
Q6DHN2 PRELIMINARY; PRT; 404 AA.
AC Q6DHN2;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DN Zgc:92202.
GN Name=Zgc:92202;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OC NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins B.S., Wagner L., Scheimen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stedlman M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Udell T.B., Toehiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.U., McKernan K.J., Malek J.A., Guneratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Myers R.M., Butterfield Y.S.,
RA Kiryianski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX Tissue=whole;
RC Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC075935; AAH75935.1; -
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR01875; DED.
DR Pfam; PF01335; DED; 1.
DR SMART; SM00031; DED; 1.
DR PROSITE; PS50168; DED; 1.
SQ SEQUENCE 404 AA; 44888 MW; 3C949DB83B07B81A CRC64;

Query Match 41.1%; Score 636.5; DB 2; Length 404;
Best Local Similarity 44.2%; Pred. No. 1.7e-38;
Matches 142; Conservative 58; Mismatches 78; Indels 43; Gaps 9;

QY 4 SCSIPAPC-----WEDECDLYYGMLSHRMFEVVGQLTECELELLAF-----LDEAP 53
DB 77 SSTRPAPAGVPEWPEEAVDAGVGLSHMFPDVGQLTRHVRVLSFLEVDVIDEY- 135
QY 54 GAAGLARARSGELLELELRRGCGGSNRLLLQQLRLVLRHDLPLHARKRRRPVSP 113
DB 136 ERGGI--RSGRPLALERQGRCDENFHVQLLITRHDLPVYTRKQOTVCPD 191
QY 114 RVSYSSTSSKRTGSCRRRRQSSSSANSQOG--QMETG-----SPTKQ--RSGRG 162
DB 192 -----PVDKYLETSVRYVSPRGTDAGQGTTHRRGQPLICCPSPGQVCPRAKP 244
QY 163 RPSGARRRRGAPAPQOQSEPARPSEGVTCIDILRVAEICEHGPALGCVASRRP 222
DB 245 APPPSRRKRSHTTADCR-----KQTCIDILRVAEICEHSAQGVAFNSKQ 294
QY 223 QALARQLDFGQATVLRSDIGSVCDIKFSELSYIDAFWGDYLSGALLQALRGVLTLE 282
DB 295 EALERQFERFQANTILSRDLSITCDIKFSELSYIDAFWRDYLNSLLALKGVFTD 354
QY 283 ALREAVGREAVRLIVSDEAD 303
DB 355 SLKQAVGHEALIKLVNVDDEED 375

RESULT 5
DEDD HUMAN STANDARD; PRT; 318 AA.
AC 075618; 060737;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Death effector domain-containing protein (Death effector domain-
DE containing testicular molecule) (DEDDpro) (FLDBD-1) (KE05).
GN Name=DEDD; Synonyms=DEDDPRO, DEFT;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```


OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=986447599; PubMed=9774341; DOI=10.1093/emboj/17.20.5974;
 RA Stegh A.H., Schickling O., Ehret A., Scaffidi C., Peterhansel C.,
 RA Holman T.G., Grunert I., Krammer P.H., Peter M.E.;
 RT "DEDD, a novel death effector domain-containing protein, targeted to
 RT the nucleus.";
 RL EMBO J. 17:5974-5986(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
 RC TISSUE=Testis;
 RX MEDLINE=99049260; PubMed=9832420; DOI=10.1210/en.139.12.4839;
 RA Leo C.P., Hsu S.Y., McGee E.A., Salanova M., Hsueh A.J.W.;
 RT "DEPT, a novel death effector domain-containing molecule predominantly
 RT expressed in testicular germ cells.";
 RL Endocrinology 139:4839-4848(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Pan G.;
 RT "PRDED-1, a novel molecule with a DED-like domain.";
 RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Thome M., Tschopp J.;
 RT "DEPPE1, a novel DED-containing protein.";
 RL Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Dendritic cell;
 RA Zhao Z., Huang X., Li N., Zhu X., Cao X.;
 RT "A novel gene from human dendritic cell.";
 RL Submitted (Mar-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Bone marrow, and Placenta;
 RX MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Kleiner S.F., Collins F.S., Wagner L., Schenker C.M., Schler G.D.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Boeck S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunatane P.H.,
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP FUNCTION, AND INTERACTIONS WITH KRT8, KRT18 AND CASP3.
 RX MEDLINE=2220288; PubMed=12235123; DOI=10.1083/jcb.200112124;
 RA Lee J.C., Schickling O., Stegh A.H., Oshima R.G., Dinadale D.,
 RA Cohen G.M., Peter M.E.;
 RT "DEDD regulates degradation of intermediate filaments during
 RT apoptosis.";
 RL J. Cell Biol. 158:1051-1066(2002).
 RN [8]
 RP INTERACTION WITH GTP33.
 RX MEDLINE=239615; PubMed=11965497; DOI=10.1038/sj/cdd/4401038;
 RA Zhan Y., Hsueh R., Srinivasula S.M., Fernandes-Alnemri T.,
 RA Alnemri E.S.;
 RT "Death effector domain-containing proteins DEDD and FLAME-3 form
 RT nuclear complexes with the TRITC102 subunit of human transcription

RT factor IIC.";
 RL Cell Death Differ. 9:439-447(2002).
 RN [9]
 RP INTERACTIONS WITH CASP8 AND CASP10.
 RX PubMed=12527898; DOI=10.1038/sj.onc.1206099;
 RA Alcivar A., Hu S., Tang J., Yang X.;
 RT "DEDD and DEDD2 associate with caspase-8/10 and signal cell death.";
 RL Oncogene 22:291-297(2003).
 CC -1- FUNCTION: A scaffold protein that directs CASP3 to certain
 CC substrates and facilitates their ordered degradation during
 CC apoptosis. May also play a role in mediating CASP3 cleavage of
 CC KRT18. Regulates degradation of intermediate filaments during
 CC apoptosis. May play a role in the general transcription machinery
 CC in the nucleus and might be an important regulator of the activity
 CC of GTP33. Inhibits DNA transcription in vitro (By similarity).
 CC -1- SUBUNIT: Interacts with CASP8, CASP10, KRT8, KRT18, CASP3 and
 CC FADD. Homodimerizes and heterodimerizes with DEDD2.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Translocated to the nucleus
 CC during CD95-mediated apoptosis where it is localized in the
 CC nucleoli (By similarity). Following apoptosis induction, the mono
 CC and/or dimerization form increases and forms filamentous
 CC structures that colocalize with KRT8 and KRT18 intermediate
 CC filament network in simple epithelial cells.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=1;
 CC IsoId=075618-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=075618-2; Sequence=VSP_003846;
 CC Note=No experimental confirmation available;
 CC -1- TISSUE SPECIFICITY: Widely expressed with highest levels in
 CC testis.
 CC -1- PTM: Exists predominantly in a mono- or dimerized form.
 CC -1- SIMILARITY: Contains 1 death effector (DED) domain.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AF083236; AAC3105.1; -
 CC EMBL: AF010034; AAD16414.1; -
 CC EMBL: AF043733; AAC80280.1; -
 CC EMBL: AJ010973; CA009445.1; -
 CC EMBL: AF064605; AAC17110.3; -
 CC EMBL: BC016724; AAH16724.1; -
 CC EMBL: BC013910; AAH13910.1; -
 CC Genew: HGNC:2755; DEDD.
 CC H-InvDB: HIX000131; -
 CC MIM: 606841; -
 CC GO: GO:0005737; C:cytoplasm; ISS.
 CC GO: GO:0005730; C:nucleolus; ISS.
 CC GO: GO:0003677; F:DNA binding; ISS.
 CC GO: GO:0006917; P:induction of apoptosis; ISS.
 CC GO: GO:0006625; P:induction of apoptosis via death domain rec. .; TAS.
 CC GO: GO:0016481; P:negative regulation of transcription; ISS.
 CC GO: GO:0007283; P:spermatogenesis; TAS.
 CC InterPro: IPR011029; DEATH_like.
 CC InterPro: IPR001875; DED.
 CC Pfam: PF01335; DED; 1.
 CC SMART: SM00031; DED; 1.
 CC PROSITE: PS50168; DED; 1.
 CC Alternative splicing; Apoptosis; DNA-binding; Nuclear protein;
 CC Repressor; Transcription regulation.
 CC DOMAIN
 CC FT 25 103 DED.
 CC FT 194 194 D -> GERIQFQKRSRLREGYKELGHWAVAYAIQY (in
 CC VARSPLIC 194 194 isoform 2).
 CC FT /FTId=VSP_003846.
 CC FT P -> L (in Ref. 5).
 CC FT SEQUENCE 318 AA; 36794 MW; FF9D5FF9B61F6BB6 CRC64;

[illegible]

RA Stegh A.H., Schickling O., Ehret A., Scaffidi C., Peterhansel C.,
 RA Hofmann T.G., Grunmt I., Krammer P.H., Peter M.E.;
 RA "DEDD, a novel death effector domain containing protein, targeted to
 RT the nucleus";
 RL EMO J. 17:5974-5986(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP Thome M., Tschopp J.;
 RT "DEP-1, a novel DED-containing protein";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N-3; TISSUE=Colon, and Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
 RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Buterfield A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Maira M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: A scaffold protein that directs CASP3 to certain
 CC substrates and facilitates their ordered degradation during
 CC apoptosis. May also play a role in mediating CASP3 cleavage of
 CC KR18. Regulates degradation of intermediate filaments during
 CC apoptosis. May play a role in the general transcription machinery
 CC in the nucleus and might be an important regulator of the activity
 CC of GTF3C3 (By similarity). Inhibits DNA transcription in vitro.
 CC -1- SUBUNIT: Interacts with CASP8, CASP10, KR18, KR18, CASP3 and
 CC FADD. Homodimerizes and heterodimerizes with DEDD2 (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Translocated to the nucleus
 CC during CD95-mediated apoptosis where it is localized in the
 CC nucleolus. Following apoptosis induction, the mono and/or
 CC dimerization form increases and forms filamentous structures
 CC that colocalize with KR18 and KR18 intermediate filament network
 CC in simple epithelial cells (By similarity).
 CC -1- TISSUE SPECIFICITY: Ubiquitously expressed.
 CC -1- PTM: Exists predominantly in a mono- or dimerized form.
 CC -1- SIMILARITY: Contains 1 death effector (DED) domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL, AJ011386; CA009604.1; -;
 DR EMBL, AF100342; AAD16415.1; -;
 DR EMBL, BC023668; AAH23668.1; -;
 DR EMBL, BC054445; AAH54445.1; -;
 DR MGD, MGI:133874; Dded.
 DR GO, GO:0005737; Cytoplasm; IDA.
 DR GO, GO:0005730; C:nucleolus; IDA.
 DR GO, GO:0003677; F:DNA binding; IDA.
 DR GO, GO:0006917; P:induction of apoptosis; IDA.
 DR GO, GO:0016481; P:negative regulation of transcription; IDA.
 DR InterPro, IPR01029; DEATH_Like.

DR InterPro, IPR01875; DED.
 DR Pfam, PF01335; DED; 1.
 DR SMART, SM00031; DED; 1.
 DR PROSITE, PS0168; DED; 1.
 KW Apoptosis; DNA-binding; Nuclear protein; Repressor;
 KW Transcription regulation.
 FT DOMAIN 25 103 DED.
 FT CONFLICT 237 237 K -> N (in Ref. 2).
 FT CONFLICT 316 316 A -> V (in Ref. 3; AAH54445).
 SQ SEQUENCE 318 AA; 36805 MW; C9A31DEC4C0E57CA CRC64;
 Query Match 39.3%; Score 608.5; DB 1; Length 318;
 Best Local Similarity 43.5%; Pred. No. 1.4e-36;
 Matches 111; Conservative 56; Mismatches 93; Indels 21; Gaps 5;
 QY 12 WEDELDLYYKGLSLHMFVVGQGLTECELELAFL-IDEPGAAGGLARASGALL 70
 DB 12 WPEERGEORHGYSLHMFVDIVGTHLTHRDVLSFLFDVIDDHERGL-IRNGDFLL 69
 QY 71 EERRGCGESNRLILGQLRLVLRHDLPLHARRRRPVSP--ERYSGTSSSKATE 127
 DB 70 ALERGRCDSESPROYQLRLITRHDLPVTLKRAVCPDLDYKLESTISRYVTR 129
 QY 128 GSCRRRGSSSSANSOGQOMETGSPPTK-----RGRSRGSPSGARRRRGAPAPQOO 182
 DB 130 ALSDEPRPPOPSKTVPHYPVCCPTSGSCMSKRPARGRTTIGSQRRK----- 180
 QY 183 SEPAPSSSGKTCYDILRLVRAVEYCEHGPALFQGVASRRPOLARQLDVFQATAVLR 242
 DB 181 -KSVPDPPEKQYCIIRLRVRAVYCOHETALQGVNFSNKPDLERQFERFNPANTLKSR 239
 QY 243 DGSAVCDIKFSELSYLDAPMGDYLSGALLQALRGVFLTEALREAVGREAVRLVSVD 302
 DB 240 DLSGIIICDIFELTYLDAPFMDYINGSLRLKGVFTIDSLKQAVGHAITLVNVD 299
 QY 303 D 303
 DB 300 D 300
 RESULT 8
 Q6GNZ8 PRELIMINARY; PRT; 243 AA.
 AC Q6GNZ8;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DE MGC80767 protein.
 OS Name=MGC80767;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
 RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC073351; AAH73351.1; -;
 DR GO: GO:0005515; F:protein binding; IEA.
 DR GO: GO:0042981; P:regulation of apoptosis; IEA.
 DR InterPro: IPR011029; DEATH_like.
 DR InterPro: IPR001875; DED.
 DR Pfam: PF01335; DED; 1.
 DR PROSITE: PS50168; DED; 1.
 SQ SEQUENCE 243 AA; 27767 MW; 57A2B89CFBD3E0BC CRC64;

Query Match 25.7%; Score 398; DB 2; Length 243;
 Best Local Similarity 40.2%; Pred. No. 2.5e-21;
 Matches 92; Conservative 31; Mismatches 52; Indels 54; Gaps 5;
 QY 12 WEEDCLDYGYGMLSHRMFEVVGQLTCECELELAFLIDEA-----PG 54
 DB 13 WEEDTCLSYETLSHIEFELVSGQLTETDVVLSFLDERVLPQGNPLDPGWTEDLP 72
 QY 53 ---PGA-----GLARASGLLELLEFRGGCGESNRLRL 89
 DB 73 EAMPSALLSMQWRNRGRTLNNDSPDLARPKGTLELLEFRGKDESNFPHLQL 132
 QY 90 LRLVLAARDLPLHAKRRRPPVSPERYSGTSSSKRTGSCRRRROSSANSQCGQ 147
 DB 133 LRLVLRHDLPLVYTKRPRAVSPERYTGPSTLDDQWMD-----RCINPNPADTREENW 187
 QY 148 EFGSPPTQRQRSGRRPGSGARRRRGAPAPQCGSEPPAPSSGKVT 196
 DB 188 ETGSNSRRKRGCTQMGCHCPKPKKVKGNTPSQ-----NPNNSKVTC 231

RESULT 9

Q6DHV2 PRELIMINARY; PRT; 244 AA.
 AC Q6DHV2;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Dedd1 protein.
 GN Name=Dedd1;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OK NCBI_Taxid=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schlier G.D.,
 RA Altshuler S.F., Zeng B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bask S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman W., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RA Strausberg R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC075865; AAH75865.1; -;
 DR GO: GO:0005515; F:protein binding; IEA.
 DR GO: GO:0042981; P:regulation of apoptosis; IEA.
 DR InterPro: IPR011029; DEATH_like.
 DR InterPro: IPR001875; DED.
 DR Pfam: PF01335; DED; 1.
 DR PROSITE: PS50168; DED; 1.
 SQ SEQUENCE 244 AA; 28051 MW; 043225AEA5D79527 CRC64;

Query Match 22.5%; Score 349.5; DB 2; Length 244;
 Best Local Similarity 37.6%; Pred. No. 9e-18;
 Matches 88; Conservative 20; Mismatches 69; Indels 57; Gaps 5;
 QY 12 WEEDCLDYGYGMLSHRMFEVVGQLTCECELELAFLIDEA-----PG 54
 DB 13 WEEDTCLSYETLSHIEFELVSGQLTETDVVLSFLDERVLPQGNPLDPGWTEDLP 72
 QY 55 AAG-----GLARASGLLELLEFRGGCGESNRLRL 86
 DB 73 PDGSPQANTPCPRLLKSWQMOPQKGCISARRPKSGVEHLLLEFRGYLSDNLRPL 132
 QY 87 GOLRLVLAARDLPLHAKRRRPPVSPERYSGTSSSKRTGSCRRRROSSANSQCGQ 146
 DB 133 LQLRLVLRHDLPLVPSQKRRVSPEROKIDYEVDFRQDEVGSNNTNIFSEVTDHN 192
 QY 147 WETGS-----PTKQRQRSGRRPGSGARRRRGAPAPQCGSEPPAPSSGKVT 196
 DB 193 WRAGSGSMTASNRKRGKHWSRKR--GPEIQQGTP-----NKVTC 238

RESULT 10

Q8BRM9 PRELIMINARY; PRT; 168 AA.
 AC Q8BRM9;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 26, Last annotation update)
 DE Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched
 DE library, clone:AB30049M9 product:similar to death effector domain-
 DE containing and DNA-binding protein 2, full insert sequence.
 GN Name=Dedd2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cortex;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.


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RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN
[3]
RC SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Cortex;
RA The FANTOM Consortium;
RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
RL "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN
[4]
RC SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata K., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RX Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN
[5]
RC SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Katsunai T., Taahiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Washiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1157-1171(2000).
RN
[6]
RC SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Cortex;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Muraoka M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Saeki D., Shibata K., Shimagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AK043908; BAC31699.1; -.
DR MGI: 1914629; Decd42.
DR GO: GO:0042981; P:regulation of apoptosis; TAS.
DR KW DNA-binding.
SQ SEQUENCE 168 AA; 17242 MW; F75D7IDC489D2425 CRC64;

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Query Match 16.4%; Score 253.5; DB 2; Length 168;
Best Local Similarity 57.1%; Pred. No. 6,1e-11;
Matches 60; Conservative 4; Mismatches 18; Indels 23; Gaps 4;

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QY 163 RPSG-----GARRRRGAPAP-----QQQSE-----ARPSSEKVTCDIRLRYA 204
DB 38 QPSGSGGAG-----ALPVPSSGGEGALQPRSSSTSSSTRSWAPPSSEKATCDIRLRYA 92
QY 205 EYCEHPALGEGVARRRRPOLAROLDVFGQATAVLRSDLGSVVC 249
DB 93 EYCEHPALGEGVARRRRPOLAROLDVFGQATAVLRSDLGSVVC 137

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RESULT 11
Q7XU10 PRELIMINARY; PRT; 531 AA.
ID Q7XU10

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AC Q7XU10;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE OSJNB0091D06.5 protein.
GN Name=OSJNB0091D06.5;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriaroidae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN
[1]
RC SEQUENCE FROM N.A.
RP PubMed=12447439; DOI=10.1038/nature01183;
RA Feng Q., Zhang Y., Hao P., Wang S., Pu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Yu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
DR EMBL: AL606459; CADD41631.1; -.
DR Gramene; Q7XU10; -.
DR InterPro; IPR008552; DUF834.
DR Pfam; PF05754; DUF834; 1.
SQ SEQUENCE 531 AA; 56907 MW; AC26AB4A459B71D CRC64;

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Query Match 7.5%; Score 116.5; DB 2; Length 531;
Best Local Similarity 27.5%; Pred. No. 2.5;
Matches 49; Conservative 18; Mismatches 72; Indels 39; Gaps 6;

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QY 53 PGAGGLARARSGLELLEERRGQC---GESNRLRLQLRLVLRH--DLPLRLRRKR 107
DB 250 PNTGGAAGARRHSLAAGTTARGAATRGDGR-----RQLTRAKAAHAREGRGAARRGR 305
QY 108 RPSV---DERYSYGTSSSSKRTGSCRRRRQ-----SSSSANSQ 143
DB 306 GPAAHHRRHRRGHGVRSAATAATRSDDHRRRQGVATPCRRPTKGRKRRREGSAHDAARR 365
QY 144 QGQMTGSPPTKGRGRSGRRSGARRRRKAPAPPOOSEARRPSSEKATCDIRL 201
DB 366 RGRRRQGTAVGLAKRTTRRSSGDGRSGGRRARPRSATB-----EGCAPADPRRR 417

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RESULT 12
Q9ZRH9 PRELIMINARY; PRT; 526 AA.
AC Q9ZRH9;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Early embryogenesis protein.
GN Name=Q9ZRH9;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriaroidae; Oryzae; Oryza.
OX NCBI_TaxID=45310;
RN
[1]
RC SEQUENCE FROM N.A.
RP STRAIN=cv. Tainung 67;
RA Tseng M.J., Wang C.S., Hsu H.R.;
RL Submitted (APR-1995) to the EMBL/Genbank/DBJ databases.
DR EMBL: U25968; AAD10369.1; -.
DR HSRP; P04776; IEXZ.
DR Gramene; Q9ZRH9; -.
DR GO: GO:0045735; P:nutrient reservoir activity; IEA.
DR InterPro; IPR006045; Cupin.

```


OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1770;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K10;
 RA Li U., Bannantine J., Zhang Q., Amosin A., Alt D., Kapur V.,
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017240; AAS06272.1; -
 KW Complete proteome.
 SQ SEQUENCE 381 AA; 41951 MW; 987D2F6155BF5E8 CRC64;

Query Match 7.4%; Score 114.5; DB 2; Length 381;
 Best Local Similarity 31.4%; Pred. No. 2.3;
 Matches 58; Conservative 14; Mismatches 58; Indels 55; Gaps 11;
 QY 53 PGAAGGLAPARSG-ELLELEERGGCGESNRLGQLRLVLRKHDLLPHLAKRRPV 111
 DB 25 PQAAGRRAARVALGAPADRRRG--GEPG-----HHALPH--RMRAVRG 67
 QY 112 PERVSGTSSSKRTGSCRRRSOSSANSOQGWETGSPPTKQRGRGRPSGGARR 171
 DB 68 PGRSGGT-----RRDPRLARRGRSAALASPARG-----APNRARRACRP---RRR 112
 QY 172 RRG--APAAPQO-----SEPARPSSEKVTCDIRLRVRAVYCEHGPALQGVASRRP 222
 DB 113 CRGPDAPAGPRHRVRPATREARAAG-----RARRPHC---PADGDLRQRNR 159
 QY 223 QALAR 227
 DB 160 LGRAR 164

Search completed: February 12, 2005, 16:29:59
 Job time : 76 secs

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OM nucleic - nucleic search, using sw model

Run on: February 12, 2005, 11:02:37 / Search time 2501 Seconds
(without alignments)
13834.635 Million cell updates/sec

Title: US-10-030-271-1

Perfect score: 909

Sequence: 1 atggcgcctatccggctgcac.....tcagtcgtgatgagctgcac 909

Scoring table: IDENTITY NTC

Gapop 10.0, Gapext 1.0

Searched: 3423544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gsa1.*
9: gb_gsa2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	907.4	99.8	1053	3	CR604307 full-length
2	907.4	99.8	1860	3	CR593642 full-length
3	907.4	99.8	1866	3	CR619301 full-length
4	907.4	99.8	1894	3	CR625070 full-length
5	847.2	93.2	1046	5	EX342837 full-length
6	822.8	90.5	1021	5	EX384448 full-length
7	802	88.2	1091	5	EX374729 full-length
8	773.6	85.1	951	5	EX375652 full-length
9	760.4	83.7	800	4	BG685173 full-length
10	738.4	81.2	837	4	BI769587 full-length
11	727.4	80.0	1089	5	BM925969 full-length
12	711.2	78.2	820	5	BP158001 full-length
13	704.2	77.5	1090	5	BM920838 full-length
14	680.8	74.9	872	4	BI523561 full-length
15	678.8	74.7	874	1	AL519410 full-length
16	653	71.8	924	5	EX442929 full-length
17	639.6	70.4	931	5	BQ923358 full-length
18	624.2	68.7	718	4	BI117988 full-length
19	607.8	66.9	1042	5	BQ072022 full-length
20	605	66.6	926	4	BG757042 full-length
21	596.4	65.6	1641	3	AK010701 full-length
22	593.2	65.3	1025	6	BY710117 full-length
23	588.8	64.8	4598	3	AK043908 full-length
24	586.8	64.6	878	4	BI756130 full-length

25	582.8	64.1	905	4	BI910528
26	582.8	64.1	927	4	BG251151
27	582.8	64.1	947	4	BI910416
28	582.8	64.1	1586	3	CR590827
29	582.4	64.1	634	4	BI907024
30	582.4	64.1	1131	2	BE907425
31	582.4	64.1	1510	3	CR599685
32	582.4	64.1	1062	5	BM908148
33	581.4	64.0	655	7	CK429257
34	581.2	63.9	1051	5	BQ073197
35	581.2	63.9	1161	5	BU902131
36	580.8	63.9	644	7	CN373290
37	579.6	63.8	678	7	CN373294
38	579.6	63.8	783	5	BU602002
39	577.4	63.5	826	6	CB991766
40	574	63.1	938	5	BU507654
41	572.4	63.0	671	7	CN373287
42	570.6	62.8	780	6	CB994488
43	570.4	62.8	931	5	BX381775
44	569.4	62.6	993	4	BM559141
45	562.8	61.9	1017	3	AK011713

ALIGNMENTS

RESULT 1
LOCUS CR604307 1053 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DL006YL09 of B cells (Ramos cell line)
Cot 25-normalized of Homo sapiens (human).

ACCESSION CR604307.1 GI:50485114

VERSION HTC; CDSIT_CDNA.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1053)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished

REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/InvitrogenCorporation1600

REFERENCE 2 (bases 1 to 1053)
AUTHORS Genoscope.

JOURNAL Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES
source location/Qualifiers
1..1053
/organism="Homo sapiens"

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DL006YL09"

/tissue_type="B cells (Ramos cell line)" Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 99.8%; Score 907.4; DB 3; Length 1053;
Best Local Similarity 99.9%; Pred. No. 2.9e-189;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGGCGCTATCCGGCTGCACCCCGGCGCTGCTGGAGAGAGATAGGCTGACTAC 60

99 ATGGCGCTATCCGGCTGCACCCCGGCGCTGCTGGAGAGAGATAGGCTGACTAC 158

DB


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QY 61 TACGGATCTGTGCTTCAACGATATGTTGAGGTGTGAGCGGCACTGACCGAGTGC 120
DB 159 TACGGATCTGTGCTTCAACGATATGTTGAGGTGTGAGCGGCACTGACCGAGTGC 218
QY 121 GAGCTGAGACTCTGTGCTTCTTGTGCTGAGTGAAGGCTCTGAGCGGCGGCACTGAGC 180
DB 219 GAGCTGAGACTCTGTGCTTCTTGTGCTGAGTGAAGGCTCTGAGCGGCGGCACTGAGC 278
QY 181 CGGGCCCGGAGCGGCTTAGAGCTCTGTGAGTGAAGGCTCTGAGCGGCGGCACTGAGC 240
DB 279 CGGGCCCGGAGCGGCTTAGAGCTCTGTGAGTGAAGGCTCTGAGCGGCGGCACTGAGC 338
QY 241 AGCAACTCTGCTGTGCTGAGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 339 AGCAACTCTGCTGTGCTGAGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 398
QY 301 GAGCTGAGACTCTGTGCTTCTTGTGCTGAGTGAAGGCTCTGAGCGGCGGCACTGAGC 360
DB 399 GAGCTGAGACTCTGTGCTTCTTGTGCTGAGTGAAGGCTCTGAGCGGCGGCACTGAGC 458
QY 361 AGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 459 AGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 518
QY 421 AATTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 519 AATTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 578
QY 481 CGGGCCCGGAGCGGCTTAGAGCTCTGTGAGTGAAGGCTCTGAGCGGCGGCACTGAGC 540
DB 579 CGGGCCCGGAGCGGCTTAGAGCTCTGTGAGTGAAGGCTCTGAGCGGCGGCACTGAGC 638
QY 541 GAGCACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 639 GAGCACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 698
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DB 759 CGGGCCCGGAGCGGCTTAGAGCTCTGTGAGTGAAGGCTCTGAGCGGCGGCACTGAGC 818
QY 721 TCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 819 TCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 878
QY 781 GCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 879 GCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 938
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DB 939 ACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 998
QY 901 GAGGCTGAC 909
DB 999 GAGGCTGAC 1007

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REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1. (bases 1 to 1860)
Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Feng Liang Email: fliang@life.techn.com URL:
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue
2 (bases 1 to 1860)
Genoscope.
Direct Submission
Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail: sequefgenoscope.cns.fr)
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1. 1860
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODK010YK16"
/tissue="Hela cells Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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Query Match 99.8%; Score 907.4; DB 3; Length 1860;
Best Local Similarity 99.9%; Pred. No. 3e-189;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 ATGGCGTATCCGGGTCGACCCCGGCGGCTGCTGAGAGAGAGAGAGAGAGAGAGAG 60
DB 71 ATGGCGTATCCGGGTCGACCCCGGCGGCTGCTGAGAGAGAGAGAGAGAGAGAGAG 130
QY 61 TACGGATCTGTGCTTCAACGATATGTTGAGGTGTGAGCGGCACTGACCGAGTGC 120
DB 121 TACGGATCTGTGCTTCAACGATATGTTGAGGTGTGAGCGGCACTGACCGAGTGC 190
QY 121 GAGCTGAGACTCTGTGCTTCTTGTGCTGAGTGAAGGCTCTGAGCGGCGGCACTGAGC 180
DB 191 GAGCTGAGACTCTGTGCTTCTTGTGCTGAGTGAAGGCTCTGAGCGGCGGCACTGAGC 250
QY 181 CGGGCCCGGAGCGGCTTAGAGCTCTGTGAGTGAAGGCTCTGAGCGGCGGCACTGAGC 240
DB 251 CGGGCCCGGAGCGGCTTAGAGCTCTGTGAGTGAAGGCTCTGAGCGGCGGCACTGAGC 310
QY 241 AGCAACTCTGCTGTGCTGAGCACTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 311 AGCAACTCTGCTGTGCTGAGCACTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 370
QY 301 GAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 371 GAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 430
QY 361 AGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 431 AGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 490
QY 421 AATTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 491 AATTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 550
QY 481 CGGGCCCGGAGCGGCTTAGAGCTCTGTGAGTGAAGGCTCTGAGCGGCGGCACTGAGC 540
DB 551 CGGGCCCGGAGCGGCTTAGAGCTCTGTGAGTGAAGGCTCTGAGCGGCGGCACTGAGC 610
QY 541 GAGCACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 611 GAGCACTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 670

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RESULT 2
LOCUS CR593642 1860 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CSODK010YK16 of Hela cells Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR593642
VERSION CR593642.1 GI:50474449
KEYWORDS HTC; cDNA;
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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QY 601 CCGGTTGAGCAGAGTACTGCGAGCATGGGCGACCTTGGAGCAGGGCGTGGCATCCCGG 660
DB 671 CCGGTTGAGCAGAGTACTGCGAGCATGGGCGACCTTGGAGCAGGGCGTGGCATCCCGG 730
QY 661 CCGGCCCCAGGCGCTGGGCGCGGCGAGCTGGAGCTGTTTGGGCGAGGCGACCGCATGTCGCG 720
DB 731 CCGGCCCCAGGCGCTGGGCGCGGCGAGCTGGAGCTGTTTGGGCGAGGCGACCGCATGTCGCG 790
QY 721 TCAAGGAGCCTGGGCGCTGTTGTTGTGATCATGAAGTTCTCAGAGCTCTCTCATCTGGAC 780
DB 791 TCAAGGAGCCTGGGCGCTGTTGTTGTGATCATGAAGTTCTCAGAGCTCTCTCATCTGGAC 850
QY 781 GCGTTCTGGGCGAGTACTGAGTGGCGCCCTGCTGAGGCGCTGCGGCGGCGTGTCTG 840
DB 851 GCGTTCTGGGCGAGTACTGAGTGGCGCCCTGCTGAGGCGCTGCGGCGGCGTGTCTG 910
QY 841 ACTGAGGCGCTGGGAGAGGCTGTGGGCGGAGGCGCTTTCGCTGCTGCTGATGTGGAT 900
DB 911 ACTGAGGCGCTGGGAGAGGCTGTGGGCGGAGGCGCTTTCGCTGCTGCTGATGTGGAT 970
QY 901 GAGGCTGAC 909
DB 971 GAGGCTGAC 979

RESULT 3
CR619301
LOCUS
DEFINITION CR619301 1866 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DC015J24 of Neuroblastoma Cot
25-normalized of Homo sapiens (human).
CR619301
ACCESSION CR619301.1 GI:50500108
VERSION HTC; CNSLT cDNA.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 1866)
TITLE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
REMARK Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1866)
REFERENCE
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source
1. 1866
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC015J24"
/issue_type="Neuroblastoma Cot 25-normalized"
/plasmid="pCMVSPORT_6"

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Query Match 99.8%; Score 907.4; DB 3; Length 1866;
Best Local Similarity 99.9%; Pred. No. 3e-189;
Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCGCGTATCCGAGGTGACCCCGGCGCGTGTGGAGAGATGATGCTCGAGCTAC 60
DB 76 ATGCGCGTATCCGAGGTGACCCCGGCGCGTGTGGAGAGATGATGCTCGAGCTAC 135

QY 61 TACGAGATGCTGTGCTTCAACCTGATGTTGAGGTGAGGCGGCGAAGTACCGAGTGC 120
DB 136 TACGAGATGCTGTGCTTCAACCTGATGTTGAGGTGAGGCGGCGAAGTACCGAGTGC 135
QY 121 GAGCTGAGAGTCTCTGGCTTTTCTGCTGATGAGGCTCTGGCGCCCGGAGGCTTAAGC 180
DB 196 GAGCTGAGAGTCTCTGGCTTTTCTGCTGATGAGGCTCTGGCGCCCGGAGGCTTAAGC 255
QY 181 CCGGCCCCAGGCGGCTTGAAGCTCTGCTGAGTGAAGGCGGCGGCGAGTGCAGG 240
DB 256 CCGGCCCCAGGCGGCTTGAAGCTCTGCTGAGTGAAGGCGGCGGCGAGTGCAGG 315
QY 241 AGCAACTGCGGCTGTGGGCGCAACTCTGCGGCTGTGCGCGCGCAAGCTTGC 300
DB 316 AGCAACTGCGGCTGTGGGCGCAACTCTGCGGCTGTGCGCGCGCAAGCTTGC 375
QY 301 CACCTGGCGGCGCAAGCGGCGCGCGCAAGTGTCTTCAGAAAGCTATAGCTATGCACTCC 360
DB 376 CACCTGGCGGCGCAAGCGGCGCGCGCAAGTGTCTTCAGAAAGCTATAGCTATGCACTCC 435
QY 361 AGCTCTTCAAAAGAGGAGCAGAGGCTAGCTGCGGCTGCGGCGAGTCAAGCAGTTCTGCA 420
DB 436 AGCTCTTCAAAAGAGGAGCAGAGGCTAGCTGCGGCTGCGGCGAGTCAAGCAGTTCTGCA 495
QY 421 AATTCTCAGCAGGCTGAGTGGAGAGAGGCTCCCGCCCAAGCGGCGAGCGAGT 480
DB 496 AATTCTCAGCAGGCTGAGTGGAGAGAGGCTCCCGCCCAAGCGGCGAGCGAGT 555
QY 481 CCGGCGCGGCGCGAGTGTGTGTCAGACGCGCGGCGAGAGGCGCGCGAGCGGCGAG 540
DB 556 CCGGCGCGGCGCGAGTGTGTGTCAGACGCGCGGCGAGAGGCGCGCGAGCGGCGAG 615
QY 541 CAGCAGTCAAGAGCGCGCGCGAGCCTTCTCTGAAGGCAAGTGAACCTGTGACATCCGCTC 600
DB 616 CAGCAGTCAAGAGCGCGCGCGAGCCTTCTCTGAAGGCAAGTGAACCTGTGACATCCGCTC 675
QY 601 CCGGTTGAGCAGAGTACTGCGAGCATGGGCGACCTTGGAGAGGAGGCGCTGGATCCCGG 660
DB 676 CCGGTTGAGCAGAGTACTGCGAGCATGGGCGACCTTGGAGAGGAGGCGCTGGATCCCGG 735
QY 661 CCGGCCCCAGGCGCTGGCGCGGCGAGCTGAGCTGTTTGGGCGAGGCGACCGCATGTCGCG 720
DB 736 CCGGCCCCAGGCGCTGGCGCGGCGAGCTGAGCTGTTTGGGCGAGGCGACCGCATGTCGCG 795
QY 721 TCAAGGAGCCTGGGCGCTGTTGTTGTGATCATGAAGTTCTCAGAGCTCTCTCATCTGGAC 780
DB 796 TCAAGGAGCCTGGGCGCTGTTGTTGTGATCATGAAGTTCTCAGAGCTCTCTCATCTGGAC 855
QY 781 GCGTTCTGGGCGAGTACTGAGTGGCGGCTGCTGAGGCGCTTGGGCGGCGTGTCTG 840
DB 856 GCGTTCTGGGCGAGTACTGAGTGGCGGCTGCTGAGGCGCTTGGGCGGCGTGTCTG 915
QY 841 ACTGAGGCGCTGGAGAGGCTGTGGGCGGAGGCTGTTGCTGCTGCTGCTGATGTGGAT 900
DB 916 ACTGAGGCGCTGGAGAGGCTGTGGGCGGAGGCTGTTGCTGCTGCTGCTGATGTGGAT 975
QY 901 GAGGCTGAC 909
DB 976 GAGGCTGAC 984

RESULT 4
CR625070
LOCUS
DEFINITION CR625070 1894 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DC001YC18 of Neuroblastoma Cot
25-normalized of Homo sapiens (human).
CR625070
ACCESSION CR625070.1 GI:50505877
VERSION HTC; CNSLT cDNA.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

	REFERENCE	1 (bases 1 to 1894)
AUTHORS	Li, W.B., Gruber C., Jessee J. and Polajsek D.	
TITLE	Full-length cDNA libraries and normalization	
JOURNAL	Unpublished	
REMARK	Contact : Peng Liang Email : liang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 1894) Genoscope. Direct Submission Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primers end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Sca I sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. Location/Qualifiers 1..1894 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CSODC001YC18" /tissue.type="Neuroblastoma Cot 25-normalized" /plasmid="pCMVSPORT_6"	
FEATURES		
SOURCE		
ORIGIN		
Query Match	99.8%; Score 907.4; DB 3; Length 1894;	
Best Local Similarity	99.9%; Pred. No. 36-189;	
Matches	908; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
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DB	89 ATGGGCATATCGGGTCGACCCCGGCCCTGTCTGGAGAGATGAGTCTTGACTAC	148
OY	61 TACGGGATGCTGTGCTTCAACCGTAGTTGAGAGTGAGGGCGGGAACAATACTGACGAGTGC	120
DB	149 TAGGGAGTGTCTGCTTCAACCGTAGTTGAGAGTGAGGGCGGGAACAATACTGACGAGTGC	208
OY	121 GAGCTGAGCTCTCTGGCTTTCTGTCTGATGAGAGCTCTGTGGCGCGCGAGAGCTTAAGC	180
DB	209 GAGCTGAGAGCTCTGTGGCTTTCTGTCTGATGAGAGCTCTGTGGCGCGCGAGAGCTTAAGC	268
OY	181 CGGGCCGCGAGGGCGCTTAGAGCTCTGTCTGAGCTTGAGAGCGCGCGGAGTGCAGAG	240
DB	269 CGGGCCCGCAGGGCGCTTAGAGCTCTGTCTGAGCTTGAGAGCGCGCGGAGTGCAGAG	328
OY	241 AGCAACCTGGCGCTCTGTGGGAGCACTCTGCGCGGTGCTGGCGCGCAAGCACTGTGCGC	300
DB	329 AGCAACCTGTGGCTCTGTGGGAGCACTCTGCGCGGTGCTGGCGCGCAAGCACTGTGCGC	388
OY	301 CACTGGGCGCGAAGCGGCGCGCGCAGGTCTCCAGAAGCTTAGCTATGGACCTTC	360
DB	389 CACTGGGCGCGAAGCGGCGCGCGCAGGTCTCCAGAAGCTTAGCTATGGACCTTC	448
OY	361 AGCTTTAAAGAGAGCAGAGGGTAGCTGCGTGCCTGTGGAGCAAGTCTTGCA	420
DB	449 AGCTTTAAAGAGAGCAGAGGGTAGCTGCGTGCCTGTGGAGCAAGTCTTGCA	508
OY	421 AATTCTAGCAGGGGTCAATGGGAGCAGAGTCTCCCGCCCAACCAACGGCAGAGGGGAGT	480
DB	509 AATTCTAGCAGGGGTCAATGGGAGCAGAGTCTCCCGCCCAACCAACGGCAGAGGGGAGT	568
OY	481 CGGGGCGGGCCAAGTGTGTGTCAGACGGCGCGGAGAGGGGCCCCAGCGCACCCAG	540
DB	569 CGGGGCGGGCCAAGTGTGTGTCAGACGGCGCGGAGAGGGGCCCCAGCGCACCCAG	628
OY	541 CAGCAGTCAAGCCCGCCAGACTTCTCTGAAGCAAGTGAAGCTTGACATCCGAGTTC	600
DB	629 CAGCAGTCAAGCCCGCCAGACTTCTCTGAAGCAAGTGAAGCTTGACATCCGAGTTC	688
OY	601 CGGGTTCAGACAGACTACTCGAGCATGGGCAAGCTTGGAGCAGAGGCGTGGCATTC	660

Df		689	CGGGTTGAGAGAGTACTGTGCAGACATGTGGCCAACTTGAGGCAAGGGGTGGATTCCGG	748
OY		661	CGGCCCCAGGCGCTGGCGCGCGCAGCTGTGAGCTGTTGGGCAAGCCACCAGTCGTGCGC	720
Df		749	CGGCCCCAGGCGCTGGCGCGCACCTGGACGCTGTTGGGCAAGGCCACCGCATGTCTGCGC	808
OY		721	TCAAAGGGAACCTGGGGCTCTGTGGTTTTGTGACATCAAGAATCTTCAGAGCTCTCTATCTGGAC	780
Df		809	TCAAGGGAACCTGGGGCTCTGTGGTTTTGTGACATCAAGAATCTTCAGAGCTCTCTATCTGGAC	868
OY		781	GCCTTCTGGGGGCGAATACTAGTAGTGGCGCCCTGTGTCAGAGGCCCTGCGGGGCGTGTCTGTG	840
Df		869	GCCTTCTGGGGGCGAATACTAGTAGTGGCGCCCTGTGTCAGAGGCCCTGCGGGGCGTGTCTGTG	928
OY		841	ACTAGAGCCCTTGCAGAGAGCTGTGTGGCGCGGAGAGCTGTTCCCTCTGTGCTGATGTGGAT	900
Df		929	ACTAGAGCCCTTGCAGAGAGCTGTGTGGCGCGGAGAGCTGTTCCCTCTGTGCTGATGTGGAT	988
OY		901	GAGGCTGAC	909
Df		989	GAGGCTGAC	997
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BX342837				
LOCUS	BX342837	1046 bp	mRNA	linear EST 07-APR-2004
DEFINITION	BX342837 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED			
ACCESSION	Homo sapiens cDNA clone CS0DL006YL09.5-PRIME, mRNA sequence.			
KEYWORDS	BX342837 BX342837.2 GI:46266793			
SOURCE	EST.			
ORGANISM	Homo sapiens (human)			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
JOURNAL	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
COMMENT	Li,W.B., Gruber,C., Jessee,J. and Polyses,D. Full-length cDNA libraries and normalization Unpublished (2001) On May 1, 2003 this sequence version replaced gi:30313128. Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 9074.r For more information about this cluster, see http://www.genoscope.cns.fr/cdna?cs=CS0DL006CP5QPL&c=9074.r. Location/Qualifiers 1. 1046 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DL006YL09" /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED" /cell_line="RAMOS CELL LINE" /clone_1pb="Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED" /note="1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."			
FEATURES				
SOURCE				
ORIGIN				
Query Match	93.2%	Score 847.2;	DB 5;	Length 1046;
Best Local Similarity	98.1%;	Pred. No. 5.2e-176;		
Matches	888;	Conservative	9;	Mismatches 3; Indels 5; Gaps 4;


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QY      1 ATGGCGCTATCCGGGTCGACCCCGGCCCGCTGCTGGAGAGATGATGCTCGACTAC 60
DB      99 ATGGCGCTATCCGGGTCGACCCCGGCCCGCTGCTGGAGAGATGATGCTCGACTAC 158
QY      61 TAGGGATGCTGTCGCTTCAACCGTATGTTGAGTGTGGCGGCACTGACCGAGTGC 120
DB      159 TAGGGATGCTGTCGCTTCAACCGTATGTTGAGTGTGGCGGCACTGACCGAGTGC 218
QY      121 GAGCTGAGAGCTCTGAGCTTTCTGCTGATGATGAGGCTCTGGCGCCGCGGAGCTTACGC 180
DB      219 GAGCTGAGAGCTCTGAGCTTTCTGCTGATGATGAGGCTCTGGCGCCGCGGAGCTTACGC 277
QY      181 CGGCGCCGAGCGGAGCTTGAAGCTCTGCTGAGCTGAGCGCGCGGAGTGCAGTGCAG 240
DB      278 CGGCGCCGAGCGGAGCTTGAAGCTCTGCTGAGCTGAGCGCGCGGAGTGCAGTGCAG 337
QY      241 AGCAACTGCGGCTGCTGCGGCGCAATCTCTGCGGCTGTGGCCCGCCAGCACTGCTGCC 300
DB      338 AGCAACTGCGGCTGCTGCGGCGCAATCTCTGCGGCTGTGGCCCGCCAGCACTGCTGCC 397
QY      301 CACCTGAGCGGAGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB      398 CACCTGAGCGGAGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 455
QY      361 AGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB      456 AGCTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 515
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DB      576 CGGCGCGGAGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 635
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DB      636 CAGCAGTCAAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 695
QY      601 CGGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB      696 CGGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 755
QY      661 CGGCGCGGAGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB      756 CGGCGCGGAGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 815
QY      721 TCAAGGAGAGCTGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
DB      816 TCAAGGAGAGCTGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 875
QY      781 GCTTTCT-GGGGGAGACTACTGAGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 839
DB      876 GCTTTCTGAGGAGAGACTACTGAGTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 935
QY      840 GACTGAGAGCGCTGAGAGAGCTGAGGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 899
DB      936 GACTGAGAGCGCTGAGAGAGCTGAGGAGCGGAGAGAGAGAGAGAGAGAGAGAGAG 994
QY      900 TGAGG 904
DB      995 TGAGS 999

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RESULT 6
LOCUS    BX384448
DEFINITION BX384448 Homo sapiens HELA CELLS COR 25-NORMALIZED Homo sapiens
CDNA clone CS0DK010YK16 5-PRIME, mRNA sequence.
ACCESSION BX384448
VERSION   BX384448.2 GI:46557783
KEYWORDS EST.

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SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1021)
AUTHORS   Li, W.B., Gruber, C., Jessee, J., and Polyes, D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On May 8, 2003 this sequence version replaced gi:30440338.
Contact: Genoscope
Genoscope - Centre National de Sequenage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segre@genoscope.cns.fr, web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
9074.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0DK010BF08QPlc=9074.f.
FEATURES
Source
Location/Qualifiers
1..1021
/organism="Homo sapiens"
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/clone="CS0DK010YK16"
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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 90.5%; Score 822.8; DB 5; Length 1021;
Best Local Similarity 97.0%; Pred. No. 1,2e-170;
Matches 877; Conservative 12; Mismatches 9; Indels 6; Gaps 5;
QY      1 ATGGCGCTATCCGGGTCGACCCCGGCCCGCTGCTGGAGAGATGATGCTCGACTAC 60
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QY      61 TAGGGATGCTGTCGCTTCAACCGTATGTTGAGTGTGGCGGCACTGACCGAGTGC 120
DB      131 TAGGGATGCTGTCGCTTCAACCGTATGTTGAGTGTGGCGGCACTGACCGAGTGC 190
QY      121 GAGCTGAGAGCTCTGAGCTTTCTGCTGATGATGAGCTCTGGCGCCGCGAGGCTTACGC 180
DB      191 GAGCTGAGAGCTCTGAGCTTTCTGCTGATGATGAGCTCTGGCGCCGCGAGGCTTACGC 249
QY      181 CGGCGCCGAGCGGAGCTTGAAGCTCTGCTGAGCTGAGAGCGCGCGGAGTGCAGTGCAG 240
DB      250 CGGCGCCGAGCGGAGCTTGAAGCTCTGCTGAGCTGAGAGCGCGCGAGTGCAGTGCAG 309
QY      241 AGCAACTGCGGCTGCTGCGGCGCAATCTCTGCGGCTGTGGCCCGCCAGCACTGCTGCC 300
DB      310 AGCAACTGCGGCTGCTGCGGCGCAATCTCTGCGGCTGTGGCCCGCCAGCACTGCTGCC 369
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DB      370 CACCTGAGCGGAGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 427
QY      361 AGCTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
DB      428 AGCTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 487
QY      420 AATTTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 479
DB      488 AATTTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 547
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Db 548 TGGGGCCGGCCCAAGTGGTGGTCCAGACGGCGGGAGAGGGGGCCCCAGCCGCACCCGA 607

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Db 608 GCAGCAGTCAAGGCCCGCCAGACCTTCTCTGAAGCAAAATGACCTGTGACATCCGGCT 667

Qy 600 CCGGGTTGAGCAGCAGTACTCGGAGCAATGGGCCAGCCTTGGAGCAGGGCGTGGCATCCCG 659

Db 668 CCGGGTTGAGCAGCAGTACTCGGAGCAATGGGCCAGCCTTGGAGCAGGGCGTGGCATCCCG 727

Qy 660 GCGGGCCCAAGGGCTGGCGCGCGCCAGCTGGAAGCTGTTTGGGCAAGGCCACCGCAGTGTCTGG 719

Db 728 GCGGGCCCAAGGGCTGGCGCGCGCCAGCTGGAAGCTGTTTGGGCAAGGCCACCGCAGTGTCTGG 787

Qy 720 CTCAAGGGAGCCCTGGGCTCTGTGTTTGTGACATCAAGTCTGACAGCTCTCCATCTGGA 779

Db 788 CTCARAGGACCTGGGCTCTGTGTTTGTGACATCAARTTCTGAGACCTTCTCAATCTGGA 847

Qy 780 CGCCTTCTGGGGCGACTACTTGTAGTGGCGCCCTGTGTCAGGGCCCTGGCGGGCGTGTCTCT 839

Db 848 CGCCTTCTGGGGSG-MTAACTGATGGCGCCCTGTGTCAGAGCCCTGGCGGGCGGTGTCTCT 906

Qy 840 GACTGAGGCCCTGGCGAGAGGCTGTGGGCCCGGAGGCTGTTGCGCTTGCTGTCAATGTGTGA 899

Db 907 GACTGAGGCCCTGGCGAGAGGCTGTGGGCCCGGAGGCTGTTGCGCTTGCTGTCAATGTGTGA 965

Qy 900 TGAG 903

Db 966 TRAG 969

RESULT 7	
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LOCUS	BX374729 1091 bp mRNA linear EST 23-APR-2006
DEFINITION	BX374729 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
ACCESSION	CDNA clone CS0DC001YC18 5-PRIME, mRNA sequence.
VERSION	BX374729
KEYWORDS	BX374729.2 GI:46557336
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	Li W.B., Gruber C., Jesssee J. and Polayes D.
AUTHORS	Full-length cDNA libraries and normalization
TITLE	Unpublished (2001)
JOURNAL	
COMMENT	On May 8, 2003 this sequence version replaced gi:30438519.

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?c=CS0DC001BB09QPI&c=9074.r>
 Location/Qualifiers
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/organism="Homo sapiens"
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/cname="CS0DC0011C18"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/cname_lib="HOMO SAPIENS NEUROBLASTOMA COT 25-NORMALIZED"
/ncore="1st strand cDNA was primed with a NOTI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

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ORIGIN

Query Match	88.2%;	Score 802;	DB 5;	Length 1091;
Best Local Similarity	96.8%;	Pred. NO. 4.7e-166;		
Matches 881; Conservative	10;	Mismatches 11;	Indels 8;	Gaps 7;

OY	1	ATGGACGTATCCGGATCGAACCCCGGCCCGTGTCTGGAGAGAGATGATGCTGTGAATAC	60
Db	89	ATGGCCCTATCCGGATCGAACCCCGGCCCGTGTCTGGAGAGAGATGATGCTGTGAATAC	148
OY	61	TACGGAGATGCTGTGCTTCAACCGTATGTTTCAGAGTGTGTGGCCGGGCAACTGACCAATGC	120
Db	149	TACGGAGATGCTGTGCTTCAACCGTATGTAACGAGTGTGTGGCCGGGCAACTGACCAAGTGC	208
OY	121	GAGCTGAGAGCTCTGTGACTTTTCTGTGATGATGAGCTCTGTGACGCGCCGACGAGCTTAGCC	180
Db	209	GAGCTGAGAGCTCTGTGACTTTTCTGTGATGATGAGGCTCTGTGACGCGCCGACG	267
OY	181	CGGAGCCCGCAGCGGACTTAGAGCTCTGTGCTGAGCTGTGAGCCCGCGGGCAATGTGCGGAG	240
Db	268	CGGAGCCCGCAGCGGACTTAGAGCTCTGTGCTGAGCTGTGAGCCCGCGCAATGTGAGAGAG	327
OY	241	AGGAACCTGTGAGCTGTGGGGCAATCCGTCGACGCTGTGACCGCGCAAGACTTGTCTGCG	300
Db	328	AGGAACCTGTGAGCTGTGGGGCAATCTCTGTGAGCTGTGACCGCGCAAGACTTGTCTGCG	387
OY	301	CACCTGAGCGCGCAAGCGCGCGCGGACGATGTCTTCAGAACGCTATGACTATGACACTTC	360
Db	388	CACCTGAGCGCGCAAA--MGCGCCGGCGCAGATGTCTTCAGAACGCTATGACTATGAGCACTTC	445
OY	361	AGCTCTTCAAAAGAGACAGAGAGGTAGCTGTGCGCTGTGCGAGTCAAGCAGTTCTGCA	420
Db	446	AGCTCTTCAAAAGAGACATAGAGTATAGCTGTGCGCTGTGCGAGTATAGCATTTCTGCA	505
OY	421	AATTCTCAGCAGGGTCAGTGGAGACAGAGCTTCCCTCCCAACCAAGCGGACGGCGGAGT	480
Db	506	AATTCTCAGCAGGGTCAGTGGAGACAGAGCTTCCCTCCCAACCAAGCGGACGGAGT	565
OY	481	CGGGGCGCGGCCAGTGTGTGTGTCCAGACGGCGCGGAGAGAGGGGCCAGCGCACCCAG	540
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OY	541	CAGCAGTCAGAGGCCCGCCAGACCTTCTCTGAAGGCAAAATGACCTGTGACATCCGACTC	600
Db	625	CAGCAGTCAGAGGCCCGCCAGACCTTCTCTGAAGGCAAAATGACCTGTGACATCCGACTC	684
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OY	661	CGGACCCCAAGCGCTGTGCGCGGACGCTGTGACGTGTTTGGGCAAGGCCACCGCAGTGTGCG	720
Db	745	CGG--CCGAGGCGCTGTGCGCGGACCGGGACGTTTGGGCAAG--CACCGCAGTGTGCTGCG	802
OY	721	TCAAGAGACCTGTGGGCTGTGTGTTTGTACATCAAGATTCTTGAAGCTCTCTATCTGTGAC	780
Db	803	TCAAGAGACCTGTGGGCTGTGTGTTTGTACAAACAAGTCTTGAAGCTCTCTATCTGTGAC	862
OY	781	GCCCTTCT--GGGCGGACACTGATGATGTGGCCCTGTGTGACGACCCTGTGCGGGGCGTTCCT	835
Db	863	GCCCTTCTGTGGGGGGAATACCTGATGTGTGGCCCTGTGTGACGACCCTGTGCGGGGCGTTCCT	922
OY	840	GACTGAGAGCCCTGTCCGAGAGGCTGTGTGGGCCCGGAGGCTGTTCGCTGTCTGTGATGTGGA	899
Db	923	GACTGAGAGCCCTGTCCGAGAGCTGTGTGGGCCCGGAGG--TGTTCGCTGTCCGATGATGTGGA	981
OY	900	TGAGGCTGAC 909	
Db	982	TGAGGCTGAC 991	

LOCUS BX375652 951 bp mRNA linear EST 26-APR-2004
 DEFINITION BX375652 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
 cDNA clone CS0DC015YJ24 5-PRIME, mRNA sequence.
 ACCESSION BX375652
 VERSION BX375652.2 GI:46573220
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 951)
 Li, W.-B., Gruber, C., Jesssee, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 8, 2003 this sequence version replaced gi:30448429.
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 9074.x
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdnas=CS0DC015DE120P1&c=9074.x.
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 primer. Five prime end enriched, double-strand cDNA was
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 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
 Query Match 85.1%; Score 773.6; DB 5; Length 951;
 Best Local Similarity 98.0%; Pred. No. 8.3e-160;
 Matches 833; Conservative 2; Mismatches 8; Indels 7; Gaps 5;

QY 1 ATGGCGTATCCGGGTGAGACCCCGGCGCTGCTGGAGAGAGATGAGTCTTGACTAC 60
 DB 76 ATGGCGTATCCGGGTGAGACCCCGGCGCTGCTGGAGAGAGATGAGTCTTGACTAC 135
 QY 61 TAGCGGATGCTGCTGCTTCAACCGATGATGAGGTGGGCGGCAACGAGAGTGC 120
 DB 136 TAGCGGATGCTGCTGCTTCAACCGATGATGAGGTGGGCGGCAACGAGAGTGC 195
 QY 121 GAGCTGAGAGTCTGAGCTTCTTGCTGATGAGGCTCTTGCGCGCGCGAGCTTAC 180
 DB 196 GAGCTGAGAGTCTGAGCTTCTTGCTGATGAGGCTCTTGCGCGCGCGAGCTTAC 254
 QY 181 CGGAGCGGAGAGGCTGAGAGTCTTGCTGAGAGTGGAGCGCGCGGAGTGGCGAG 240
 DB 255 CGGAGCGGAGAGGCTGAGAGTCTTGCTGAGAGTGGAGCGCGCGGAGTGGCGAG 314
 QY 241 AGCAACTGCGGCTGCTGGGCAACTCTGCGGCTGCTGGCGCGCAAGCTGCTGCG 300
 DB 315 AGCAACTGCGGCTGCTGGGCAACTCTGCGGCTGCTGGCGCGCAAGCTGCTGCG 374
 QY 301 CACCTGCGCGCAAGCGCGCGCGAGTGTCTCCAGAACGCTATAGCTATGACCTCC 360
 DB 375 CACCTGCGCGCAAGCGCGCGCGAGTGTCTCCAGAACGCTATAGCTATGACCTCC 432
 QY 361 AGCTCTTCAAGAGAGAGAGGAGTACCTGCTGCGCGCTGCGAGTCAAGAGTTTCCA 420
 DB 433 AGCTCTTCAAGAGAGAGAGGAGTACCTGCTGCGCGCTGCGAGTCAAGAGTTTCCA 492

QY 421 AATTCTCAGAGGGTACATGTTGGAGAGAGAGTCTCCCCCAACCAAGCGGACGC- 479
 DB 493 AATTCTCAGAGGGTACATGTTGGAGAGAGAGTCTCCCCCAACCAAGCGGAG 552
 QY 480 TCGGGGCGCGGCGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 539
 DB 553 TCGGGGCGCGGCGCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 612
 QY 540 GCAGAGTGCAGAGCGCGCGAGAGTCTTCTTGAAGGCAAGTACCTGTGACATCCG 599
 DB 613 GCAGAGTGCAGAGCGCGCGAGAGTCTTCTTGAAGGCAAGTACCTGTGACATCCG 672
 QY 600 CCGGAGTTCAGAGAGTACTCGAGAGTGGGCGGAGTGGAGAGGCGCTGAGCTCCG 659
 DB 673 CCGGAGTTCAGAGAGTACTCGAGAGTGGGCGGAGTGGAGAGGCGCTGAGCTCCG 732
 QY 660 GCGGCGCGGCGGCGGCGGCGGAGTGCAGTGCAGTGTGTGTGTGTGTGTGTGTGT 719
 DB 733 GCGGCGCGGCGGCGGCGGCGGAGTGCAGTGTGTGTGTGTGTGTGTGTGTGTGT 792
 QY 720 CTCAGAGGAGTCTGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 779
 DB 793 CTCAGAGGAGTCTGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 851
 QY 780 CGCTTCTGAGGAGTCTGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 839
 DB 852 CGCTTCTGAGGAGTCTGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 909
 QY 840 GACTGAGGCC 849
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RESULT 9
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 LOCUS 602637058F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4764639 5',
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 VERSION BG685173.1 GI:13916570
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 800)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNCM622 row: d column: 16
 High quality sequence stop: 794.
 Location/Qualifiers
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 /note="Organ: B-cells, Vector: pOTB7, Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAAGAG(G). Size-selected >500bp

QY 421 AATTCTCAGCAGGAGTCTAGTGGAGAGAGAGGCTCCCCCAACCAAGCGGAGCGGAGT 480
| | | | |
Db 460 AATTCTCAGCAGGAGTCTAGTGGAGAGAGAGGCTCCCCCAACCAAGCGGAGCGGAGT 518
| | | | |
QY 481 CGGGGCGGCGCCAGTGTGTGTGCCAGACGGCGCGGAGAGAGGCGCCAGCGGCA -CCCCA 539
| | | | |
Db 519 CGGGGCGGCG -CGAGTGTGTGTGCCAGACGGCGCGGAGAGAGGCGCCAGCGGCA 577
| | | | |
QY 540 GCAGCACTCAGAGCGCGCCAGACCTTCTCTGAAAGGCAAGTGAACCTGTGACATCCGAGT 599
| | | | |
Db 578 GCAGCACTCAGAGCGCGCCAGACCTTCTCTGAAAGGCAAGTGAACCTGTGACATCCGAGT 637
| | | | |
QY 600 CGGGGCTTCAGACAGTACTGCGAGCA -TGGGCGAGCGCTTCGAGCAGGAGCGT -GGCAATCC 657
| | | | |
Db 638 CGGGGCTTCAGACAGTACTGCGAGCAATTTGGGCGAGCGCTTCGAGCAGGAGCGTGGGCAATCC 697
| | | | |
QY 658 CGGGGCGGCGCGGCGCTGCGCGCGGAGCTGTGTTGGGCGAGGCGCACCGCAGTCTGTG 717
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Db 698 CGGGGCGGCGCGGCGCTGCGCGCGGAGCTGTGTTGGGCGAGGCGCACCGCAGTCTGTG 757
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QY 718 CGCTCAAGGAGACCTGCGCTCTGTGTGTGTGACATCAAGTTCTCAGAGCTTCTCTATCTG 777
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Db 758 CGCTCAAGGAGACCTGCGCTCTGTGTGTGTGACATCAAGTTCTCAGAGCTTCTCTATCTG 817
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Db 818 GAGCGCTTCTGCGGCGACTA 837
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RESULT 11
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LOCUS AGENCOURT_6649774 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5764272
DEFINITION
BM925969
BM925969.1 GI:19376336
EST.
Homo sapiens (human)

ORGANISM
Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabds-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LIML at:
http://image.llnl.gov
Plate: LIML2817 row: h column: 01
High quality sequence start: 14
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Location/Qualifiers

FEATURES
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1.1089

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Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
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primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber

ORIGIN
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."

Query Match 80.0%; Score 727.4; DB 5; Length 1089;
Best Local Similarity 95.7%; Pred. No. 1.2e-149;
Matches 780; Conservative 0; Mismatches 31; Indels 4; Gaps 3;

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| | | | |
QY 61 TACGGATGCTGTGCTTCAACCGATGTTGAGGTGTGGGCGGCAACTGACCGATGTC 120
| | | | |
Db 131 TACGGATGCTGTGCTTCAACCGATGTTGAGGTGTGGGCGGCAACTGACCGATGTC 190
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QY 121 GAGGTGAGTCTCTGCGCTTTCTGTGATGATGAGCTCTTGCGCGCGGAGCTTAACC 180
| | | | |
Db 191 GAGGTGAGTCTCTGCGCTTTCTGTGATGATGAGCTCTTGCGCGCGGAGCTTAACC 250
| | | | |
QY 181 CGGGCGGCGAGCGGCGCTGAGCTTCGTGAGTGGAGGCGCGGCGGAGTGGGCGAG 240
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Db 191 GAGGTGAGTCTCTGCGCTTTCTGTGATGATGAGCTCTTGCGCGCGGAGCTTAACC 250
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QY 251 CGGGCGGCGAGCGGCGCTGAGCTTCGTGAGTGGAGGCGCGGCGGAGTGGGCGAG 310
| | | | |
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| | | | |
QY 311 AGCAACCTGCGGCTGTGAGGCGCAACTCTGCGGCTGAGCGCGGCGCAAGCTGCTCCG 370
| | | | |
Db 301 CACCTGCGGCGGCGAGCGGCGCGGCGAGTGTCTTCAGAACGCTTAATGCACTTCC 360
| | | | |
QY 371 CACCTGCGGCGGCGAGCGGCGCGGCGAGTGTCTTCAGAACGCTTAATGCACTTCC 430
| | | | |
Db 361 AGCTCTTCAAGAGGAGAGAGGAGTGTGCTGCGCGGCGGAGTGAAGAGTTCGCA 420
| | | | |
QY 431 AGCTCTTCAAGAGGAGAGAGTGTGCTGCGCGGCGGAGTGAAGAGTTCGCA 490
| | | | |
Db 421 AATTCTCAGCAGGAGTCTAGTGGAGAGAGGCTCCCGCCCAACCAAGCGGAGCGGAGT 480
| | | | |
QY 491 AATTCTCAGCAGGAGTCTAGTGGAGAGAGGCTCCCGCCCAACCAAGCGGAGCGGAGT 550
| | | | |
Db 481 CGGGGCGGCGCGGAGTGTGTGCCAGCGGCGGAGAGAGGCGGCGGAGCGGCGAG 540
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QY 551 CGGGGCGGCGCGGAGTGTGTGCCAGCGGCGGAGAGAGGCGGCGGAGCGGCGAG 610
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Db 541 CAGAGATCAAGAGCGGCGGAGTGTGTGCCAGCGGCGGAGAGAGGCGGCGGAGCGG 600
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QY 611 CAGAGATCAAGAGCGGCGGAGTGTGTGCCAGCGGCGGAGAGAGGCGGCGGAGCGG 670
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Db 601 CGGGTTCAGCAGAGTACTGCGAGCATGGGCGGAGCTTGGAGAGAGGCGGCGGAGTCCCGG 660
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QY 671 CGGGTTCAGCAGAGTACTGCGAGCATGGGCGGAGCTTGGAGAGAGGCGGCGGAGTCCCGG 730
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Db 731 GGGGCGGCGGCGGAGTGTGTGCCAGCGGCGGAGAGTGTGGGCGAGGCGCAAGCGGCTGCG 790
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QY 719 GCTTAAGAGAGCTGGGCT--CTGTGTGTGTGACATCAAGTTCACAGCTCTCTATCT 776
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Db 791 GCTTAAGAGAGCTGGGCTCTGTGTGTGTGACATCAAGTTCACAGCTCTCTCAATT 850
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QY 777 GAGCGCTTCTGCGGCGACTACTGAGTGGCGGCGC 811
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Db 851 GAGCGCTTCTGCGGCGACTACTGAGTGGCGGCGC 885
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RESULT 12
BP158001 820 bp mRNA linear EST 30-DEC-2003
LOCUS BP158001 full-length enriched swine cDNA library, adult spleen sus
DEFINITION scrofa cDNA clone SP1010019D12 5', mRNA sequence.
ACCESSION BP158001
BP158001.1 GI:40407474
KEYWORDS EST.

SOURCE	ORGANISM	REFERENCE	TITLE	JOURNAL	COMMENT
Sus scrofa (pig)	Sus scrofa	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.	1 (bases 1 to 820)		
Uenishi, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H., Okumura, N., Hamaeima, N. and Anata, T.			PERE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries	Nucleic Acids Res. 32 (1), D484-D488 (2004)	Contact: Hirohide Uenishi

Email: huenhshia@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and SRAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
library
Vector sequences were eliminated by Repetasker version 2002/07/13
and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.
Translation/Peptide confirmed

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FEATURES
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    Location/Qualifiers
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        /mol_type="mRNA"
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        /clone_lib="full-length enriched swine cDNA library, adult
spleen"

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Query Match	78.2%	Score 711.2	DB 5	Length 820
Best Local Similarity	92.6%	Pred. No.4.5e-146		
Matches 759	Conservative 0	Mismatches 58	Indels 3	Gaps 1
QY	44	ATGAGTGCCTGAGACTACTACGGAGATGCTGTGCTTCAACCGATATGTCAGGTGGGCG	103	
Db	1	ATGAGTGCCTGAGACTACTACCGGATGCTGTGCTTCAACCGATATGTCAGGTGGTGGCG	60	
QY	104	GGCAACTGACCGAGTGCAGCTGAGACTCTTGCCCTTTCCTGAGATGAGCTCCTGCG	163	
Db	61	GGCAACTGACTGAGTGCAGCTGAGACTGTAGCTTCTCTGAGACAGAGTCCAGGCG	120	
QY	164	CCGCGGAGAGCTTATGCCCCGGGCCCGGACGGGCTTAGAGCTCTGTGAGCTGAGAGCC	223	
Db	121	CCGCGGCGGCTTAGCCCGCCGCGCAGCGGCTGAGACTCTGTCTGAGCTGAGAGCC	180	
QY	224	GCGGCGAGTGGCGGAGAGCAACTGCGGCTGTGAGGCAACTCTCTGCGGTGCTGGGCC	283	
Db	181	GCGGCGAGTGGCGAGAGCAACTGCGGCTGTGAGGCAACTCTCTGCGGTGCTGGGCC	240	
QY	284	GCCAGCACTGCTGCCGCACTTGCGCGCAAGCGCGCCGACAGTCTTCCAGAACGCT	343	
Db	241	GCCAGCACTTGTCTCCGCACTTGCGCGCAAGCGCGCCGACAGTCTTCCAGAACGCT	300	
QY	344	ATGACTTAGGCACCTCCAGCTCT--TCAAAGAGACAGAGGATGCTGCCGTC	400	
Db	301	ACAGCTTAGGCACATCCAGCTCTTCTCAGAGAGAACTGAGAGAGCTGCGGCGCTC	360	
QY	401	GGCAGTGAAGAGTTTCGCAATTCCTCAGCAGGATCACTGGGAGACAGGCTCCCCCAA	460	
Db	361	GGCAGTGAAGCCGTTCTTCAATTCCTCAGCAGGATCACTGGGAGACAGGTTCCCTCCAG	420	
QY	461	CCAAGCGGAGCGGAGTGGGAGCGGCGCCCACTGGTGTGCCAGACGAGGCGAGAG	520	
Db	421	CCAAGCGGAGCGGAGTGTGGCGGCTCCCAATGGTGTGCCAGAGAGGCGGAGAG	480	

OY	521	GGGGCCCCAGCCGACCCCGAGCAGAGTCAAGACC	CGGCAGACCTTCTCTGAAGGCAAG	580
Db	481	GGGGCCCCAGCCGACCCCGAGCAGAGCCAGGCC	AGCCAGGCCACTTCAGAGGCAAG	540
OY	581	TGACCTGTGACATCCGGCTCCGGGTTCCAGCAG	AGTACTGCAGCAGTGGCCAGCCTTGG	640
Db	541	TGACCTGTGATATCCGGCTCAGGGGTCCAGCAG	AGTACTGTGAGCATGGGCCAGCCTTGG	600
OY	641	AGCAGGGCGTGGCATCCCGCGGGCCCCAGCGC	CTGGCCGCGACGTGTGTTGGGC	700
Db	601	AGCAGGGCGTGGCATCCCGCGGGCCCCAGCGC	ACTGGCCCGCAGCTGATGTGTTGGGC	660
OY	701	AGGCGACCGGAGTGTGCGCTCAAGGGGACTGG	GGCTGTGTGTTTGTGACATCAAGTCT	760
Db	661	AGGCGTACAGCAGTGTGCGCTCAGAGGGACTGG	GGCTGTGTGTAATCAAGTCT	720
OY	761	CAGAGCTCTCTTACTGTGGACGCTTCTGGGGG	CGACTACCTTAGTGTGACCCTGTGCAGG	820
Db	721	CAGAGCTCTCTTACTGTGGACGCTTCTGGGGG	TACTTAGTGTGGGACCTTGTCTGCAGG	780
OY	821	CCCTGCGGGGCGTGTCTGTACTGACTGAGGC	CCCTGCAGAGGC	860
Db	781	CCCTGCGGGGCGTGTCTGTACTGACTGAGAGC	820	

RESULT	13
LOCUS	BM920838
DEFINITION	BM920838 1090 bp mRNA linear EST 12-MAR-2002 AGNCOCURT 6706034 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5752092
ACCESSION	BM920838
VERSION	BM920838
KEYWORDS	EST. GI:19371217
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 1090)	NIH-MGC	http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D. Email: cgaabs-remail.nih.gov			
	Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)			
	DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov			
	Plate: LLM12785 row: 1 column: 13			
	High quality sequence, stop: 625.			

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FEATURES
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/clone="IMAGE:5752092"
/lab_host="DH10B"
/clone_1ib="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-Sport6; Site 1: NotI; site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age 23-27; 1
male lung, age 27; and 1 male testis, age 65. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
ORIGIN
Query Match 77.5%; Score 704.2; DB 5; Length 1090;

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Best Local Similarity 95.5%; Pred. No. 1.6e-144;
Matches 780; Conservative 0; Mismatches 28; Indels 9; Gaps 5;

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Db 102 ATGGCGCTATCCGGGTGACCCCGGCGCTGGGGAGAGATGATGCTGAGACTAC 161
OY 61 TACGGAGATGCTGTGCTTCAACGATATGTCAGAGTGTGGGCACTGACCGAGTGC 120
Db 162 TACGGAGATGCTGTGCTTCAACGATATGTCAGAGTGTGGGCACTGACCGAGTGC 221
OY 121 GAGCTGAGAGCTTCTGGGCTTTTCTGCTGATGAGGCTCTGGGCGCCGAGGCTTAC 180
Db 222 GAGCTGAGAGCTTCTGGGCTTTTCTGCTGATGAGGCTCTGGGCGCCGAGGCTTAC 281
OY 181 CGGGCCCGCAGCGGCTGAGCTCCTGCTGAGCTGAGCGCCGCGGCACTGGCGGAG 240
Db 282 CGGGCCCGCAGCGGCTGAGCTCCTGCTGAGCTGAGCGCCGCGGCACTGGCGAG 341
OY 241 AGCAACCTGCGGCTGTGGGGCAACTCTGCGCGCTGTGGCGCCGCAAGCTGTGCG 300
Db 342 AGCAACCTGCGGCTGTGGGGCAACTCTGCGCGCTGTGGCGCCGCAAGCTGTGCG 401
OY 301 CACCTGGCGGCAAGCGCGCGCGCACTGTCTCCAGAACCTATAGCTATGCACTTC 360
Db 402 CACCTGGCGGCAAGCGCGCGCGCACTGTCTCCAGAACCTATAGCTATGCACTTC 461
OY 361 AGCTCTTCAAGAGAGACAGAGGTAGCTGCGCGCTGCGGAGTCAAGAGATTGCA 420
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OY 421 AATTCTGAGAGGTTCAGTGGAGACAGAGCTCCCCCAACCAAGCGGCAAGCGGAGT 480
Db 522 AATTCTGAGAGGTTCAGTGGAGACAGAGCTCCCCCAACCAAGCGGCAAGCGGAGT 581
OY 481 CGGGCGCGGCGCACTGTGTGCTGCAAGCGCGCGGAGAGGGGCCCAAGCCGAC 540
Db 582 CGGGCGCGGCGCACTGTGTGCTGCAAGCGCGCGGAGAGGGGCCCAAGCCGAC 641
OY 541 CAGAGTCAGAGCCCGGCACTTCCCTGTAAGGCAAGTGAACCTGTAATCCGAGTC 600
Db 642 CAGAGTCAGAGCCCGGCACTTCCCTGTAAGGCAAGTGAACCTGTAATCCGAGTC 701
OY 601 CGGGTTGAGAGAGTACTGCGAGCATGGGCAAGCTTGTGAGCAGAGGCGTGGATCC 660
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OY 661 CGGCTCCAGAGCGCTGGCGGCAAGCTGATGTTT--GGGCAAGGCCAGCGAGTGTG- 717
Db 762 CGGCTCCAGAGCGCTGGCGGCAAGCTGATGTTTGGGCAAGGCCAGCGAGTGTG- 821
OY 718 CGGTCAGAGGAGCTGGGCG--TCTGTGCTTGTGACAT--CAAGTCTGACAG---CTGTC 771
Db 822 CGGTCAGAGGAGCTGGGCGCTTGTGGGGTGTGAACTTCAAAAGTTCTCAGAGCTCTCCT 881
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Db 882 ATCTTGAGAGCGCTTTGGGGGGGCACTTACTTGAG 918
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RESULT 14
B1523561 872 bp mRNA linear EST 29-AUG-2001
LOCUS B1523561
DEFINITION 60317585.F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240077 5',
mRNA sequence.
ACCESSION B1523561
VERSION B1523561.1 GI:15348353
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 872)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.lnl.gov>
Plate: L16M1605 row: f column: 14
High quality sequence start: 28
High quality sequence stop: 805.
Location/Qualifiers

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/clone_lib="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."

ORIGIN

Query Match 74.9%; Score 680.8; DB 4; Length 872;
Best Local Similarity 98.8%; Pred. No. 2.2e-139;
Matches 759; Conservative 0; Mismatches 2; Indels 7; Gaps 7;

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Db 108 ATGGCGCTATCCGGGTGACCCCGGCGCTGGGGAGAGATGATGCTGAGACTAC 167
OY 61 TACGGAGATGCTGTGCTTCAACGATATGTCAGAGTGTGGGCACTGACCGAGTGC 120
Db 168 TACGGAGATGCTGTGCTTCAACGATATGTCAGAGTGTGGGCACTGACCGAGTGC 227
OY 121 GAGCTGAGAGCTTCTGGGCTTTTCTGCTGATGAGGCTCTGGCGCCGAGGCTTAC 180
Db 228 GAGCTGAGAGCTTCTGGGCTTTTCTGCTGATGAGGCTCTGGCGCCGAGGCTTAC 287
OY 181 CGGGCCCGCAGCGGCTGAGCTCCTCTCTGAGAGTGGAGCGCGGCGAGTGGCGAG 240
Db 288 CGGGCCCGCAGCGGCTGAGCTCCTCTCTGAGAGTGGAGCGCGGCGAGTGGCGAG 347
OY 241 AGCAACCTGCGGCTGTGGGGCAACTCTGCGCGCTGTGGCGCCGCAAGCTGTGCG 300
Db 348 AGCAACCTGCGGCTGTGGGGCAACTCTGCGCGCTGTGGCGCCGCAAGCTGTGCG 407
OY 300 GCACTTGGG--CGGCAAGCGGCGCGGCACTGTCTCAGAAAGCTATAGCTATG- 357
Db 408 GCACTTGGGCGGCAAGCGGCGCGGCACTGTCTCAGAAAGCTATAGCTATGCAAC 467
OY 358 TCCAGCTCTTCAAGAGAGACAGAGGTAGTGTGCGCGCTGTGGCAGTCAAGAGTTC 417
Db 468 TCCAGCTCTTCAAGAGAGACAGAGGTAGTGTGCGCGCTGTGGCAGTCAAGAGTTC 527
OY 418 GCAAAATTCTGAGAGGATCAGTGGAGACAGAGCTCCCCC--AACCAAGCGGAGCGGCG 476
Db 528 GCAAAATTCTGAGAGGATCAGTGGAGACAGAGCTCCCCC--AACCAAGCGGAGCGGCG 587
OY 477 GAGTGGGCGCGGCGCAAGTGTGTGTCAGACGCGCGGAGAGAGGGGCCCAAGCGGAGC 536
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